

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
12396	42764	A	12471	3771	4703	SFQFFCSVFSPSLWVFYLLLWFDD GDVQMRFRCCCPFCLLWFLLTD RTLSCRSVGIPCRVRCQCA  LG GASQLGCSGVKGSRDPLEEAV CPFSSDL QLRAGGNTALFKAVR QGHLSLQRLLSFVCLCPAPRG GAYRGQQASLSCGGHLHPV*AS  RLLCLPKQAWAMAGAPPASL LAPCILJSDCCASNQRDGSVGVP S/ERPGVGYSLLVVRRLFSRER NIRGGIVTRFSRCPSPSLTRK GNSLTPCASQSEGNAICPAFGF AHGARTHWALRPTVWHSLCE MNPVQMEMQKSPVFCVAHA GGCRPEL
12397	42765	A	12472	1	1038	
12398	42766	A	12473	27	428	LADRSAIPGFAIFAVTFLLALVG AVLYLYPWTLLKPC*SHY*GIN LVVAV*VKTT*GKNCMKMV*L IL*RVTLPS*RFGLRLEKAF*M GHLIKT*LGKNNMKMPCSNWS LF*GTS*KNEKEGTSVNIFSLTP
12399	42767	A	12474	107	362	NKPCEEFYFLAALIYLHGRK KADTKIPP*ISRFFLYLPSHELTI FIVIHIMCDLGCTWAICFLTTSE EVQKKLYEEINQVFG
12400	42768	A	12475	193	637	TSSEVVKKQIAQVHNFAVIMQL ARENILSS/EDLLVIKVPLY*GV NENMLTEVPSFSFFYDVP*NRL QLHEGIFILFFPSHVFIK*PI*KAF SNLRPNCAMILLEANDFLIIFKC TTHYHLCNRHISKTKHMLAEG HVLGLWVGEPFI
12401	42769	A	12476	1	1930	
12402	42770	A	12477	1	362	
12403	42771	A	12478	58	160	GVSLQSTSEEGRGMRQE*TERE IKVTCRSHYRLA
12404	42772	A	12479	3	410	
12405	42773	A	12480	1	807	
12406	42774	A	12481	154	375	
12407	42775	A	12482	2	512	
12408	42776	C	12483	29	455	
12409	42777	A	12484	209	433	
12410	42778	A	12485	11	1546	
12411	42779	A	12486	3	931	
12412	42780	A	12487	1	363	
12413	42781	A	12488	1	351	
12414	42782	B	12489	82	263	
12415	42783	A	12490	1	1878	
12416	42784	A	12491	24	242	
12417	42785	A	12492	1	3558	

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12418	42786	A	12493	2	478	HNSLKS DENKENS FSA DHV ITA VEKS KES QVT ADD LEE KAKA ELIM DDD RTV DPL LSK SQS ILIS TSAT A SSK KTI ED RNI K NK K STN NRASSA SAR LMT SEFL K K SSK RRTPS TTT SSS HYL GTI KVL DQK PFT ETEA*EP DRAD NI RG SCL FR
12419	42787	A	12494	1	1047	
12420	42788	A	12495	1	1055	
12421	42789	A	12496	212	611	
12422	42790	A	12497	2	195	YVMGRNDGGYLMIDSKTAEIK FVKNMNRDSTIVNKTTAEV L AID RYSGKNCNLLISWSYICG
12423	42791	A	12498	1	429	
12424	42792	A	12499	1	503	
12425	42793	A	12500	3	825	GTT KWQ T VRR QK REWI K FAAA CREG ED NSK RNPI A K *SDL QNS LLP ALY *K H I RSD C E S N Q K I T Y RIS GV GIDR P P YGV F T I N P R T G E I NITS VV DRE I T P L FLY I C R A L N S R G E D I L E R P L E L R V K V M D I N D N A P V F S Q S V Y T A S I E E N S D A N T L V V K L C A T D A E E N H L N S K I A Y K I V S Q E P S G A P M F I L N R Y T G E V C T M S S F L D R E Q H S M Y N L V V R G S D R D G A A D G L S S E C D C R I K V L D V N D N F P T / F R E N F K Q N S S R F S N S L L S S F D Q W R K L
12426	42794	A	12501	986	4030	K Q R L T W T F S P G K S E T M M G L F P R T T G A L A I F V V V V I L V H G E L R I E T K G Q Y D E E E M T M Q A K R R Q K R E W V K F A K P C R E G E D N S K R N P I A K I T S D Y Q A T Q K I T Y R I S G V G I D Q P P F G I F V D K N T G D I N I T A I V D R E E T P S F L I T C R A L N A Q G L D V E K P L I L T V K I L D I N D N P P V F S Q Q I F M G E I E E N S A S N S L V M I L N A T D A D E P N H L N S K I A F K I V S Q E P A G T P M F I L S R N T G E V R T L T N S L D R E Q A S S Y R L V V S G A
12427	42795	B	12502	1	3572	
12428	42796	A	12503	1	594	
12429	42797	A	12504	1	612	
12430	42798	B	12505	200	532	
12431	42799	A	12506	2	735	
12432	42800	A	12507	5	400	

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12433	42801	A	12508	2	1260	GQAASPAASPASPAMAWAA LLGLLVALLLLLLLSSRRRTRRP GEPLLDLGSIPWLGYALDFGKD AASFLLTRMKEKHGDIITLVGG RYVTVLLDPHSYDAVVWEPR RLDFHAYAIFLMERIFDVQLPH YSPSDEKARMKLTLLHREIQLAL TEAMYTNLHAVLLGDATEAGS GWHEMGLLDF/CLQLPAQSRLP DSLRLN*GAATHP*KPGPGPRLPS *CLPHLSPARPAAPQTGPWLVP SGGQGPHVQCQKSPVEAIPSQ AGQAGPPEQMAGELPAAPGGD GCVRGDAGTGPGAAAVGHTGE YGSRCLLAPALPSQES*SPGCCP RRAREYPLASGAACLAADDHSP EGSRQHTC/DLIAC*VRASGLQL PPSSPRL\GGPGHAAHGRERI PATW*PPPLPLPEPPERPRNLH RPRGI
12434	42802	A	12509	3	466	
12435	42803	A	12510	1	1134	
12436	42804	A	12511	2	1211	
12437	42805	A	12512	2	405	HEMLLASEIKHLPRLLIGQERE TQTSELKIKRGNGNEEAPS/PPPS AYERGTKR/DDRYDTPTSKKK VRJKDRNKLSTEERRKLFEQEV AQREAQKQQQMQNIGMTSP LPYDSLGYNAPHHPFAGYPPGY PMQA
12438	42806	A	12513	191	898	
12439	42807	A	12514	1	270	
12440	42808	A	12515	2	1328	
12441	42809	A	12516	1	2868	
12442	42810	A	12517	1	1254	
12443	42811	A	12518	1	576	

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12444	42812	A	12519	1919	3044	HQGPSTPPSWAMSGPPTPLSRE DWHQGPSTPPSWAMSEPP/SSI QGLASGAVHTILLGDVRATYTS IQGVTSGVSVQSVRAAQMAVPSS RILQLSKPKAPATLLEWDPVP KPKPHVSDHNRLLHLAKVPRK EGSGKKVGAFFPEIKGPEAFRDK ARAMESQSNDMPFDELLALYG YEASDPISDRESEGGDVPDNL DMTLKEQIAKDLLSGEEEEET QSSADDLTPSVTSHEASDLPN RSGCLLAGEAESSRGLLPRAQP VPRGAGLADNSRGALLRAHGT VRVGTATTVKPADATPPESPRDR RSRNDSHRPTGPSESERQPQSN QPTLLLRGHGTIRVRTTATVKP ADAPAEPRDRRSRNDSHGQSS
12445	42813	A	12520	413	1412	
12446	42814	A	12521	293	412	NHLSVAGNGSSPCGL*AGALGL LLWLASSGHRLVSGMI
12447	42815	A	12522	2	181	
12448	42816	A	12523	1	277	
12449	42817	A	12524	1	739	
12450	42818	A	12525	1	326	
12451	42819	A	12526	3	566	
12452	42820	A	12527	1	465	
12453	42821	A	12528	1	1167	
12454	42822	A	12529	260	395	EVATATPTLSNHYPDQSAAIN/D QG*PLHQQKDHLQKAQMNSI F
12455	42823	A	12530	209	958	FRCVLISFWSHKLHLWYHEGRI VPSDRIVPPPHGIVVSSHGVALPQR ILMRQFTLLEGLNLKDGRFLIQLS GTAPWSSYFNSVAKFGVIHRH SFFLSHNGHKAVAPL DLLS NVG GSCLCGDASSFVTPSRITMTSK SWLARSVAEMS YR/WTALVN VADDQRGHQKNVIALDWV NVQLVNRNHLPPRCSFCFLDHD AHRGTTNDHAFPQVTHSEHEAQ LAISDGNHSMAAENQSFCPVS LSCFHENAA
12456	42824	A	12531	1	1965	
12457	42825	C	12532	520	684	

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12458	42826	A	12533	701	1307	GRHLTTNHTAAVVVFPRPLCS SFFRYSGFRGVAGATASGRGQG PAG*DNCQRAWRGAFYKFQAT LSAGAGTRAEEGSDGDGEAAE PGAGTAREPARLRGYRSRRFVL DGRRCCLCYFKKNPHDPLPLGHIL DIAEACFSYQRADEAAEQPAHF QVRSAGAATVLEVGTRALRGV HLLRAHRGIWQAQWSPVSFLQ AVLPAWLL
12459	42827	A	12534	1	1356	
12460	42828	B	12535	1	1449	
12461	42829	A	12536	3	2449	
12462	42830	A	12537	1	3327	
12463	42831	A	12538	1	1359	
12464	42832	A	12539	1	672	
12465	42833	A	12540	1	1281	
12466	42834	A	12541	1	399	
12467	42835	A	12542	1	399	
12468	42836	A	12543	171	426	PVSCATGEEEDNVLFPGDDLP R**PGKLWCEFHASSISQLGQ HPRRSVLDTDQSHVPLVRRKTT CFSQRAMISPDDPSQEAGALS RNNLLAPYSALTFMENGNCLL QLFQLGKLLVQASHLHGQLLV FVQKIIISM
12469	42837	A	12544	1	988	
12470	42838	A	12545	3	129	LFHPCQDSQQHH*CVCCRLTGH GAA*VHGPCQAVQTYRASH
12471	42839	C	12546	532	1101	
12472	42840	A	12547	197	355	
12473	42841	A	12548	1	1275	
12474	42842	A	12549	3	131	

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12475	42843	A	12550	1746	3504	ESDPSNNTSMDRTLL/MSSIVP RLPSACRILPTGFTIPE*SCVHRT ASLIPPLPPGSRKYSPPPLNLSI FLKN/SAYTAVPALQTDWATSP ISLHLRTSFNSPHLYPPPEELIYFL DRSSKTSPTDISHQQAAALLRTY LKNLSPYINSTTPPIFGPLTTQTTI PVAAPLICISWQRPTGIPGLGNLSP SRCSTLHLRSPTTNINETIGAF QLHITDKPSINTDKLNKNISSNYC LGRHLPCISLHPWLSSPCSSDSP PRPSSCLLIPSPENNSERLLVDT RRFLIHHENRTFPSTQLPHQSP1. QPLTAALAGSLGVVVWVQDTPF STPSHLFTLHLQFCLAQGLFFLC GSSTYMCPLANWTGTCITLVFL TPKIQFANGTEELPVPLMPTQ QKRVIPLIPLMVGLGLSASTVA LGTGIAG1STSVMTFRSLSDNS ASITDISQLSVLQAQVDLAA VVLQGQLRGLDLLTAEKGLCI FLNEECCFYLNQSGLVYDNNIKK LKDRAQKLANQASNYAESPWA LSNWMSWVLPIVSPLIFLLL FGPCIFRLVSQFIQNRIQAITNHS IRQMFLLTSPQYHPLPQDLPSC
12476	42844	A	12551	2	394	
12477	42845	A	12552	1	882	
12478	42846	A	12553	45	409	
12479	42847	A	12554	1	1035	
12480	42848	A	12555	118	312	
12481	42849	A	12556	1	1083	
12482	42850	B	12557	1	1122	
12483	42851	A	12558	97	439	
12484	42852	A	12559	1	450	
12485	42853	A	12560	1	471	

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12486	42854	A	12561	2	1407	WGKRNRAEKLETLKSRVPLLLQ RNAVPHQQWNKAGRRTMLTS* EKKASDD/PNYSKLQEEIQTKG KEVKHFEKNLDECITRITNREK CLKELMELKAKARELREECRSL RSQCDQLEERVSVMEEIQTITIRE YYKHLYENKLQNLEEMDKFLD TYTLRRLNQEEVESLNRPITGSE IVAIINSPTKSPGPDGFTAKF YQRYKEELIPFLLKLFQSIEKEGI LPNSFYEAISIILIPKQGRDTKK ENFRPFIPLMNINAKILNKILANR QQHIKKLIHHHDQVGFIQGMQG WFNICKSRNVIIHHINRTKDKNH MIIISIDAEKAFDKIQQPFMLKTL NKLGIDETYLKIIRAIYDKPTAN IIILNGQKLEAFPLKTGTRQGCPL SPPLLNFIVLEVLRALARQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVISAQNLFELISNFSKVSGY KINVQISQAFLYTNYRQSAKS
12487	42855	A	12562	1	846	
12488	42856	A	12563	1	1281	
12489	42857	B	12564	1	274	
12490	42858	B	12565	1	2265	
12491	42859	A	12566	1	2742	
12492	42860	A	12567	1	1272	

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12493	42861	A	12568	222	2130	RKKKKKK*TKPPRNMGLRETKSMSDWCT*K*RGEW/NQV/AKTLCRILSRRTY/PNLARQADIQIQEIQRTPQRYSSRRATPKHIVRFTKVEVKEMKMLRAAREKGRTVHKGKPIRLTADLSAETLQARREWGQJFNI.I.KEKNFQPRISYPAKL SFISEGEIKPFTDKQML.RDFVTTRPALKELLKEVLNMRERNRKKLNRPITGSEIIVAIINSPLTKKSPGPDGFTAEFYQRYKEELVPFLLKLFQSKKEGEIHPNSFDEASIIJIPKAGRDTTCKDNFRPISLMNIDA KILNKILANQIQQHIIKLIJHDQVGFIGPMQGWPNICQSIINVQHINRTKDKNHWIISIDAEEKAFDKIQQRFLMLKTLNKLGLIDRMYLKIIRAIYDKPTANIIJNGQKLEAFPLKMGTRQGCPLSPPLLNFIVLEVLA RAIHQKEIJKHQLGKKEVILSFADDMIVYLENSIVSAQNLNLKJISNFSKVSGYKINVQKSHAFLHTNNRQTESQIMSELPTTIAKRJKYLGQLTQDVKDLFKENYKPLLNEIKEDTKWKHIPCWSVGRINIVKMAILPKVIYRFNAPIKLPMTFFTELEKTTLKFIWQNKRATHAKSILSQKNKAGGITLPDFQLYCKATVTKTAWY
12494	42862	A	12569	1	474	
12495	42863	A	12570	1	1197	
12496	42864	A	12571	1	1518	
12497	42865	A	12572	1	3189	
12498	42866	A	12573	1	2199	
12499	42867	A	12574	3	2820	ENKDTTYQNL\WDAFKAVCRGKFIALNAHKRKQERSKIDTLTSQLKELEKQEQTHSKASRRQEITKIRAELEKEIETQKSLQKINESRSWFFERINNIDRPLARLJIKKKREKNQIDTIKNDKGDIITDDPTEIQTTRYYKHLYANKLKNLEEMDKFLDTYTLPLRNQEEVESLRNPITGSEIVTIINSPLTKKSPGPDGFTAEFYQRYKEELVPFLLKLFQSIKEGILPNSFYEASIIJIPKPGRDTTKKENFR
12500	42868	B	12575	1	1593	

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12501	42869	A	12576	1	3549	MGDFNTPLSTLDRSRRQKVNDTQEELNSALHQVLDIYRTLHKSTEYTFPSAPHYTSKIDHVGSKALLSKCKRTEIITNYLSDHSAIKLELRKLNLTQRNSTTWKLNNLLNDYWIHNKMKAEIKMFFETNKNKDITTYQNLWDAFKAVCRGKFIALNAHKRKQERSKIDLTSQLKELEKQEQTSHSKASRQEVTKIRAELEKEIETQKTLQKINESRSWFFERINKIDRMLARLIKKREKNQIDTIKNDK
12502	42870	A	12577	1	2724	
12503	42871	A	12578	1	3567	
12504	42872	B	12579	709	2064	
12505	42873	A	12580	1	3370	
12506	42874	A	12581	1	2024	MGFYHVGGAGTELLTSNDPLTSASQSARITGKALQKPTEVPPVYEKMLQDQSAIJVQGLPEGVAFKHPENYDLATLKWLIENTAGISFIINSATIEPPAAQPMMSFTHMGHSLCVLVVETHAKPVAQVSSFTRNPEVISLEVAAVTVKEESEDPDYDYITFKDLPGIAYTEKAYVLWPQLSKICSKNGDKNNKAYRGQQCRLRQQNPLAALTGKISVSVYVSHPSLRSVSIGWTRQVARQTMQKDRDGPLKNEGEKNCAGSEKNTLTSQLKELEKQEQTHSKASRRQEITKIRAELEKEIETQKTVKEKINESRSWFFERINKIDRPLARLIKKREKNQVDAIKNDKGDDITDPTEIQTITREYYKHYANKLENVEMDKFLDTYTLPRLNQEEVESLNRPITGSEIVAIINSPLTKKSPGPDGFTAEFYQRYKEELVPFLKLKFQSIEKEGILPNSFYEASIILIAKPGRTTCKENFRPISLNMNIDAKILNKILAKRIQQHIIKKLIIHHDQVGFIPGMQGWPNIRRSINVIQHINRAKDKKKHMIISIDAEKAFDKIQQPFMLKSLNKL/DIGKNYFKVHMGPKKSPCRQVNPKPKEQSWRHHST*LQTILQGYSNQNMSMVLVPKQRYRSMEQNTALRNNATYQLSDL*QT*EKQAMGKGFPI**
12507	42875	A	12582	722	4214	

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12508	42876	A	12583	228	1152	KNRDYNKLSLRPQCNCQTRTQN *ESHSKPLNYMETEQPAPE*LL DT*RMKAEIKMFFETENKDT TYQLNLWDAFKATASKTNKEKE KNQIDTIKNDKGDITTPTEIQT TIREYYKHLYANKLENLEEMD KFLDITYTLPRLNQEEVESLNRP TGAEIVAVAINSPLTKKSPGPDDGF TAEFYQRYKEELIGWLRESVK ICLKFDHQVQVITGRLIIRQFIAF GTVVLCQLTRHIDFVGKRLA NARFAPSLLGGAPDLFTLKPCFV AVETQGDLQPATTVVIDGCL GK PANVQVALDLDVKGFQQW
12509	42877	A	12584	1	2028	
12510	42878	A	12585	2	2264	
12511	42879	A	12586	1	2130	
12512	42880	A	12587	1	2900	MENDFDELREEGFRQSNYSEL REDIQTKGKEVENFEKNLNEECITR JTNTCKLKELMELKTKAQUELR EEWRSRLSRCDQLEERVSAME DEMNEMKGEGKFRERKIRKNE QSLQEIWWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIIVRFTKVEMKEKML RAAREKEIQTTEYYKHLYTN KLENLEEMDKFLDTYTLPNTLNQ EEVESLNRPJTGAE
12513	42881	A	12588	1	2745	
12514	42882	B	12589	1	3288	
12515	42883	A	12590	1090	2526	
12516	42884	A	12591	1	3242	
12517	42885	A	12592	3862	8976	RAKSPANIIMTGSNSHTILT LNVNGLNSPIKRHLASWIKSDQP SVCCIQETHLMCRDTHRLKIG WRK1YQANGKQKKAGVAILVS DKTDFKPTKIKRDRDEGHYMMV KGSIQQEELTILNMVYAPNTGAP RFIKQVLSLQRDLDHSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDYRTLHPKST EYTFPSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNTQSR
12518	42886	A	12593	1	1000	

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12519	42887	A	12594	1	979	MNNAKENFLGRFQDGRIGTAP VYSPQHQRRRRRVISALPTEPPL VIPRQTGFVGVLQQTPTDQLQR VLTIVRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMRNQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKTYTEVGFRQLVI TNFSELVEDVQTHHKEAKNLE KRLDEWLTRNSIENTLIDLME KTMARELRDSCSTSFSRQFDQVE ERVSVIEDQMNEMKREEKFRE KKMLEVLPRAIQEKEIKGQQL GKEEVKLSLFA DNMTVYLENPI ISPKIISL* **ATSAKSQDIKSMC KNHKHSYTPITDKQRAKS
12520	42888	A	12595	1140	2210	KPWHKNFVTHAQASIA DLIKW KKGYQ* LKIKLMK*SKKTRNTN YHQNTNISMQIN*KI*KKWRNS WTHTLSQY* TRKKLN* IDQ*Q ALKL/QAIYSLPTKNVQGQMD SQSNTRVWGILARA IRQEK E KDIQLENEEVKLSLFA DDDMT VY LENSIVSAQNL LLKRLIKYLGQL TTDV KDLF KENYKPL LN KIKED TNK W K N I P C S W I R G I N M K M A I L P K I Y R F N A P I K L P M T F T E L E K A T L K F I W N Q K R A H I A T L S K K N A G G I M L P D F K L Y Y K A T A T K A A W Y W Y Q N R D I D K K L T Q I Y K K K T N P I K K W A K D M N R H L S K E D I Y G A N R H M K C S S L V I R E K Q I K T T M R
12521	42889	A	12596	520	697	GLCSVPLLCISVLPV P V P C C F G Y C S L V V * F E V R * S D A S S F V L L A * D F L G N A V S F L V P Y E L
12522	42890	A	12597	1	1410	
12523	42891	A	12598	1	1461	
12524	42892	A	12599	77	457	QALKLRQ* LIA Y Q P K R V Q D Q M D S Q T N S A R G T K R S W Y H S F * N Y S N P T E K E G I L L N S F Y E A G I L I P K P G R D T T K K E N F R P I S L M S I N A K I L N K I L A N R I L Q H K K L I N T I K S A S S L G C K A G S T Y A N Q

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12525	42893	A	12600	1	919	MGDFNTPLSTLDRSTRQVKNK DIQELNSALHQADLIDIVRTLHP KSTEYTFSSAPHTYSKIDHLG SKALLSKCKRTEIIITNCLSDHSA IKLELRRIKLTQNCSTTJKLNN MLLNIDYWEHNKMKMAEIKMFF ETNKNKDDTYQNLWDTLKAVC RGKFKALNAHKRKERSQIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAEELKETETQKTLQRLMN PGAVLEVLRALARQEQEIKGQL GKEEVKLSLFADDMMIVYLENP MSQPKISLS**ATSAKSQDIKSIY KNHQHSYTPIRDQKQRAKSI
12526	42894	A	12601	1	1264	MDKFLDTYTLPRLNQEEVESLN RPITGSEIEIAINSLPTQKSSGP GFTAEFYQRYKEELVPFLKKLF QSIEKEGILPNSFYEAISIILPKPG RYTHKKNNFRPISLMNIDAKIL NKILANRQQHIIKKLIIHQDQVGI IPGMQSFWNIHKSINVQIHINRT DKKNHMIISIDAEEKAFDKIQQQPF MLKTLNKLLENKIPKPNPTYKGCE GPLQGELQITAQRNKGRHKQM EEHPMLMDRKNEYHKGNTHTPK VIYRFNVIPIKLPMTFFSELEKST LKFIFWNQKRARIAKTILSQKNK AGGIMLPDFKLYKKATVTKTA WYWYQNRDIDQWNRTEPESEM TPHIYNHLIFDKPDKNKQWGK DSLFLNWKWCWENWLAIGRQLKL DPFLTPYTKINSRWIKDLNVRP KTIKTLEENLGNTIQDISMGKDF MSKTPKAMATKAKMDKWDLI KLKSFTAKETTIRQSWPEMTK FTFSSNTDVKNWKHGKNNIGR HKTTSVNTCKMDSGLVLERWM EWNPFGPLSIDAKCHKDLPRDI QFDSEKGVDVFLNYSKANMR WAGSMFL*FIESF*HEWLLNFV KGKFCIY*DNHVVFVFGSVYML
12527	42895	B	12602	1	1827	
12528	42896	B	12603	13	1377	
12529	42897	A	12604	557	664	KTPLSQPKISLS**ATTAKSQDT KSVYKNQQHSYT

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
12530	42898	A	12605	77	1866	QAPKLRQ*LIAYQPKKVQDQTD SQPNSTRGTTKKSWSYHSF* NFSN/ PIEKEGIFPNLFYEA NIIILIPKPGR DTTKKENFRPISLMNVNAKILN KLLANQIQQHKKLJHHNQVGF PGMQGWFNICKSINVQHINRT KDKNHRSSISIDAFKAFNPKIQQPF MLKTLNKLDDMIVYLENPIVSA KNLLKLISNFSKVSGYKINVQK SQAFLYTNNRQAESQMSAVSF TIASKRKYLGQLQLTRDVKDLFK ENYKPVLNIKEDETDNKWKNIPS LWIGRNVNIMKMAILPKVIYRFN AIPIKLPMTTFTELEKTTLKFIW NQKRAHIAKTI LSKKNKAGGIT LPDFKLVYYKATVTKTAWHWY QNRDIDQWNRTEPSEIPIYHNH LIFDKLDKNKTLGKDYL FNKRC WENWLAICRKLKLDPFLTRYT KINSRWIKDLNIRPKTIKTEEN LGDTIQDIGMGKDFITKTPKAM ATKAKIDKWDLILKLSFCTAKE TTIRVNRQPTEWENIFAIYPSDK GLISRIYKELQIYKKKSNNP KWA KDMNRYFSKEDIYAA NR HMKKCSSLALREM QIKTTMR YHLPVRM AJIKKSGNNRCW
12531	42899	A	12606	67	243	GLCCVPLIYISVLVPVPCCFGYC SLVV*FEVR*HDASSFVLLA*D* LGDVGSLV PYEL
12532	42900	A	12607	1554	1692	
12533	42901	A	12608	640	816	GLCSVALVCISVLVPVPCCFGY CSLVV*FEVR*HDASSFVLF A*D *LGNVDSLLV PYEL
12534	42902	A	12609	1626	1739	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
12535	42903	A	12610	I	2014	MKREGSLEKKRIRKRNQLQEI CDYVKRANRLRIGGPESDGENG TKLENTLQDMQEKFPNLARQA NIQIQEIQRTPQRYSSRRAATPRHJ IVRFTK VEMKEKMLRAAREKG QVTHKGKSIRLTAADLSAETLQA RREWGPIFNILKEKNFQPRISYP GKLFSIFSEGEIKSFTDKQMLRDF VTTRPALKEELLKEALNMEKNK QYQPQPKHAKLTREARANTFK PSRRREITKIRAEKIEITPKTAQ KINESRSWFSERINKIDRPLARL RKKKREKNQIDTIKNDEGDTT HPTEIHTIIREYYKHYLYANKLEN LEEMDKFLDTYTLPRPNQEEVE SLNGPIAGSEIQAIIINSLPTKKSP GPDGFYQRYKEELVPFRLKLFQ SIEKEGILPNSFYEASIIILPKPGR DTTKKENFRPISLLNINAKILNKI LANRQQHIIKKLMHHQDQVGFP GMQGWFNIRKSIINVQHINERTK DKNHMIISIDAEKAFDKIQQPF MLKTLNKLGIIDGTYHKIRANY DKPTANIIJLNGQKLEAPPLKTGT RQGCPPLSPLLFNIVLEVALARIR QEKETEGIQLGKEEVVKLSLFAD DMIVYLENPMSPQPKISLS**ATS AKSQDTKSMCKNHKYSYTPIT DKQRAKSSVNSPFTIASKRKYL GIQLTRYVKDLFKERSMK
12536	42904	A	12611	I	700	MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLSTKKS PGD GFIAQFYQRTKDKNHHMIISIDAE KAFDKIQOHFMLKTLNKLGIIDG TYLKIIARVYDKPTASIIINGQK LEAPPLKTGTRQGCPPLSPLLFNI VLEVALARIRQEKEIKGIGQLGKE EVKLSSLFAADDMIVYLENPMSPQPKISLS**ANSAKSQDIKSMCKN LKHSYTLITDKQRAKSSVNSHS QLLORE
12537	42905	A	12613	I	1765	
12538	42906	A	12614	I	2310	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12539	42907	A	12615	1	836	MENEFDELTEVHFRRVITVNTSELKEHVLTQCCEAKNLARRNKLENLEEMDKFLATYTFPSLNQE EVESLNRPITSSEIEAAINSLPTK KHPGPDGFTAKFYQRYKEELHI NRAKDKNHNMIISDAEAKFDKI QHPVKLKILNKLGIDGTYLKII AIYDKPTANLILNGQKLEAFPL KTGTRQGCPPLNFNIVLEVLA RAIRQEKEIKGIQLGKEEVKLSL FADDURLYI*GTPLSQPKISLS** ATSAKSQDTKSMYKNHKHSYT PTTDKQRAKS
12540	42908	A	12616	355	4502	QSARFRGRRTLRRPGVGYSLVV *FEVR*CDASSFVLLA*DCLGN AGSFLVPYEL
12541	42909	A	12617	248	362	
12542	42910	A	12618	529	680	YYTRCSKWWNCSVLP*IYIYNF HLPHGKLKNTDYIKKKLHDFFF KNSKHI
12543	42911	A	12619	1	641	
12544	42912	B	12620	36	48	
12545	42913	A	12621	1	326	
12546	42914	A	12622	1	444	PGSTHASAHACERLQRTLRAF SSQRFPATASRASLSSNMAKIS SPTETERCIESLIAVFQKYAGKD GYNYTSLKTEFLSFMTNTELAAF TKNQKDPGCP*PHDGRKLGQPT VDGQLDFSEFLNLIGGQAMAC HDSFLKAVPSQKRT
12547	42915	A	12623	2	6008	
12548	42916	A	12624	530	856	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, =Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12549	42917	A	12625	1	952	MAARGTGDKVKPGCEEAGAAF ELPPSVYAAALHESHQHQCPA GGARARQRVPGGIVTEPLCTPP KDMVFLSDDGGDDDDDDND GGGDDDDNGNDNDGNDNGD DDDGDNDDDGGDNDNGDNG NDGDNDNDGGDNDNSDNGND GDGDDDGVD-DDDNGD DDDDSDDDGGDSNGYDDGD GNDDDDGGDSDDDSDNGDGD NGDGDDGGGGDNDNGHDD DGDMMMMIVMMVMMVMMVV MMVMMVMMVMMVQLRKRAEA SVSEAKCSINVSDDNDGDN DGDDDDSDGDDDDGGGGD SELTNQFPTNHSGMKASKLRK DSDHREW*W**WWWWCN*GR EQRPVFLKQSAQLMSVMM VMVMMVMMMIIVMVMMMT VVMVIVVNSPINSRLITQA
12550	42918	A	12626	3	380	
12551	42919	A	12627	5	765	RQWEVGRWSGTTIFSCFKKT YFTNPSSSSSLT VTLRREVTH/CGGAPEQRYQIIPV CVAARLPT RAQDVLD LAHSEVNA VRGP SSLLATGG GADRILH WNVVGSR LEANQT LEGAGGS ITSVDF DP VRNSAP VA WDCAL SDLHT GQG YQV LA TYN QAA QLW KVGEA QSKET L SGH KDK VTA AKFKLT RHQAV TGS RDR TV KEW DLG RA YSP KR QR PSRT GH DD GGF VE KKR GK CGE KRD QIV TV SV
12552	42920	B	12628	1	2802	
12553	42921	A	12629	458	708	QNRHRHHGPF SMVA V SSQL LD TPA ERL S LHT WKIA Q P GR GT P H F PD GA V VQA ETLP P TQ G P G R G T P H F PD GA A SS FG Y C S L VA
12554	42922	A	12630	2300	6491	EGLEALIH QERLSY WAN QV SED RPV CKAI QGK QF EGL V DTG AD V S HAL LNQ WP KN WP K Q AV T VG I G T A SE V Y Q S M E I I L H C L G P DN Q E S T V Q P M I T S I P L N L W G R D L L Q Q W G A E I T M P A L Y S P T S Q K I M T K M G Y I P G K G L G K N I P E D G I K V P E A K I N Q E R E G I G Y P F L G A V T V E P P K I P L T W K T E K P V W V N Q W P L K Q K L E A L H L L A N E Q L E K G H I E P F S P W N S P V F V I Q K S G K W H T L T D L R A V N A V

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
12555	42923	A	12631	1	434	MTVSKNKCHTKGGKGTEKK VVASFSKIVWYNVKAPAMFSR NIGKALVIGTHGTDPSVSDGFKG GLIEIPDSIGKDKEACRSIYPLH DVFVRKVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
12556	42924	A	12632	1	642	
12557	42925	A	12633	260	534	
12558	42926	A	12634	1	438	
12559	42927	C	12635	391	750	
12560	42928	A	12636	199	451	
12561	42929	A	12637	120	992	RDRIPGPVCKGKWKKNKERILIFS SRGINFRTRHLMQDLRMLMPH SKHDTNMARSNDNLSVINEGCE MNNWLRCIYFEAKKKQDLYM WLSNSPDGPSAKFLVQNIHTLA ELKMTGNCLKGSRPLLSFDPAF DELPHYALLKELLIQIIFSTPRYH PKSQPFDHVFTFTILDNRIWFR NFQIEEDAALVEIGPRFVLNLIK IFQGSFGGPTLYENPHYQSPNM HRRVIRSITAAKYREKQQVKDV QKLRKKEPKTLLPHDPAADF VTPAAEKPIEQWVWPETKVDL KASV
12562	42930	A	12638	1	342	
12563	42931	A	12639	1	580	PGWEKRMRSRSS/GVNTQEALPT AAIPTDAKVRVYYFNHITNASQ WERPIGNSSSGKGNGQGEPARV RCSHLLVKHSQSRRPSWRQEK ITRTKEE\ALELINGYI\QKIKSGE EDFE\SLASQFSDCSSAA\RGD LGFSFRGQMQKPF*RTPRFA\ RTGGDERGPGCFTD\SGIHIILPHL SEGGKPRPGLGAGQGG
12564	42932	A	12640	3	116	
12565	42933	A	12641	2	253	
12566	42934	A	12642	3	512	EDYLERKRQ/VPTECQTHSKLG GPMTLKREVKP/KVDSVPSKKG PLIQHITLLIVCHVRIFYPGSIQ/ VRWFNLNGRKKTAGVSPNLR NGDWT/FQILVMLEM/TPQQGD VYTCQVEHTSLDSPVTEWKA QSDSARSKTLGAGGFVLGLIIC GVGIFMRRSKK\FNEDLHKQG
12567	42935	A	12643	1	363	
12568	42936	B	12644	70	1229	
12569	42937	A	12645	1	430	
12570	42938	B	12646	1	1321	
12571	42939	A	12647	3	446	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12572	42940	A	12648	1	417	
12573	42941	A	12649	269	452	TILRSFGYFFRRINIMLTEEKIKS DHRKISQLIFLQKLCQTLQSENV SQGGMLYRAKA*H*T*TLVWV *HIVMSYPHKGLGLMLSCLCSVK HSTLRDVFTL
12574	42942	A	12650	83	1385	
12575	42943	A	12651	1	974	MNPLECVDRSSQPWGNPTWTS SGMRSVTFLVGFKLTFLAQT LNAAASLTGQELLAGFPGVINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLFKANNLFE SGNMRHMQVSLFALAGKVKT KRPOSGVDIGIKYSEKQEQNFS DAAMKAGQCVIGLQMGTNKC TSQLGMLTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGFLPPCLGPSQE
12576	42944	A	12652	1	1103	MNPLECVDRSSQPWGNPTWTS SGMRSVTFLVGFKLTFLAQT LNAAASLTGQELLWNFPFLLMF AWKIAPALCCGNTVVIKPAEQT PLSALYMGALIKEAGFPGVINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLFKANNLFE SGNMRHMQVSLFALAGKVKT KRPOSGVDIGIKYSEKQEQNFS DAAMKAGQCVIGLQMGTNKC TSQLGMLTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGFLPPCLGPSQE
12577	42945	A	12653	1	729	
12578	42946	A	12654	259	390	SFCSANFEVRLTAQQ*FVR*H ALSHIF*G*V*SFPKSTKRVNF
12579	42947	A	12655	68	735	
12580	42948	A	12656	1	825	
12581	42949	A	12657	3	470	
12582	42950	A	12658	1	1683	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
12583	42951	A	12659	1	1748	MNKPYIRNLSENAAPLDLEGIL KDAKIPVSGPFLVKIGYAFVDC PDEIWALKAIESTLGSKIELHGKP IEVEHSVPKRQRIRKLQIRNIPPH LQWEVLDS*LVQYGVVESQQ VNTDSETAVVNNTVYSSKDQAR QALDK/LLDKLNGFQLENFTLK VAYIPDEMATQQNPFLQPRGRR GLGQRGSSRQGSPGSVKQKPC DLPLCLLVPDQFVGAIKGEGAT IRNITKQTQSKIDVHRENAGA AEKSITILSTPEGTSAAKSILEI MRKETQDVFKTEEIPLKILAQN NFVGRIGKEGRNLKKIEQDTD TKITISPLQELMQYNPHEHTITAK GNVETCAKAEEIMKKIRER*E NDITSM/N/LQAHLLPGLNLNAL GLFPPTSGMPPPTSGPPSAMTPP SPQSEQSESETVHLFIPALSVRA LISKQQHQIKQLSFRAGASSKIA PVEAPDAKVRMVMIAGSPEAR FKAQGRIYGKIKEENFVSPKEE VKLEAHIRVPSFAAGRIVGKGG KTVNELQNFSSAEVVVPRDQTP DENDQVVVKITGHYACQVAQ RKIQEILTQVKQHQQQKALQSG
12584	42952	A	12660	3	803	
12585	42953	B	12661	1	330	
12586	42954	C	12662	127	342	
12587	42955	A	12663	324	491	
12588	42956	A	12664	1	891	
12589	42957	B	12665	1	1869	
12590	42958	A	12666	2	136	
12591	42959	A	12667	108	355	
12592	42960	A	12668	2	811	FGMRGSRGWAGEMAASGES GTSGGGGSTEEAFMTFYSEVKQ IEKRDSVLTSKNQIERLTRLPGSS YFNLPNPFEVLDQIDPEVTDEEIKK RFRQLSILVHPDKNQDDADRA\  QKAFEAVDKAYKLLLDQEQKK RALDVIQAGKEYVEHTVKERK KQLKKEGKPTIVEDDPELFKQ AVYKQTMKLFAELEIKRKERE AKEMHIERKRQREEEIEAQEKA KR/EREWQKNFEE\$RDGRVD SWRNF/QAFRRGKKEKKNRTF LRPPESKNGSNVE
12593	42961	A	12669	731	850	
12594	42962	A	12670	201	377	LMTLPCPKIPSPGSSWLIKISPIEHL MTPTPASQRTTPFDCNPLPTQI L*NGPTPISLH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12595	42963	A	12671	742	2982	KIFPPFDASFLPCLHKFNFLKGKG NSKGFKMAEKFESLMNIHGFDL GSRYMIDLKPLGCGGNGLVFS VDNDCDKRAIKKIVLTDPOQSV KHALREIKIIRRDLHDNIVKVFE ILGPSGSQLTDDVGSLTELN YIVQEYMETDLANVLEQGPLLE EHARLFMYQLLRLGKLYIHSAN VLHRLDKPANLFINTEDLVLKI GDFGLARIMDPHYSHKGHLSE GLVTWKYRSPRLLSPNNYTK AIDMWAAGCIFAEMLTGKTLF AGAHELEQMQLILESIPVVHEE DRQELLSVIPVYIRNDMTEPHK PLTQLLPGLSREALDFLEQILTFS PMDRLTAAEALSHPYMSIYSP MDEPISSHPPFHIEDEVDDILLMD ETHSHIYNWERYHDCQFSEHD WPVHNNDIDEVQLDPRALSD VTDEEEVQVDPRKYLGDREK YLEDPAFDTNYSTEPCWQYSD HHENKYCDLECSHTCNYKTRS SSYLDNLVRESEVNHYEPK LIIDLNSNWKEQSKEKSDDKGKS KCERNGLVKAQIALEEAQQLA GKEREKNQQGFDFDSTIAGTIHL SSQHEPTDVGIDKLNDLNSSVS QLELKSLISKSVSQEKQEKGMA NLAQLEALYQSSWDSQFVSGG EDCFINQFCEVRKDEQVEKEN TYTSYLDKFFSRKEDTEMLET PVEDGKLGERGHEEGFLNNSGE
12596	42964	A	12672	826	1041	WKITVKGGVFLWWAGVGDTK VLSGGAF*ARMSQEEDFHKV SSVKARTGHLHFCCGGMSSVK AGQQGPFSVLL
12597	42965	A	12673	1	1482	
12598	42966	A	12674	3	488	
12599	42967	A	12675	2	114	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
12600	42968	A	12676	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQLVQSTKRPA RAIAPHAGYTYCGSCAAHAYK QVDPSITRTRIFILGSPHIVPLSRC ALSSVDIYRTPLYDLRIDQK1YG ELWKTGMFERMSLQTDDEDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQFGKLFSKYL ADPSNLVVSDFCHWQRFR YISYYDESQGEIY*SIEHLDKMG MSIIEQLDPVFSFSNYLKKYHNTI CGRHPIGWVLLNAITELQKNGM NMSFSFLNYAQSSQCERNWQD SSVSYAAGALTvh
12601	42969	A	12677	2	114	
12602	42970	A	12678	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQLVQSTKRPA RAIAPHAGYTYCGSCAAHAYK QVDPSITRTRIFILGSPHIVPLSRC ALSSVDIYRTPLYDLRIDQK1YG ELWKTGMFERMSLQTDDEDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQFGKLFSKYL ADPSNLVVSDFCHWQRFR YISYYDESQGEIY*SIEHLDKMG MSIIEQLDPVFSFSNYLKKYHNTI CGRHPIGWVLLNAITELQKNGM NMSFSFLNYAQSSQCERNWQD SSVSYAAGALTvh
12603	42971	A	12679	1	912	
12604	42972	A	12680	1	156	
12605	42973	A	12681	112	1120	
12606	42974	A	12682	33	415	NMNKPITPSTYVRCLNVGLRK LSDFIDPQEGWKKLAVAIKKPS GDDRYNQFHIDAVPKTANTLP SKEAITVQQKQMPFCDKDRTL MTPVQNLEQSYPDPSSSPENK SLEVSDTRFHFSFYELKN
12607	42975	A	12683	3	311	
12608	42976	A	12684	1	1125	
12609	42977	A	12685	1	1365	
12610	42978	A	12686	3	141	VVSTVVVPDS/AHKLFIGGLPNYL NDDQCHGLSKGYAFCEYVDIN VTV

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
12611	42979	A	12687	1	1255	GTRSTSSLRQMKNIVHNYSEA EIKVREATSNDPWPGPSSLMSEI ADLTYNVVAFSEIMSMIWKR NDHGKWRHVVKAMTLMEYL IKTGSERVSQQCKENMYAVQT LKDFQYVDRDGKDQGVNVRE KAKQLVALLRDEDRLLREERAH ALKTKEKLAQTATASSAAVGS GPPPEAEQAWPQSSGEEELQLQ LALAMSKEEADQEEIRRGDDL R\RRWQSRRARGRLGARRSRPS WTLLTSSRQPQLP\RPQTPGGAQ HPWLLPSPRLPPRTPGAAPLSL Q\LLIPGEVQPPRPLGTPGGLP LQDPQLTLGVGPQPLQLGRGPR LIHGEVPMVGSRSGVGPQPPJPGH RPRPSQIPGEGHLPSPAPMAQQ QPGDSTRSPITSSLTLTDARHCR PPGAQQESWSCWQERCRCPEAL
12612	42980	A	12688	116	1541	
12613	42981	A	12689	3	415	
12614	42982	A	12690	1	1440	
12615	42983	C	12691	117	314	
12616	42984	A	12692	3	120	
12617	42985	A	12693	1	729	
12618	42986	A	12694	79	870	EWSSVRRSLVEKRALRRPHPC LCFRMKTILSNQTCRPPFENVD  ITLKG\RPVIV\GPAEGTLR\RD  NH\LQW\*NLSLSWKEKKRGSR VDK\W\WGNRKGNWPTV\RTYL VVHVQ\N\MIKGVLP\PLGLPVTKD EGLVVA\ FPHPTL\VIPGRNGSS LLKSRN\FLGVKNTSRRVSG\*RP GIVACSVVSSPRKDEFNPLKG DIGACFQISAGFGFQQAPHTCL KTRDIQGNFWDGYPMV\WKK GTVSARAGWNKDLKEFTWATE RKMPG
12619	42987	A	12695	2	293	
12620	42988	A	12696	1	273	TRGPWCDSVLRGCSLEQRFSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG\SLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS
12621	42989	A	12697	1	1308	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mol. wt	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ~=possible nucleotide insertion)
12622	42990	A	12698	124	1135	DKNSMGLPGVIPSCAAVLWSSILHSSSALSPTISACRHPMEDSM DMDMSPLRPQNYLFGCEKLAD KDYHKVVDNDENEHQQLSLRTV SLGAGAKDELHIVEAEMNYE GSPIKVTLATLKMVSQPTVSLG GFEITPPVVRLKCGSGPVHISG QHLVAVEEDAESDEEEEDVK\LLSISGKRSAPGGGSKVVPQKK\W KLAAD\EDDD\DDDEEDDDDEDD \DDDDF\DDEEAEEKAPVK\KSI\ RDTPAKNAQKSQNQNGKDSKPS STPRSKGQESFKKQEKTPKTPK GPSSVEDIKAQMQSIA/EKGGS LPKVEAKFINYVKNCFRMTDQ EAIQDLWQWRKSL
12623	42991	A	12699	201	416	
12624	42992	A	12700	2	678	
12625	42993	A	12701	3	2149	
12626	42994	A	12702	1	219	
12627	42995	A	12704	267	437	
12628	42996	A	12705	507	845	
12629	42997	A	12706	426	704	SRRWGGVHSCPPSPPPTAGHWT LLILCAKARRSEAAMVLASRRR RPGPRPRRRRLPVLGSRGGAG PARGRGPGSGWPGLPRAAPSP*PSSTV
12630	42998	A	12707	195	892	
12631	42999	A	12708	1	893	
12632	43000	A	12709	1	777	
12633	43001	A	12710	1	439	KTQVAPSTDGIQP\PSNSNSRTDE REFFIASYNRKKEDEGEVNWIA KSSAGAKGEGILISSEASELLDFI DNQAOQVHV\QKYLEHPLLEPG HRKFDIRSWVLDHQVNIYL REGVLRATASEPYHVVDNFQDKT CHLTNHCIQKKKKK
12634	43002	A	12711	1	394	SGTRPVFLVPHITIGI\HPAIVTP QVKQEHPHTSDLMHVKPQHE QRKEQEPKRPHIKKPLNAFMLY MKEMRANVVAECTLKESAAIN QILGRRWHALSREEQAKYYEL ARKERQLHMQLYPGWSARDN
12635	43003	A	12712	1	789	
12636	43004	A	12713	1	870	
12637	43005	A	12714	1	729	
12638	43006	A	12715	1	828	
12639	43007	A	12716	1	213	
12640	43008	A	12717	1	664	
12641	43009	A	12718	1	695	
12642	43010	A	12719	96	269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
12643	43011	A	12720	3	241	
12644	43012	A	12721	213	660	EGPARHRLSPVRASKMTKKR RNNGRAQKRAARHVRGPGSPLK/ CFPSGPLPPNCAR/CVPKDKAIAK KFWIIRNVEAAA/AR/DISEASV FDAYLALPKL/VVVKLHVYCVSCA/ HKQK^SGNRSS^SPAKTRTPPR FRPGG^LPHGPTTKSP
12645	43013	A	12722	1	303	
12646	43014	A	12723	610	928	FLSLPTFLFV/ISGEEEELLVLALV FLSLFFFFFLRWNSFAVVAQAV/ VQWHINLSSLPFGFKQFSCLSLP SSWDYRCPPPRPANFCIFTRDG VSPCCPGWSRTSDLR
12647	43015	A	12724	1	2775	
12648	43016	A	12725	1	6039	
12649	43017	A	12726	2	3661	
12650	43018	A	12727	1	1173	
12651	43019	A	12728	1	1632	MPNPKNSKGGRKNKRANSSGD EQENGAGALAAAAGAGAAAAG GALAAAAGCGAAAAGAGPAG GAAGAGGAGTGAANAAAAG AAAAGDAKNEAPCATPLICSGF RPVDLEKDDYQKVVCNNEHC PCSTWMHLQCFYEWESSILVQF NCIGRARTWNEKQCRQNMWT KKGYDL/AFRFCSCRCQQGNL KKDTDWYQVQVCRMQDEKKKK GSEKNTGRPPGEAAEAEAKKCRP PNPKOKGPSPHDLPRRRHSMDRQ INSQEKAVGAAAYGARSPGGSP GQSPPTGYSILSPAHFSGPGRSSR YLGEFLKNAIHLEPHKKAMAG GHVFRNAHFDSPLAGLAVHRC GHFDTPVQFLRLDLSELLTHIP RHKLNTFHVRMEDDAQVGQG EDLRKFILAALSASHRNVNCA LCHRALPVFEQFPLVDTGLFLSP SRHDEIEYDVPCHLQGRLMHL YAVCVDCLEGVHKIICIKKCSR WDGSWHQLGTMTYDILAASP CCQARLNCKHCGKPVIDVRIG MQYFSEYSNVQQCPHCNGNLDY HFVKPFSSFKVLEAY
12652	43020	A	12729	1	1485	
12653	43021	A	12730	1	1074	
12654	43022	A	12731	2	3394	
12655	43023	A	12732	1	2190	
12656	43024	A	12733	1	1251	
12657	43025	A	12734	1	1710	
12658	43026	A	12735	3	679	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/\$40,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ~ =possible nucleotide insertion)
12659	43027	A	12736	209	337	
12660	43028	A	12737	365	538	
12661	43029	A	12738	2	196	
12662	43030	A	12739	1	2639	
12663	43031	A	12740	3	173	
12664	43032	A	12741	1	1479	
12665	43033	A	12742	1	921	
12666	43034	A	12743	1	798	
12667	43035	A	12744	2	773	
12668	43036	B	12745	75	321	
12669	43037	A	12746	321	738	
12670	43038	A	12747	1	3190	
12671	43039	A	12748	287	1636	ACGAMERAPPDGPLNASGALA GDAAAAGGARGFSAAWTAVL AALMALLIVATVLGNALVMLA FVADSSLRTQNFFFLLNLAISDF LVGAFCIPLYVPPVLTGRWTFG RGLCKLWLVDYDYLCTSSAFNI VLISYDRFLSVTRAVSYRAQQG DTRRAVRKMLLVWVLAFLLYG PAILSWEYLSGGSSIEPGHCYAE FFYNWYFLITASTLEFTPFLSV TFFNLSIYLNQQRTRLRLDGAR EAAGPEPPPEAQPSPPPPGCWG CWQKGHEAMPLHRYGVGEA AVGAEAGEATLGGGGGGGSA SPTSSGSSSRGTERPRSLKRG KPSASSASLEKRMKMSVQSFTQ RFRLA\DRKEAKSLAVIVSIFG LCWAPYTLMIIRAACHGHCVP DYWYETSFWLLWANSAVNPV LYPLCHHSFRRAFTKLCPQL KIQPHSSLEHCWK
12672	43040	A	12749	1	2142	
12673	43041	A	12750	3	7II	VWWNSDLMVINRSITTELPLTV SYDKVSLGRLRFWIMQDAVY SLQQFGFSEKDADEVKGIFVDT NLYFLALTFFVAAFHLLDFFLA FKNDISFWKKKSMIGMSTKA VLWRCCFSTVIFLFLDEQTSLL VLVPAGVW/AAJELWES*RK/ VI*RWTFWRLMPFQFGTYS ESERKTEEYDTQAMKYLSYLL YPLCVGGAIVSLLNIKYKSWY SWLINSFVNGVYAFGFLFMLPQ
12674	43042	A	12751	1	2025	
12675	43043	A	12752	494	747	ATVKWITLCRNRNIKLPFTIKKE GTGKAPKKSRKSVLGLGP~VHT SPGDPAAEAEGLPAGERPDGNLS QSPNSLRFYIKKKAYK
12676	43044	A	12753	9	731	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
12677	43045	A	12754	143	641	RSWVLLGVGARGSTPRTYQVPSPSLAPSALC*VS*VPLESLSCSHADNWKQELTKFISPQLPVEFGGTMTDPDGPNPKCLTKINYGGEVPKSYYLCKQVRLQYEHTRSVGRGSSLQVENEILPFGCGLRVLRFYNTYSLVHSKRISYTVEVLLPDQTFMEKMEKF
12678	43046	A	12755	1	1506	
12679	43047	A	12756	2	526	CQPVRAA*RHGNTPLATV*PAST/WWKWSEKQKEEQEMQNWR <sup>E</sup> SAS/VS <sup>G</sup> YPQDILSCAMSQNP <sup>R</sup> KRKPRRNV <sup>S</sup> APPVHQMAQM <sup>N</sup> I <sup>S</sup> VEQMETSKTHQATPLTWGQM <sup>K</sup> RLAHVAEE <sup>N</sup> LRSQNKPL <sup>T</sup> TSN <sup>I</sup> LMVAMM <sup>V</sup> VLAVS <sup>L</sup> PVAGAD <sup>Q</sup> NYIYWAY <sup>I</sup> PFPH
12680	43048	A	12757	1	1443	
12681	43049	A	12758	3	766	
12682	43050	A	12759	29	253	
12683	43051	A	12760	34	252	
12684	43052	A	12761	1362	1611	SSVLHPWDARLVQHTKSIHHIHJNRTNDKNHMIISIDAEKAFDKIQLPKIQQDFMLKTLNKLGDGTYLKIVRATYDKPTASIILNG
12685	43053	B	12762	1	1755	
12686	43054	A	12763	1	2109	
12687	43055	B	12764	1	1497	
12688	43056	B	12765	1	1527	
12689	43057	B	12766	1	1746	
12690	43058	B	12767	1	2853	
12691	43059	B	12768	1	1479	
12692	43060	B	12769	1	1932	
12693	43061	A	12770	1269	1581	NTGKPNPAAHQKGYP <sup>R</sup> SSGPHPWDARLVQHTKSIHHIHJNRTDKNIIMIISIDAEKAFDKIQLPKMLKTLSKLGVS <sup>Y</sup> NMFTRL <sup>T</sup> IP <sup>I</sup> AQVDTGRGNQLPSYL <sup>I</sup>
12694	43062	B	12771	1	4404	
12695	43063	B	12772	56	2080	
12696	43064	B	12773	1	5445	
12697	43065	B	12774	295	2831	
12698	43066	A	12775	89	459	
12699	43067	A	12776	2	980	
12700	43068	A	12777	1	378	
12701	43069	A	12778	1	363	PGVALPGR <sup>C</sup> RQAPADLLP*MRAYWPDIYFSANRSR <sup>F</sup> WKHEWEKHGTCAAQVDALNSQNKYFGTSLELYRELDLNSVLLKLGKPSINYYQVADFKDALARVYGVIPKIQCLPPSQDEDRQ

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, =Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12702	43070	A	12779	1	577	QRFKNDCRDPRDTGPVHGLWPD KSEG/CNRSW/PFNLEEKDLCP EMRAYWPDVHHSFPNRSRFWK HEWEKGHTCAAQVDAALNSQK KYFGRSLELYRELDL\NQVADF KDALARVYGVIPKIQCLQLPSQD EEVQTIGQIEI.CLT\TKQDQLQLQN CTEPGEQPSKQEVWLANGAA ESRGLRVCEDGPVFPYPPPDKTK
12703	43071	A	12780	1	624	MRPAALRGALLGCLCLALLCL GGADKRLRASVSPFSPLEHPEP GHCLDLDLHRLRAYPAR\WSS\*PWP QDFWVR\PTWES\VS DLLPEMR AYWPDVHHSFPNRSRFWKHEW EKHGTCAAQVDAALNSQKKYFG RSLELYRELDLNRGERVPTQFP RELVNVRSLAPPPTPGFLSGHV SVHTSSPLPSAMSGSFLRRLPEA ESGMLLQGPADP
12704	43072	A	12781	1	612	
12705	43073	A	12782	113	1149	RGAPRGPGRQGCCGHSRSPAR GPRDTGLGRPRAPGAPGGRCCS GGSAARGLGDSVSPGSLPRAA GGKWEPERQLAAFSPQVGTMR PAALRGALLGCLCLALLCLGG ADKRLRDNHEWKKLIMVQHW PETVCEKIQNDCRDPDYWTIH GLWPDKSEGCGNRSWFPNLEI KDILLPEMRAYWPDVHHSFPNRS RFWKHE/WPKRHGTCAAQVWD ALNSQK\YFGRSLELYRKLDL NSVLLKLGKIPSNYYQQVADFK DALARVYGVIPKIQCLPLTSQGE\ EVQTIGQ\IDLCLIKARTQLQN\ CTEPGEQ\PSPKQEVWLANGA\ AESRGLRVCEDGPVFPYPPPDKT
12706	43074	A	12783	2	515	
12707	43075	B	12784	62	359	
12708	43076	B	12785	219	523	
12709	43077	A	12786	1010	1550	DTENIPSSRRERSK VPYIVRQC VEEERRGMEEVGIVHVSGR\V AADIQALKAANVSECRAQD GMEVWA VVSAMRSQSAQPRRH VTSFSVSFLHLSGSSRRLHFR LSNNKDVSVMMSEMDVNAIA GSLKLYFRELPEPLFTDEFYPNF AEGIGEHWRPWPWHGRRLLHVH CCPQRL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
12710	43078	A	12787	2	951	GSNLYCTLEGDSFGYFVNKAK TRVYRD/THADPNWNEEFIEL EGSQTLRILCYEKCYNKTIPKE DGESTDRLMGKGQVQLDPQAL QDRDWQRTVIAMNGIEVKLSV KFNSREFSLKRMPRSRKQTGVFG VKIAVVTKRERSKV^PYI^VRQC VEEIEPPKALEGGWASTACPAG VATDIQALKAFFDGNKNDVSV MMSEMDVNNAIAGTFLNLYFREL PEPLFT^DEFYPNFAEG/IRVAEK EAVNNM^SLIHNLATVFGPTLLR PSEKESKLPANPSQPIITMDSW SLEVMSQVQVLLYFLQLEAIPA PDSKRQSILFSTEV
12711	43079	A	12788	3	644	
12712	43080	A	12789	168	378	
12713	43081	A	12790	1	486	
12714	43082	A	12792	83	536	
12715	43083	A	12793	1	662	
12716	43084	A	12794	3	357	
12717	43085	A	12795	2	421	
12718	43086	A	12796	2	908	
12719	43087	A	12797	1	846	
12720	43088	C	12798	87	413	
12721	43089	A	12799	1	508	MCQGDTYAWGGHMCRGGHLR RGHSHERDTPRGPERPPRPPAR DRESKDERRRPPPKDPPAVRTC PDSPLSTATPPPPPPPPPPPPPP PAAPSAFAAALRLRGPGRKWT RGQLPLPATAPEARVRALPRGG YSSPGRATSARGPAPWPLPSRT GKPPRPCSANTQEHC
12722	43090	A	12800	1	393	
12723	43091	A	12801	1	582	
12724	43092	A	12802	1	1422	
12725	43093	A	12803	1	1080	
12726	43094	A	12804	2	261	SCPFGNCFYKHA^YDGRREEP QRQKVGTSSRYRAQRNRHFWE LIEERENSNPFDNDEEEVVTFEL GEMLLMLLAAGGDELTSN
12727	43095	B	12805	60	802	
12728	43096	A	12806	2	238	
12729	43097	A	12807	1	1017	
12730	43098	B	12808	1	939	
12731	43099	A	12809	1	708	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12732	43100	A	12810	1	2653	MGDFNTPLSTLDRSRMRQKVNK DIQELNSALHQADLID1YRNLP ESTEYTFSSPAHHTYSKIDHILG SKAPLSKYRRSEIKINCLSDHSA IKLELRKKLTQNRSTTWKLNN LLLNDYVWHNEMKAIEKMFPE TNENKDITTYQNLWDTLKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQE1 SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLLARLIKKKR EKNQHAIKNDKGDMSTNHTE1 QTTIREYYKHLYANKLENLKEI DKFLETYSLPLRNQEEVESLNR PITGSEIEAIINSLPNKRSRPGPDG FTAKFYQRYKEELLISNFSKV5 GYKINVQKSQAFLYTNNRQTES QIMSEL/PFTIASKRMKYLG1QPT RDMKDLFKENYKPLLNEIKEDT NWKWNIPCSWVGRNIVKMAIL PKNWKKTTLKF1WQNQKRARIA KSILSQKNKAGGIMLPDFKLYY KATITKTAWYWYQNRD1QOW NRTEPSEIMPHIYNHLIFDKPDK NKKWGKDLSLFNKWCWENWLA ICRKLKLDPLTPYTKINSRWIK DLNVRPKTIKTLEENPGNTIQLD1 GMGEDFMSKTEAMATKAKID KWDLIKLKSFCATAKETTIRLNR PPTEWEK1FA1YSSDKGLISRIYN ELQQIYEKKTNP1KKWAKDM NRHLSKEDIYAAKRHMKKC8
12733	43101	B	12811	1	2748	
12734	43102	A	12812	1	1962	
12735	43103	B	12813	1	1833	
12736	43104	A	12814	176	421	QQPASPTRSVLLFPKTAHISGSP APPNVGLLNPSTGAAQKKTMT SAGLGRSLSL*K*NLPPECVACA GETWVTSMMSGNQCN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in ISSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
12737	43105	A	12815	1	1615	LISNFSKVSGYKINVQKSQAFLYTNNRQTESQIMSELPTIASKR MKYLGQPTRDMKDLFKENYKPLLNEIKEDTNKWKNIPCSWVG RINIVKMAILPKNWKKTLKFIWNQKRARIAKSILSQKNKAGGI MLPDPKLYYKATITKTAWYWYQNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKWKGDLSLFNKWCWENWLAICRKKLDPFLTP YTKINSRWIKDLNVRPKTIKTEENPGNTIQDIGHGEDFMSKTP AMATAKAKIDKWDLKLKSFCTAKETTIRLNRPTEWEKIFAIYS SDKGLISRIYNELQQIYEKKTNNPIKKWAKDMNRHLSKEDIYAA KRHMKKCASSLAIREIQLKTTMRYHLPVVRMAMIIKKSGNNRRCW RGCGEIGTLLHCVWDCKLVQP LWKSIVRFLRDLEIIPDPAIP LLGIYPKDYKSCCYEDTCTHMF IVALFTIAKWTWNQPKCPTMIDW IKKMWHIYTMEEYIADIKKDEF MSFVRTRMKLETTILSKISQIEK KTKHRMFSLIGGN
12738	43106	A	12816	1	996	
12739	43107	A	12817	1	756	
12740	43108	A	12818	1	1428	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
12741	43109	A	12819	1	2377	MNIDAKILNKILANRIQQHKKL IHHDQVGFIPGMQGWFNIRKSI NIVQHINRTNDKNHMIISIDEAK AFDKIQQRQFMLKTLNKLGLDGT YLKIIIRAIYDKSTANIVLNGQKL EAFLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKIEKIGQLRKEE IKLSSLFADDMIVHLENPIVSAQN LLKLIDNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPTIA SERIKYLGQLTRDVKDLFKEN YKPLNDIKEDTNWKWNTPRS WVGRINIMKMAILPKVYRFNA IPIKLPMTFTTELEKTTLKFIVN QKGARIAKSILLYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYYYKATVKVTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIEDKDPDKNKKGWNDS LFNWKWCWENWLAICRKLKLDP FLIPYTKINSRWKDLNVRPKTI KTLEENLGNTIQDIAMGKDFMS KTPKAMATKAKIDKWDLNLK SFCTAKETTIRVNRPQPIWEKIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSSLAIREMHI KTTMRHHLTSVRMIAIKKLG DWCRWCGCEIGRLLHCWWD KLVQLWKSVWRFLRDLELET PFDPATULLGIYPKDYKSCCYK DICT/RVCVPAALFTIANTWNPT
12742	43110	A	12820	1	4840	
12743	43111	A	12821	578	630	EYKNR*GLSLNPWGKTVHISW DVWSVGSSAKRWNESWES*C RGIQKKASLRSRTGNHSASSGI* ESRV*GLGTTGYRGITASLMSL RSCTRLLH
12744	43112	A	12822	8	214	EEWPKRKSEIRERPRP*SWPSDK QTLVQVQRGOKMEQANHPDPTD HMSQLMWTA <sup>v</sup> CPKGLGIALICL VRH
12745	43113	A	12823	33	240	GGGRNTWLQAVPGFPGW*RTL RTAVWDRRLTLRKPHCPGGS QFPGPQRQVIGLHHFLSSLNHQ GWV

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12746	43114	A	12824	1	411	MSTITQRKEENPSVFWELWEA /CKKIYSPVTRLTRGSIDPKR*V YYAISHRYQQKAPKPSPGI*TK SGGIKPGNLGVLY*GPRGTGQ KGKARSEKGCSLSHGPOQTNPK WWFREDRKWSRPITWYGLFS WFARTP
12747	43115	A	12825	1	611	
12748	43116	A	12826	120	493	KYRAQRRMIARWLPQDLERGE AMLPNSSGWYKSLKGIVLISEA FSCKCRAASLTIAWDLV*KQHS SPKKVQSPPPSAVRRSKWPQFW RVTAAKQSIWDCRVRIIDFVISC KLRNPLRVCGSRLL
12749	43117	A	12827	1	2195	VGEEGPAGVEGLNPAQSSRRP GPQQCSPGAEQGASARARRRP RPRPAAMVPVGVPGAVLTLCLW LAASSGGSWRPAPARLCAAAG RVAVCRERPARIASCRCLSLQI TRISAFFQHFQNNGSLVWCQNH KQCSKCLEPCKESGDLRKHQ QSFCCEPLFPKKSYECLTSCEFLK YILLVKQGDCPAPEKASGFAAA CVESCEVDNECSGVVKCCSNG CGHTCQVPKTLYKGVPPLKPRK ELRFTELQSGQLEVWKSSKFN SIEPVIVYVVQRRRNWYGIHPSED DATHWQTVAQTTDERVQLTDI RPSRWYQFRVAAVNVHGTGRF TAPSKHFRSSKDPSAPPANLR LANTVNSDG/AV*TVTIVWDL PEEPDIPVHHYKVFWSWMVSS KSLVPTKKRRKTTDGFQNSVI LEKLQPDCDYVVELQAITYWG QTRLKSAKVSLSHFTSTHATNNK EQLVKTRKGGIQTQLPFQRRRP TRPLEVGAPFYQDGQLQVKVY WKKTEDPTVNRYHVRWFPEAC AHNRTTGSEASSGMTHENYIIL QDLSFSCKYKVTVQPIRPKSHS KAEAVFTTPPCSALKGKSHKPI GCLGEAGHVLSKVLAKPENIL ASFIVQDVNTGHFSWKMAKA NLYQPMTGFQVTWAEVTTESR QNSLPNSIISQSQLPSDHVYLTV PNLRPSTLYRLEVQVTPGEG
12750	43118	A	12828	1	1410	
12751	43119	A	12829	2	299	
12752	43120	B	12830	81	510	
12753	43121	A	12831	3	436	
12754	43122	A	12832	1	769	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
12755	43123	A	12833	15	413	ERMCAGPWRKGAETGPYFCND TVRHRKASLLCPF*RMNGDQN SDVYAAQEKKQDFVQHFSQIVRVL TEDEMGHPEIGDAIARLKEVLE YNAIGGKYNRGLTVVVAFREL VEPRKQDADSLQRAWTVGWC VELLQA
12756	43124	A	12834	1	795	MNGDQKSDVYAAQEKKQDFQHF SQIVGVLTEDEMGHSEIGDAIA RLKDVLEYNAIGGKHYRGLTV LVAFQELDAINYAILEACIYYL LKLVCQAQPYLNLIELFLQISC QPEIGQTLTLTAP/QDNVDFFGR FT/EKQHANA*KILLEI/GEFFQI QDGYLDLFGDPTVTRKVGTDIQ DNKCSWLVVQCLQRSTLEQYQ ILKENYQKKAKKVQVQKALY EELDLPAVFLQYEEDGYSHIMG LTEQYAAPLLPAMFLGLVYKIV
12757	43125	B	12835	1	328	
12758	43126	A	12836	2	868	
12759	43127	B	12837	118	1138	
12760	43128	A	12838	100	374	KHISPALKALELPFERNLII/PLQ LLKVRILKEGEML/DI*HWFL** GMGTVQKGMPHKCYHGKTGR VYNVTQHAVGIVVNQKVK*VV
12761	43129	A	12839	1	1035	
12762	43130	A	12840	13	600	INPPPPPFRPELPSSNSPKMTDH KGERGEATRYMFMSRPFKKTMG VVPPLGHNN*RFVYKKGDIVDIK GMGYCVCQNGMP/HKCPWPKL EGVLQLLPQHA/VAIVVNQPV GQSFPPRE*IVRIEHIKF/EPEIS FLK/RVLKENDSEKERSPEKG TWGSNLKRHLAPPQKHTL*R TNGKEPELLEPIPYPEFHGHN
12763	43131	A	12841	1	317	QRPSEAKEIKLYAQIPPIEKM DA SL SMLANCEKLSLSTNCIEKIAN LNGLAEAVGDTLEELWISYNFIE KLKGHIHMKKLKILYMSNNLVK DWGTPVIKGDEEEDN
12764	43132	A	12842	155	588	
12765	43133	A	12843	1	954	
12766	43134	A	12844	1	486	
12767	43135	A	12845	1	367	
12768	43136	A	12846	1	190	LISRAKEDDMTLNIAEGVHPSY NIVLNTLHT/CGISVKSTWRPSK GAAP*ARMPGGTAGPCLAS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12769	43137	A	12847	1	2376	MRGQAQKATNVNLKSEDIQGKE ESPTQFYERLWEAYRMYTPFPD DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFVNRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLLHQAKLTFHPTVNPSTLL GFPAAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRAWWQQLPC\YKIVPSILRIS SSDGKYKAFSTCGSHLLAVC
12770	43138	A	12848	1	636	MRGQAQKATNVNLKSEDIQGKE ESPTQFYERLWEAYRMYTPFPD DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFVNRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLLHQAKLTFHPTVNPSTLL GFPAAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRAWWQQLPC\YKKQIS
12771	43139	B	12849	180	811	
12772	43140	A	12850	1008	1265	FLGVPTLGGWRPIQHELRK/PRE VTPVLLRLDILRRFRPPLWIGSDN GPAAFLAALVQKTAKGQNNITG GVYTLCDIDSHIIIFRSGY
12773	43141	B	12851	1	996	
12774	43142	A	12852	1251	1424	DSPRGAEAS\*LPEKLEMSG NRLVDNKDPGKKQTQRRIPHSP SQIPVPLPEIWCT
12775	43143	A	12853	1	1121	
12776	43144	A	12854	189	621	
12777	43145	A	12855	2207	2308	
12778	43146	A	12856	1	762	
12779	43147	A	12857	1	678	
12780	43148	A	12858	3	496	
12781	43149	A	12859	107	258	NALGKRTSFTNRNFLASGRLFD SVTYARRLQQYPAPL\*KTA\*SF SLLNH
12782	43150	A	12860	2	410	SPDPWVSTYKSTCHIAQEIAEKI HLRNQYERKGE\*APRSNLMSE DANGGAPNPWLFEPEETIGW GFDEIRQQQHNIIR\*QDAGLDA LSSIIISRKQM\GIEIGNELHEQN EIIDDLANLMENTDEKLRNETR RVN
12783	43151	A	12861	3	1402	

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12784	43152	A	12862	1	711	MAPDPWFSTYDSTCQIAQEIAE KIQQRNQYERKGEKAPKLTVT RALLQNLKEIALLKDLLRAV STHQITQLEGDRRQNLLLDDLV RERLLLASFKNEGAEPDLIRSSL MSEEAKGAPNPWLFEPEEPETR GLGFDFEIRQQPQKII EQEQDARL DALSSIISSQKQVMGQEIGNELD EQNEIIDD LANLVENTDEKLRN ETRRVNMVDRKSASC GMIMIV LLLLVAIVVVAVWPTN
12785	43153	A	12863	1	936	
12786	43154	A	12864	1	1023	
12787	43155	A	12865	1606	2238	
12788	43156	A	12866	3	347	
12789	43157	A	12867	1	1665	
12790	43158	A	12868	1	589	
12791	43159	A	12869	19	1677	
12792	43160	A	12870	1	906	
12793	43161	A	12871	1	228	
12794	43162	A	12872	1	320	
12795	43163	A	12873	1	398	TSKAPGAQGEQGFEECFLAVAL AGRPLPSLWALFQATT PVLQG LKEAFRPEVP\LR RDPL LLLFR\  TQTS DPAM LPTMIGLAEARR AGCL SYQTSLVSDGETWHVMG ISSLLPSLEGW KQ\H VTEAFQF HF
12796	43164	A	12874	3	322	SAGGSGRRTLHSRTMAQFVRN LVEK TPA LVNA A\VT YSKPRLAT FW YYAKV ELV PPTPAEIPRAIQS LKKIVNSAQTGSFKQLTVK VTT G\*MKT DVHNRKCLPLGFF
12797	43165	A	12875	91	425	WTFHPTTMAFPVRDLGEKTPA LGKAATVYLKPRLA AFW YYH\  QVELV PPTPAEIPRAIQSLKKIVNSAQTGT NSAQTGSFKQLTVK EA\I.LNDL VATEVSTW FYVREITKG RIGI* NV
12798	43166	A	12876	179	664	HSSPAVPGRTDFSHSQNPWPQF CPVTLVGEDP RALVNAAVT/YT RKPRIGLHF WYYA\KVELV PPT PAEIPRAIQSLKKIVNSAQTGT LANSSHVKEAV\I.NGLVATEV\  LMWFLCSERLLGKR GHLS LGY CFEDQSF NIWII FWI FILELFVW DHVVD PDC
12799	43167	A	12877	25	164	
12800	43168	A	12878	2110	2260	
12801	43169	C	12879	32	1429	
12802	43170	A	12880	172	322	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12803	43171	A	12881	1060	12039	
12804	43172	A	12882	1	810	
12805	43173	A	12883	3	146	
12806	43174	A	12884	1	1211	GPQDGNNQQPAPPEKVGWVRKF CGKGIFREIWKNRVYVVLKGDQ LYISEKEVKDEKNIQEVFDSLSD YEKCEELRKSRSKKNHSKFT LAHSKQPGNTAPNLIFLAVSPEE KESWINALNSAITRAKNRILDE VTVEEDSYLAHPTDRAKIQHS RRPPTRGHLMAVASTSDGM LTLDLQEEEDPSPEEPTSCAESFR VDLDKSVAQLAGSRRRADSDRI QPSADRASSLSPWKEFTDKGAT YTPQAPKKLTPTEKGRGASLEEI LSQRYAASAHTLQLRAEPPPT ALPNPGQLSRIQDVLVARKLEET QELLAEVQGGLGDDGKRKAKDPP S/RSPPDSESEQLLLIETERLLG EASSNWSQAKRVLQQVRELRD LYRQIMDLQTPDISHLRQTPH S\Q\YRKSLM
12807	43175	A	12885	617	1041	TTLINPGGPAPLLSLPTTSITGFT TFYHPNLKPLRTPCS*VQAWPC RHPID*SDYQRDAEPTTCISKLL GENIRRDEFWVKVQIKARSGETE QNPRSTAFAGELPLANREELNN LLLNKGILPLCDQRQEIESECAF TIFCAGDANCFFPSPTHLPLTAL QQRPGCGLGSASKEAWGNSLV CGPRGDTLPMIAKPHRSASKH STLHQYPTPPRSLCHQHRDEQP TNHLOTLNTIWAHTKWPVPGL DHINKPWRSCSSSQSAYLFYHW LHYFLPPKLKTSKDLISAGLA MSAPHILJFRVSAITSNSSCKPSS TSKACEELFKEHQCLGSTDIPIH IQGGAPFSAVSPQRVLVRGSQD GSHMVRPRLPFPDSAGLANFHLSKLFID
12808	43176	A	12886	1	606	
12809	43177	A	12887	174	350	VSWRFVQVFI*V\AGGSRICAAAGLSPGTTPPCATSLIGACSLIFIPRLLSLFCGDEAL
12810	43178	A	12888	3	265	
12811	43179	A	12889	1	1209	
12812	43180	A	12890	53	369	VAHQEKGIAEPLRPTGDSRQT HRRLDVERSTSVQEHMMGGCHF SPFPEREKLSTLRGIHQQAPAL WQATDQWIDIEF\GLGQPEESL GR*ITRLQGKTIILPFGSPIC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hood	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12813	43181	A	12891	1	345	
12814	43182	A	12892	2	451	
12815	43183	A	12893	2	286	
12816	43184	A	12894	217	1071	GENPRSENTRLATILEVACCHF GSSPPPS\GSSGRKDPPLTFGDII EGTAKAEPSPALGLTP\HGNV GHAARIQQPGPLSLWSRKAGK GVQDCYIDLKQIKIDLDKFSDN PDGYIDVLQGLQGSFDTWRFNI MLLLNQTLTPNERSATITAARE FGDLWYLSQVNNDRIAEEKREK FLTGQQAVPSVGSIIWDTSEEH GDWCRRHLLTCMLEGRLKTRK KPMNYSMMSTITQGKEENPTA FLERLREALRKHTSLSLDIEGQ LILKDTFITQSAADIRK\NFKSPP
12817	43185	A	12895	1	756	
12818	43186	A	12896	473	1015	
12819	43187	C	12897	152	322	
12820	43188	A	12898	146	1079	PPCAVVCLLWIAAVYCLSTTF APLCGQNTWLPKPCRHVNRRA SNASVSLSTVTLFSRLS\PQRKG SELLDSSGPLPASPSLPLCSGV PRAGLGSAWPKIPFLGIREAKN PRSENTRLATILEAAGRHLGTS VSKDHPVTFWPRRDLQSDLK QIKIDLGKFSDNPDGYIDVLQEL GQSFDTWRFDMLLNQTLTPN ERSATITAAREFGDLWYISQVV AAVAGLVSEAVKIIQGSYCVDI HDVNGILTAKGDLWLSDNHLL KYQALLLEGPVRLRRTCATLNP ATFLPDNEEKIEHNCQQVIAQT
12821	43189	A	12899	189	1798	

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12822	43190	A	12900	194	1729	NPAAQTPFFVVKKGGKRGAGL LHRQYPLRLEAKQGLKKIVKDL KAQGLVTPCSCPNTPLAVQK PNGQWRLVQDRLRIINEAVVPLY PAVPNPYIILS!QIPEEA!WFTVL DLKDAFFCIPVHPD!SQFLFAFED PSNPMQLTWTVLPQGFRDSLH LFGQALAQDLSQFSYLDLTVLQ YMDLLLVT!HSETWCQHQA LLN!FLATCGYKVSKQNAQLCS QQVKNLGLKLSKGTRALSEERI Q!PILAY!P!PKTLKQLRGFLGITS FCRIWIPRIKAVKLQ!IQLMEPQ MOSMTIYHGPLDRPTSPSSNV NDIEGTNASDFPFLSQVLEQVV SPKGSK!EAQCCVLRPLGCESNL KQIKIDLGKFSDT!PDGY!DVLQ GLGQPYYL!TWRD!MLLDQ!TL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAVP SVDPHWDT!SEHGD!WCHRYLL TDVLEGLRKTRKKP!N*SMISTI TQGKEENPTAFLERLREALRKH
12823	43191	A	12901	1	642	
12824	43192	C	12902	54	254	
12825	43193	A	12903	32	221	NGVGHNRMGTN!GGGEWG!P PAPASA*GCSLASAFASAPRW WFEMGCRGIYDAQQVALSRSF
12826	43194	A	12904	203	538	
12827	43195	B	12905	131	536	
12828	43196	A	12906	1	1251	
12829	43197	A	12907	38	475	ESERRGEFCLCKI!ISEQGRAVCV EDEQTSHFALTGNNG!YRKSQQ QWQQELSDLARDPPA!QCSAGP VGDDMFHWQATIMGPNDSPYQ GGVFFLTIHFPFTDYPFKPKVAF \\TTRIYHPN!NSNG!SICLDILRSQ WSPAFNQFPKSS
12830	43198	A	12908	282	849	QSCPAA!GIIKSFGRTFEHPTPREV RKPD!DKHTLLALKRINKDLSL ARDPPA!QCSAGPVGDDMFHW QATIMGPNDSPYQGGVFFLTH FPTDYPFKPP*GLHFTTRFY!H \\NINSKWAA!FCLRYS*DSQW!SP ALTS!SKVLLS!CSLL!CDPNPD!D DPLVPGDWHGSY*NRTGDKYN RISREW!TQKYAM
12831	43199	A	12909	1	397	
12832	43200	A	12910	245	535	
12833	43201	B	12911	68	333	
12834	43202	A	12912	265	562	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
12835	43203	A	12913	1	872	MVNTECQLDWIEGCKVLILGVSK KEASQGLGGRSRRGNVRQSTD ADIRPTSEKDAEMLMTQEDN ISVDQRGFLSGVQKKSGCANGL KGSCVCGGFYWWMAVIRMGVG KAMGLNLKLGKFEIKKGYLGK CRDSLRLSPTGFGKFTATSHEV AATVPIKVVELTLQTHKILRG VFAHLSCLQLHSLPPGSSMDS AKARRQLQVAGQGHSLVKQK GFHVEAPDHHPVQLSDISCKSY RWGHKLIKINFILPPLWWYDDL EEVKREQSEEKQQAKIMADIIG DALNAQKAFKGNPKGHKPLPF SAGQMENW*CPECPKSI
12836	43204	A	12914	7	231	
12837	43205	A	12915	1	223	MEILTTCDKGLIFTGNTRKSETS TSECTCPLDINCSLSHSSPPSPDE ETQHHTDSDLHVRPRKGYLLCIV HIPDIVAVMVNIQQLQDWEIGC KVLFLGVSVKVLPKEINTGIGSL GKADPPSIWKS*QHVTKDLYLQ VILENQQLVLPANALVRWILTVP FPTLRLALQMRKHSTTLTVCMS DRGKDIYCASTIYQI
12838	43206	A	12916	1083	1273	NKMSFKLKEDCFGRSKCNL*T* CWKSINEA*K/DLELQLQFGPQE KLFALEQQVKKKLNLVPDA
12839	43207	C	12917	1	1506	
12840	43208	A	12918	3	1219	
12841	43209	A	12919	1	735	
12842	43210	A	12920	2	94	
12843	43211	A	12921	362	460	WLILSVNLIGLKDAKYCSCVCL *GCCQRLTF
12844	43212	A	12922	1235	1474	
12845	43213	A	12923	1	250	
12846	43214	A	12924	1	261	
12847	43215	A	12925	2	85	
12848	43216	A	12926	1	291	
12849	43217	A	12927	1	321	
12850	43218	A	12928	1	370	
12851	43219	A	12929	1	684	
12852	43220	C	12930	1	210	
12853	43221	A	12931	2	91	
12854	43222	A	12932	1	243	
12855	43223	A	12933	2	353	WMKLETHLSKLS*GQKTKHRS SSLIGSTDQQLRVVKNVQGRVC PGSTGHGAWEAWTAMRKVDS PLQTGSLRPGWCRQVGSHARS GSAEAAGNPGI.HPGICPRVEDG IQVAENFPEV

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12856	43224	C	12934	1	289	
12857	43225	A	12935	1	1194	
12858	43226	A	12936	140	237	
12859	43227	A	12937	1	292	
12860	43228	A	12938	2	178	
12861	43229	B	12939	1	1245	
12862	43230	A	12940	2	241	
12863	43231	A	12941	1	675	
12864	43232	A	12942	1515	1920	TPTNLQEKNKQPHQKVGEGYE QTLLKRRHLCSQKTHGKNAHH HWPSEKCKSKPQ/WIPSISHQLE WOSLKSQETTGTWMKLETIILS KLLQQQKTKHHMFSLIGGNRT RRTHGHRKGNITLWGGLSDSV NCASSSG
12865	43233	A	12943	608	891	
12866	43234	A	12944	1	3956	MGSCPGGFTAEFYQRYKEELVP FLLKLQFQSIEKQGTLPNPSFYEA IIIPKPGRDTTKKENFRPISLMN IDAKILNKILTNRQHQHKKLIHH DQVGFHGMQGWFNIRKSINVI QHINRTNDKKHMIISIDAKEAF DKIQQPFLMLKTLNKLGTWMKL ETIILSKRSQGQKTHRMFSLIV NIIPTIKILKQNMTAMETLCPIF KLEGDTMDNPIANRRVRTA TSVVCLHVGTPEARLPHGPMI TAQSPFG
12867	43235	A	12945	1	855	
12868	43236	A	12946	1	255	
12869	43237	A	12947	273	3484	
12870	43238	A	12948	3	377	
12871	43239	A	12949	85	333	
12872	43240	A	12952	22	308	
12873	43241	B	12953	30	383	
12874	43242	A	12954	3	448	
12875	43243	A	12955	1	453	
12876	43244	A	12956	3	491	
12877	43245	A	12957	2	749	
12878	43246	A	12958	155	637	
12879	43247	A	12959	1	510	
12880	43248	A	12960	2	559	RPHASAHASGRQRSQDVTTMV WALLLLTLLTQGTGSWAQSL TQPPSASGSPGQSITISCTGLIND VASYNFVSWYQQHPGKAPKL MIYEVTKRPSG/VPDRFSGSKSG NTASLDHLWGSRLEDEADYYC LLICRRLHPGGGIRRWDPRTV LGSQAQRPTPTVTSGRSPSSEGAP SQQGHTSVSDQ

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12881	43249	A	12961	1	1958	MSVQRKDRVRVTTQGGGSVASSMLTQEPVGSVALGQSARDRDPDCSDSVSVYLMDTWQSIVIIGFAE SAATLGDPPPELPMHPEGSEASYELTQPPSVSVPGQTARITCSGD ALPKQYAYWYQQKPGQAPVLVIYKDSERPSGIPERFSGSSGTT VTLTISGVQAEDADYYCQSADSSGTYPTVTQADRETPTHQYSR HPSYAKGFVFLWGSWAQSALTQPASVSGSPGQSITISCTGTSSD VGSYNLVSWYQQPQKGKAPKLMIYE/VDSKRPSGVSNRFGSKSGINTASLTISGVPGRLRDEGIDYY CCSYAGSVASYELTQLPSVSPGQTARITCSGDVLLGENYADWYQQKPGQAPELVIYEDSERYPGIPERFSGSTSGNTTTLTISRVLTEADYYCCLSGDEDNPSPVTQADGEDTGIRSHYEGTLALYLYPEPVKATCSVTSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWWYQQKPGQAPVLVVYDDSDRPSGIPERFSGNSNGNTATLTISRVEAGDEADYYCQLSSTLGPKTLGDTVLRPMIYSVSIQASGVPDGFSGSKSGNTASMTISGFQAEADYYCNSHRRGSVSSLETQDPAVSVALGQTVRITCQGDLSRYYASWYQQHPGKAPLIIYDGH
12882	43250	A	12962	2	367	
12883	43251	A	12963	2	376	QTYSLRRATPRHIIIVGFTKVEMKEKVLRRA/NKPIRLTVDLAETLQARKEGGPIFNLKEKNFQPRI SYPAKLSFISEGEIJKSFTDKQMLKDFVTRPALQELLKEALNMRNNQYQPLQKHAKW
12884	43252	A	12964	2	1178	
12885	43253	A	12965	1	732	
12886	43254	B	12966	99	716	
12887	43255	A	12967	1	1011	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
12888	43256	A	12968	3	1263	GRTIQTGKEV <sup>EN</sup> FEKNLEECITRITNT <sup>E</sup> KCLKELMELKTKAREVRE <sup>C</sup> RSLRSQCDQLE <sup>E</sup> EV <sup>R</sup> SAM <sup>ED</sup> EMNEMKQEGKFREKIKRN <sup>E</sup> QSLQ <sup>E</sup> IWDYV <sup>R</sup> KRPNLRLIGVP <sup>E</sup> SDV <sup>E</sup> NGTKL <sup>E</sup> NTLQD <sup>I</sup> QENFP <sup>N</sup> LARQANVQ <sup>I</sup> QERQ <sup>R</sup> T <sup>P</sup> QRYSS <sup>R</sup> RATPRHII <sup>V</sup> RFTK <sup>V</sup> EMKEKG <sup>M</sup> LLVPNWT <sup>N</sup> HSP <sup>L</sup> FRAIL <sup>F</sup> DYKG <sup>G</sup> FCRG <sup>F</sup> TT <sup>H</sup> QTG <sup>F</sup> SPAGANQ <sup>R</sup> GP <sup>G</sup> LAATL <sup>S</sup> GP <sup>G</sup> GE <sup>G</sup> Q <sup>S</sup> AV <sup>A</sup> RLT <sup>L</sup> QD <sup>I</sup> Q <sup>E</sup> ENFP <sup>I</sup> SLARQANVQ <sup>I</sup> Q <sup>E</sup> IQR <sup>T</sup> Q <sup>P</sup> R <sup>Q</sup> YSS <sup>R</sup> RATPRHII <sup>V</sup> RFTK <sup>V</sup> EMKEKG <sup>M</sup> KMLRAAREKGR <sup>V</sup> TLKGKPIRL <sup>R</sup> TADLSAETL <sup>Q</sup> AR <sup>R</sup> EWGP <sup>I</sup> FN <sup>I</sup> KEKNFQ <sup>P</sup> RIS <sup>Y</sup> PAKL <sup>S</sup> FISEGEIK <sup>I</sup> SFTDKQ <sup>M</sup> LRDF <sup>V</sup> TR <sup>T</sup> PALKELL <sup>L</sup> KEALN <sup>M</sup> ERNNNRYQ <sup>P</sup> PLQNHAK
12889	43257	A	12969	1	1392	
12890	43258	A	12970	1	1224	
12891	43259	A	12971	1	970	
12892	43260	A	12972	1	954	MDGDLHKGVA <sup>V</sup> FWPPDAA <sup>G</sup> GH <sup>T</sup> CC <sup>C</sup> RS <sup>M</sup> VCR <sup>S</sup> LLGG <sup>A</sup> QWKF <sup>H</sup> S <sup>F</sup> R <sup>C</sup> R <sup>I</sup> R <sup>F</sup> EL <sup>L</sup> H <sup>M</sup> IQ <sup>E</sup> RNS <sup>N</sup> IS <sup>I</sup> Q <sup>K</sup> D <sup>V</sup> H <sup>T</sup> E <sup>T</sup> P <sup>S</sup> E <sup>T</sup> H <sup>H</sup> Q <sup>R</sup> PKV <sup>D</sup> K <sup>S</sup> SKM <sup>M</sup> R <sup>R</sup> NQ <sup>C</sup> CK <sup>K</sup> A <sup>E</sup> NS <sup>K</sup> NQ <sup>K</sup> ASS <sup>P</sup> PK <sup>H</sup> NS <sup>W</sup> R <sup>R</sup> A <sup>R</sup> E <sup>Q</sup> N <sup>W</sup> T <sup>E</sup> N <sup>F</sup> D <sup>K</sup> L <sup>T</sup> E <sup>V</sup> G <sup>F</sup> R <sup>R</sup> W <sup>V</sup> IT <sup>N</sup> S <sup>S</sup> EL <sup>K</sup> E <sup>H</sup> I <sup>L</sup> T <sup>Q</sup> CK <sup>E</sup> AK <sup>N</sup> L <sup>E</sup> K <sup>T</sup> LE <sup>E</sup> LL <sup>T</sup> R <sup>I</sup> T <sup>S</sup> LE <sup>K</sup> N <sup>I</sup> N <sup>D</sup> LM <sup>L</sup> KL <sup>K</sup> NT <sup>A</sup> * <sup>E</sup> L <sup>L</sup> RE <sup>A</sup> Y <sup>T</sup> S <sup>I</sup> N <sup>S</sup> Q <sup>I</sup> S <sup>Q</sup> A <sup>E</sup> E <sup>R</sup> I <sup>E</sup> S <sup>I</sup> E <sup>J</sup> D <sup>Q</sup> L <sup>N</sup> E <sup>M</sup> K <sup>H</sup> E <sup>H</sup> R <sup>I</sup> R <sup>E</sup> K <sup>R</sup> M <sup>K</sup> R <sup>N</sup> K <sup>Q</sup> S <sup>S</sup> F <sup>Q</sup> E <sup>I</sup> W <sup>D</sup> Y <sup>V</sup> K <sup>R</sup> PN <sup>L</sup> R <sup>L</sup> IS <sup>V</sup> P <sup>E</sup> SD <sup>G</sup> EN <sup>G</sup> NK <sup>N</sup> * <sup>E</sup> N <sup>I</sup> LQ <sup>D</sup> <sup>I</sup> Q <sup>E</sup> N <sup>F</sup> PN <sup>L</sup> ARQAN <sup>I</sup> Q <sup>I</sup> Q <sup>E</sup> IQR <sup>T</sup> Q <sup>P</sup> Q <sup>R</sup> YSS <sup>R</sup> R <sup>A</sup> TPR <sup>H</sup> II <sup>V</sup> RFT <sup>K</sup> V
12893	43261	B	12973	1	1346	
12894	43262	A	12974	1	318	GSRGELLLS <sup>L</sup> CYNPSANSIIVN <sup>I</sup> I <sup>I</sup> KARNLKAM <sup>D</sup> IGGTS <sup>D</sup> PYV <sup>V</sup> KV <sup>W</sup> L <sup>M</sup> YKD <sup>K</sup> R <sup>V</sup> E <sup>K</sup> K <sup>K</sup> T <sup>V</sup> T <sup>M</sup> KR <sup>N</sup> L <sup>N</sup> NP <sup>P</sup> NES <sup>E</sup> FAFD <sup>I</sup> P <sup>V</sup> TE <sup>K</sup> \L <sup>R</sup> ET <sup>T</sup> <sup>I</sup> I <sup>I</sup> T <sup>V</sup> MD <sup>K</sup> DK <sup>L</sup> SLRND <sup>V</sup> IG <sup>K</sup>
12895	43263	A	12975	17	389	SWGP <sup>H</sup> CT <sup>H</sup> KL <sup>K</sup> KS <sup>L</sup> PM <sup>E</sup> MT <sup>D</sup> AM <sup>D</sup> RE <sup>R</sup> M <sup>/</sup> R <sup>G</sup> SK <sup>K</sup> D <sup>V</sup> /R <sup>V</sup> LG <sup>G</sup> CAAT <sup>W</sup> T <sup>P</sup> R <sup>A</sup> GG <sup>R</sup> QQ <sup>S</sup> PG <sup>T</sup> TV <sup>D</sup> K <sup>R</sup> E <sup>D</sup> TP <sup>D</sup> C <sup>A</sup> MC <sup>D</sup> Q <sup>S</sup> TS <sup>H</sup> P <sup>I</sup> SA <sup>S</sup> PS <sup>S</sup> LLPG <sup>S</sup> FT <sup>T</sup> QT <sup>F</sup> PP <sup>G</sup> IA <sup>Y</sup> HR <sup>A</sup> AS <sup>F</sup> LIV <sup>A</sup> Y <sup>Y</sup> PS <sup>N</sup> KN <sup>S</sup> K

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, -=possible nucleotide deletion,  =possible nucleotide insertion)
12896	43264	A	12976	84	282	GEGQVGWPQGEVQQDEEVIEE VGA*DAGSGYQEEE EG PQSLR EVVGVELVVGADPSGEGPKED
12897	43265	A	12977	1	1179	
12898	43266	A	12978	3	634	
12899	43267	A	12979	234	619	CYVVQEVLPSLLCHCLVICSRP GRTAEWPPG*GF*SPPHRGWW GC*GHD/HRRGTSIPTH/V*SPP ASYPGSLCRPGQEEEREREGEW QREGRRPGTR*CGAEAEARGW RAAAKATAVAGARNRRPGISG
12900	43268	A	12980	1	1182	
12901	43269	A	12981	3	763	
12902	43270	A	12982	32	949	
12903	43271	A	12983	1	1299	
12904	43272	A	12984	1	1176	
12905	43273	A	12985	1	421	
12906	43274	A	12986	81	404	VKFGPEIWCRDSDQGRGGVGT SLGRSIPCPALCSVRKIVLRLP VLRPTSPRNISPILNRDPTVQLT WQPLPEPLELWPKAL*LTPSQT SA*RLKTDAA RLPRKPPR
12907	43275	A	12987	1	378	
12908	43276	C	12988	1	751	
12909	43277	A	12989	302	629	ICLSYPAPPCKRFPHYTRVLVH* SLFNENTSQSCFTSR/WKLESFT TRAIERHQIPLL*ATLTLIRWL KKLAQQLLSLTASFSPSYQLPP TPPLKLPPSISSHTRQMV
12910	43278	A	12990	14	380	
12911	43279	A	12991	189	608	QSDLASQHGLFPLATEVRSSG AASCPCDSDSICPAPIA PGRATP PQANCWASEGTLRYQALP GNR APVSQVSQAGGANLCVQQP KILTNFKSGKRPLFTLFSNLQGP RSRPVAFLSKQLDLTVLWGP CL\VQQLLPP
12912	43280	A	12992	1	513	
12913	43281	A	12993	2	462	WSMGLP RRS GCVSLQPLSQEDL GRSOSESLG PEFQGLW EWLPEQ LPRSF IQALG SLSYFPRTLMNLS WPLCLRK WGYL/SYLYLPFQVGL PSTV PWPLILPSK VPEEEGQLQS TLC PGIKL LPPVFTSHH A FLGVFC NQWVSDVFL ALFL M KLLGAQ
12914	43282	A	12994	59	213	
12915	43283	A	12995	1	1159	
12916	43284	C	12996	1	864	
12917	43285	A	12997	1	1155	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12918	43286	A	12998	879	1163	SRRPLFMGLVRVLCKMSGRGP LCFPGGHIVFLWGGTVLWLW T*SPHWHRKAN*DLFLQKLPLR *VSHQCDPCLPVCHLWNCLFL PLWGPPAG
12919	43287	A	12999	1	179	
12920	43288	C	13000	1	410	
12921	43289	A	13001	42	365	FGLRLSLLAPPFCMFPLTT*HS*P SVLPASFPAAALGIPQARAVTPFV SP*LLASLSFWAPPCSLCLDA *HGSHLWHAQSSCRLRWSFGL AASQMPEEPSSHGPRRK
12922	43290	B	13002	1	741	
12923	43291	A	13003	8	265	
12924	43292	B	13004	1	646	
12925	43293	A	13005	1	1158	MKLVTIFLLVTISLCYSGYWPE NEQMSVGGGDDNGEVLYSALR GASEVIGQCQSSATKPRRSGKE SVREPWARVPAGALGVGVREID QTLGIIDTILCHHHERLLQSHYGI HKSSLLMSVGNNSQVAALYQLNV YVVADTVGLIINKSNSILDSVQPN YCSNKHIELRTQVGGARNLRA NSPMTSSYNQESSSMENVSALS LLTVESPTSMFDYCDDSLERVK SALDIIFSMIIYTVTFFLAGNG LVIWVVGFMSCVTNTCLPSDP HLHGPLTCDPVANLVLEQLHTS KGNSGALEDLAFGNLFLCSLLD LQGNSWWKVSPLSYNQYDLQ NETQGSHQLWKEIIIPW*PSAFV V/SSGYWPENEQMSVGGDDN GEV/RVFRPEGGFRGDRAVSVF SH*AEKIWEGISQRAL/VPEFQG LWEWV/CREIDQTLGIIDTILCHH HERLLQSHYGIHKSSLLMSVGNS QVAALYQLNVYVVADTVGLII KSNSILDSVQPNYCNSNKHIELRT QVGGARNLRLANSPTTSSYNQE SSSMENVSALSLLTVESPTSMF DYCDDSLERVKSAldIFSMIIYT VTFFLAGNGNLVIVWVVGFM SCTVNTCLPSDPHLHGPLTC VANLVLEQLHTSGKNSGALED LAFGNLFLCSLLDLQGNSWWK VSPLSYNQYDLQNETQGSHQL WKEIIIPWHTQLVTTAHHFFGFF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Motif	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
12926	43294	A	13006	3	371	AGARFNRVSH*RNDRVRPHRD VYSLQGRLSDHSPTFQGCQTQ GRLPWSFTLSGKFRFSGEGATT SPAIIKNFQTPEPQWPGLPPEPPP TGACYTCRSGSHWAKECPQAR IPPKPHICVGPH
12927	43295	A	13007	77	332	RWKKNCNLSPPRMS*QR*WKP* MQQAACS VGETQPPCTQVK*T ALLTQSLSFGGLFTRKTHMKFGA VTRIGGPPGLDQSPVLLFAP
12928	43296	A	13008	1048	1349	RVVEQDDAERLFRRAA/GDL PYGAFGEIF*ETQQCMEMQQLAE DHASVTMISLEAWRLYRKVMC RJWASMLRLSVCHLCAPKRVW SLISRNGYHLPGSIH
12929	43297	A	13009	213	499	PEQRTSHRQQQRQQPPQPSRS*P FCPSLPRSA LSLSFLCDGYAAP* AYRE*IPVTEDHFAE*I/ISWCPC *YREALGQLLAKMRR*SARKRF QLSP
12930	43298	A	13010	2	431	
12931	43299	A	13011	2	367	
12932	43300	B	13012	1107	2083	
12933	43301	B	13013	1	627	
12934	43302	A	13014	712	2671	AHVGRGST*ALPRAMGSDAF*C PLQ*MTPASFGSKAALSRSVFIKE ALMMEDPCVVVKPLSAHMTA WWCRIWKAYLESV
12935	43303	A	13015	50	1362	WEQIPHGLVLSQQLPRRSGSIS LQPLSQEDLGRSQESL LGPEFQ GLWQWLSDFQT*HQWFVSGFQ AFSDRLKAALSASLLRFGDSD WLPSSSACKCLMLGLHFVIVGN ICATLKEKYSSMLHLDVTMKK NGEKRTRLQKRKKGMPHPAY EDLNIAA1TLPANVVLHQPSGR TSGQLDPVWWWSLTDAAHEIWC QDPGLGSGDFPWEITPLSSYSSL HEKDPPITSGPQT DQPKKHLTN FKSKTKE TGFHIGPKTAPVTD WEGLSPLVFNHCRDTSLIHPCF KGVRPRRDA CLGSPLAASPAF LEKGQDLINLAFKVYNNRKKL QFLASTVRQTPATSPAHKNFQT TEPQQPGVPPPEPPPTGACYMC KIWPLGQANARSPGFLSRRVPS VWDPTGNRTVQLTWQPLPEPL ELWPKALCLTDSPFDLGLAA
12936	43304	A	13016	1	507	
12937	43305	A	13017	5	271	
12938	43306	A	13018	1	618	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
12939	43307	A	13019	1	429	
12940	43308	A	13020	1	3567	
12941	43309	A	13021	1	353	
12942	43310	A	13022	1	338	
12943	43311	A	13023	1	1175	
12944	43312	A	13024	3	326	
12945	43313	A	13025	150	494	PSPSLGYLVGTRGTALRL* DAR AAMRPFDPSTLLPTCW/DYWTY AGSLTTPLTESVTWIIQKEPVE VAPSQSLAFRTLFLSALGEEEK MMVNYYRPLQPLMNRKVWAS FQATNEG
12946	43314	A	13026	2	975	DSREHHPLQTGVSGNRPKMLG RNTWKTSASFVLEQWMWPLW SRSMRPGRWCSQRSCAWQTSN NTLHPLWTPVPSVPGTRQSPI NIQWRDSVYDPQLKPLRVSYE AASCLYIWNNTGYLFQVEFDDA TEASGISGGPLENHYRLKQHFH HWGAVNEGGSEHTVDGHAYP AELHLVHVNSVKYQNYKEAV VGENGLAVIGVFLKLGAHHQT LQLRVDILPEIHKH(DARAAMR PFDPSTLLPTCW/DYWTYAGSLT TPPLTESVTWIIQKEPVEVAPSQ LSAFRTLFLSALGEEEKMMVN NYRPLQPLMNRKVWASFQATN
12947	43315	A	13027	1	1233	
12948	43316	A	13028	761	1000	IPFISFSCLIALARTSNTMLNKG ERGHPSLVPVFIGNASSCPVSM ILAVGLS*IAIILRYVPSIPNLLR VFSMKG
12949	43317	B	13029	697	1527	
12950	43318	A	13030	1	1695	
12951	43319	A	13031	434	925	VAKIFSHFVCCFLTMVVSFAV QKLFSLIRSHLSILSFVAIDFGVL DMKSLPMPMS*MVMPRFSSRV FIVGLTFKSLIHLELIFV*GVRK GSSFSFLHMASQFSQHHLLNRE SFPHCLFFSGFSKIR*L*CGIISE GSVMFH*SISLFWYQYHAVLVT VAL
12952	43320	A	13032	1124	1234	KITPKKQIRQSPNLTQNTGQQ*S LQLWEHFQISTHF
12953	43321	A	13033	929	1261	
12954	43322	A	13034	1118	1354	IPFISSCLIALARTSNTMLNRSGE RGHPCLVPVFKGNASSFFPSMI LAVGLS*IAIILRYIPSILSLRV FSVKGC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12955	43323	A	13035	2	348	HQHLLFPDFLMIAILTGMRWYL IVVLICISLRASDDEHF/YHVS GCINVFF*EISVHLRPLFDGVV* FFLVNLFKFFVDSGYEPFVRWV DCKNVLPFCRLPVHSDGSFFC AEAL
12956	43324	A	13036	578	712	LISNFSKVSGYKINVPKSQAFLY TKNRQTAKS*VNNSHSQLLQRE
12957	43325	A	13037	1	1833	
12958	43326	B	13038	1	1587	
12959	43327	B	13039	1	1851	
12960	43328	A	13040	1349	1444	
12961	43329	A	13041	953	1277	MVLPRFSSRVFMVLGLTFKPLI HLELIFV*GVNFV*GSSFSFPHM ASQFSQHHLNNRESPFHFLLSG LSKIR*L*MCGLISEGSVLHW ESLFWYQYHAVLVTVAL
12962	43330	B	13042	804	4236	
12963	43331	A	13043	1	744	
12964	43332	A	13044	137	797	
12965	43333	A	13045	210	418	
12966	43334	A	13046	1	927	
12967	43335	A	13047	1	1415	MGFLGTGTWILVLVLPPIQAFPK PGGSQDKSLHNRELSAERPLNE QIAEAEEDKIKKTYPENKPGQ SNYSFVDNLNLLRAITEKEKIEK ERQSIRSSPLDNKLNVEDVDST KNRKLIIDDYDSTKSGLHDHKFQ DDPDGLHQLDGTPLTAEDIVHK IAARIYEENDRAVFDKIVSKLLN LGLITESQAHTLEDEVAEVLQK LISKEANNYYEEDPNKPTSWTEN QAGKIKEPKVTPMAAIQDGGLAK GENDETVSNTLTLTNGLERRTK TYSEDNFRRDFQYFPNFYALLKSI DSEKEAKEKETLITIMKTLIDFV KMMVKYGTISPEEGVSYLEGL DEMIALQTKNLEKINATDNIS KLFPAPSEKSHEETDSTKEEAA KMEKEYGSLKDSTKDDNSNPG GKTDEPKGKNRSPIWKPIRK\NI EWLKKHDKKGNKEDYDPFQR* EVSFNNKADA\YVEKGILDKEE AEAIIKRIYSSL
12968	43336	A	13048	1	879	
12969	43337	A	13049	3	640	
12970	43338	A	13050	134	382	DGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLGVW SQALGQSAPSLTASLPCVSKCW ENIPPWMN/WPPH*IKHIQS
12971	43339	A	13051	87	500	

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12972	43340	A	13052	1	1356	
12973	43341	A	13053	1	447	
12974	43342	A	13054	3	107	
12975	43343	A	13055	3	2377	
12976	43344	A	13056	1	2193	
12977	43345	A	13057	1	2724	
12978	43346	A	13058	253	490	QSSIPAIMSSFLGTGAETMPVPL GAGMRRTSTEPQRVCFCGTGIIIF KTSSLREAPRKKSMSIDSLMGR E/WMPVTKLGLRLVKDMKIKSLE EIYLFSLPIKESEIIDFFLGLASLKD EVLKIMPVQKQTRCGSVLVRLI PAPRGTGIVSAPVPKKLLMMA GIDDCYTSARGCTATLGNF/AK ATFDAISKTYSYLTPDLWKETV FTKSPYQEFTDHLVKTHTRVSV QRTQAPAVATT
12979	43347	A	13059	1	819	
12980	43348	A	13060	1	623	MARRKNGKWESEIIDFCLGGSL KDEVLKIMPVQKQTRAGQCTR FKAFAVIAIGDYNGHIGLGIKCSK E/LATAIRRAIIHLAKLSIVPVCRG YWGNKISKPHIVPCRTGIVSA PVSKKLLMMASINDCYTSARG CTAIGNFDKATFDAISKTYSYL TPNLWKETVFTKSPYQEFTDHL VKVYTRVSMQSTQAPALAKLP RVAVQRAEV
12981	43349	A	13061	1	949	KWRITPVPTGRP/GGPGPGMG KPRCF/RGEVFGIVIRAGSPGP TGPGRG/GEAGAKAED*EWM PVTKLGLRLVKDMKIKSLEEYL FSLAIKKSEIMSFLGGGLLSRDE VFE*LCPVQEQTTRAGQ/RATRF KAFVALTTLGTTNGVHVGGLC* VPPREVAUTGNSWGPFLQQLAH SSPVRRGLLGGTAKNSAKPPTLV PWQR*PRAACGLCAGYAFIPLQ PRGQLASVSA/PVP/KKLLMMA GTDG/CNNSSQRGGCTATVG/INL AKATTFDAISKTYSYLTPDLWK ETVFTKSPYQEFTDHLVKTHTRV VSVQRTQAPAGATT
12982	43350	A	13062	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVAMERFGSRN GKTSKKITIADCGQLE

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12983	43351	A	13063	2	797	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIGLFADKVPKTAENFR/A L*SIEEKFGFL*GVPFCFHRLFPR VLCVRGGDFHTAINGT\GGKSI\Y YGEK\FEDENFILKHTGPGILSH GKMLDPNTNGSQQFFCTAKT\VE WLDGKH\WFGKVKEGMNIVE AMEAVFGSRDCKTSKKITIAIDF GQLRIKFDFVFLSLTTKISFCAL LSGEHPLHPIWLGVILESMWLS LAVPFWVPCFCPCSLPCLAGLQS
12984	43352	A	13064	1	720	
12985	43353	B	13065	98	2074	
12986	43354	A	13066	596	841	
12987	43355	A	13067	66	326	
12988	43356	A	13068	1	441	
12989	43357	A	13069	2	325	WCPSQAAAAGARATRDMPEGS MTCLCRALWWLFSWLKVHR\*R QGQQGRPAAPSAGPAKPTPTRN SSWLLLAAPVPTRTSPSTPPCKL REPAPALASPERGSHSAAVG
12990	43358	A	13070	38	1066	
12991	43359	B	13071	1	324	
12992	43360	A	13072	2	680	
12993	43361	A	13073	2	165	
12994	43362	A	13074	1	1110	MASLLKSARPQTHWKEETPETS KRLKEQTDPJPSLRAVTLIAKVN SFipeVCETKNPLEGIHSGHILAP NVGPsPSRRQARVQFENVS ATKSDLPQSSLWSRRKRTTVSAA ASKKTSKEISKGPKQPGY/PVT SPSSCRGRGIWPNP/EYMSTPS LI*/SQIKVDLGKISDDPDRYIDV LQGLGQTLDSLWRDVMLLDQ TLAFNEKNAALAAAQQEFGDTW YLSEVNDRMTAERDKFPTED GEPIKCDCQQIIVQTYAAQDDIL EVPLANPDNLNYTDGSSFVENG IRRAGYAIVSDVTILERPNLFRA IQQVVKACEVCQRKNPPLVHPP NYLYKTLNLTHSLLNQSNPSLA NDCWLCSSLSVSAEPYN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
12995	43363	A	13075	450	1776	RGGRACLRP*AA/SPGPSTP*WP PPRGVQAAAILSGPPRAPPKG AASQRQLCGGFVEARQAVWGR GGRGPVGETQPPPSVIVQPPSRG AG/PRDQQPAMPEPPPTPSVGSC AARASQISAACPSTAPSIDHPR AEECRRTVWDWQAAPPAAQV RDPLGEASWAPESGGDVENLY VLLRDCKYTSQHPVSSSGVNA PIDTLYLATLLRDCKYTNRHSV SSSRFVNTPISTVSSSEFANAPID TLHLATLKEETPNTSEHQEQT PDMPPLRTVTATARVRFILDV SETKNPPIPDTFWPRPWRDRLRQS PSNQTLAFNEKNAALAAQEF GDTWYLSQVNDRMTAEERDKF PTEFIPSSGFLVLLTSRMKPQT AASVTALKDGVSRSVCSFCRVQS FFLPSADWCYKPLARYRALIG AFLQSAHWCVYKPLARHSVLI GAFTNL
12996	43364	B	13076	1	1999	
12997	43365	A	13077	3	469	
12998	43366	A	13078	224	410	
12999	43367	A	13079	478	675	
13000	43368	C	13080	55	237	
13001	43369	A	13081	109	239	
13002	43370	A	13082	2	88	
13003	43371	A	13083	2	178	
13004	43372	C	13084	278	460	
13005	43373	C	13085	50	217	
13006	43374	A	13086	3	251	
13007	43375	A	13087	1	759	
13008	43376	A	13088	2	604	
13009	43377	A	13089	1	558	
13010	43378	A	13090	3	1055	
13011	43379	A	13091	1	466	MDKFLDTYTLPRLNQEEVESLN RPITGAIEIVAIINSLPTKKSPGP GFTAEFYQRLISNFSKVSGYRIN VQESIQAFLYTINRQTESQIMSA LPLTIASKRIKYLGQLTRDVKD LFKENYKPLLINEIKEDTNWK NIPCSWVGRINIVKMAII.PK
13012	43380	A	13092	2	848	
13013	43381	A	13093	458	625	
13014	43382	A	13094	482	745	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=-possible nucleotide deletion, +/+possible nucleotide insertion)
13015	43383	A	13095	1	742	MNIDAKILNKILANRQIQQHKKL IHHDQVGFIQGMQGWIFNIRKSI NVIWHINRTRKDKNHMIISIDAE KVFDFKIQQPQFMLKTLNKLGDG TYLKILRAIYDKPTANILNGQK LEAFPLKTGTRQGCPPLSPLLFNI VLEVLRALARQKEIKEIQLGKE EVKPSLFAADDVIVYLENPUSVQ NLLKLISNFSKIKYLGQLTRNV KYLFKENYKSLLNEIKEDETNK WKNIPCSWIGRINIVKMAILPK
13016	43384	A	13096	1	1458	
13017	43385	A	13097	2	1624	
13018	43386	A	13098	1	1095	
13019	43387	A	13099	1	2913	
13020	43388	A	13100	2	1887	
13021	43389	A	13101	1	972	
13022	43390	A	13102	1	873	
13023	43391	A	13103	1	1365	
13024	43392	A	13104	1	867	
13025	43393	A	13105	1	591	
13026	43394	A	13106	1	990	
13027	43395	A	13107	1	2109	
13028	43396	A	13108	1	843	
13029	43397	A	13109	1	1203	
13030	43398	B	13110	1	1221	
13031	43399	A	13111	1	1092	
13032	43400	A	13112	1	931	
13033	43401	A	13113	1	1293	
13034	43402	A	13114	1	544	
13035	43403	A	13115	3	718	
13036	43404	A	13116	693	1397	ARAEVKLSLFAADDIVIVYLENPII *ARAEVKLSLFAADDIVIVYLENP IISAOQLLKLISKFSKVSRYKIN QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVVKDL FKENYKPLLNEIKEDETNKWKNI PCSWIGRINIVKMAILPKVYIYRF SAIPIKLPMITFFFTELEKKNWLAI CRKLKLDFFFIPYTKINSRWIKD LNVRPKTMKTEESLGNTIQDI GIGKDFMTKTPKAMATKAKRA SAQQKKLPSE
13037	43405	A	13117	1	2814	
13038	43406	A	13118	1	1302	
13039	43407	A	13119	1	1542	
13040	43408	A	13120	3	1327	
13041	43409	A	13121	1	1023	
13042	43410	A	13122	1	1448	
13043	43411	A	13123	1	1038	
13044	43412	A	13124	3	1711	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met ind	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
13045	43413	B	13125	1	1756	
13046	43414	A	13126	1	923	
13047	43415	B	13127	1	1515	
13048	43416	B	13128	1	1560	
13049	43417	A	13129	1	4032	
13050	43418	A	13130	1	2684	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSQLQRDLDSHTL MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTHL PKSTEYTFPSAPHHTYSKIDHIV GSKALLSKCKRTEIITNLYSDHS AIKLERIJKNLTSQRSTPWKLN NLLLNDYWVHNEMKAEIKMFF ETNKNKDTTYQNLWDAFKAV CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTSHSKASRRQ EITKRAELKEIETQKTLQKINES RSWFPPERINKIDRPLARLIKKKR EKNQIDTIKNDKGDITTDPTEIQ TTIREYYKHLHYANKLENLEEM DTFLDTYTLPLRNQEEVESLNR PITGSEIVAIINSLPTKSPGPDG FTAEFYQRAIYDKPTANIIANGQ KLEAFPLKTGTQRQGCPPLSPLL NIVLEVLRALARQKEKEIKGQIQLG KEEVKLSLFADDMMIVYLENPIV SAQNLKKLISNFSKVKSGYKINV QKSQAFLYTKNRQTESQLMSEL PFTIASKRKYLGLIQLTRDVKDL FKENYKPLLNEIJKEDTNKWKNI PCSWVGRINIVKMAILAPKVIYR FNAIPIKLPMTFTTELEKTTLKF WNQKRARIAKSILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIIPIHYN HLIFDKPEKNKQWGKDSLFB WCWENWLAICRRLKLDPFLTP
13051	43419	A	13131	1	1149	
13052	43420	A	13132	127	329	
13053	43421	A	13133	1	1132	
13054	43422	A	13134	1	1020	
13055	43423	A	13135	803	2009	
13056	43424	A	13136	1	1944	
13057	43425	A	13137	1	1282	
13058	43426	A	13138	1	2423	
13059	43427	A	13139	1	2694	
13060	43428	A	13140	1	1195	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13061	43429	A	13141	6082	6984	KLAQQRDALSPPLLFNIVLEVL ARAIQEKEIKGIGLGEKEVKLS LFADDMIVYVLENPIV\SAKPSPL RLISNVSKV*GYKIN\WQKS\QA FLYTNNTDKQESQIMSEL\PFTT ASKRIKYLGIQL\TRDVKDLFKE NYKPLLKE\UKED\TNKWKNIPCS WVGRINIMKMAILPKVN\YRFI NSMPSIPIKL\PM\TTFTELEKNYF K\VHMEPKKSPHCQVNPKTKEQ SWRHQRYLTSNYILQGYSNQK STISMVLVPKQHGTGKTE\IDQ WNRTEPSEITPHI\NYLIFDKPL LEKNKQWGKGFP\
13062	43430	A	13142	193	335	MVEEKLTLPKDEK*SKKQRSIY RKT\QELKNKNEKRNRKNKW QVKTH
13063	43431	A	13143	131	427	
13064	43432	A	13144	1	360	
13065	43433	A	13145	2	376	
13066	43434	A	13146	1	360	
13067	43435	A	13147	2	376	
13068	43436	A	13148	3	469	
13069	43437	A	13149	224	410	
13070	43438	A	13150	478	675	
13071	43439	A	13151	32	161	
13072	43440	A	13152	1	1671	
13073	43441	A	13153	1	1656	
13074	43442	A	13154	62	1295	
13075	43443	B	13155	149	320	
13076	43444	A	13156	12	89	
13077	43445	A	13157	28	417	
13078	43446	A	13158	2	440	
13079	43447	A	13159	190	553	EIVREGASFSIRHLRWSRHRKC RFSVKT\LTGEDPSTL\VEPS\DT I\ENVKAKI\QDKEGI\PPDQQR\I/ VSFAGKQL\EDGRD\SLSGY\NIQ KGSL\LLHPCV*DFRGGA\KKEE ESLYTTISPRKD
13080	43448	A	13160	3	415	PVK\VGA*GGQVINGVLAQV*L TVGPVGPRTHPVVIFPVPECRIG RDILSSWQNPH\TGS\LTGRVRAF MVGKAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A\TIKLNRRG VVIPTTSRFNSPIWPVQKTDGS W*TAADY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13081	43449	A	13161	5	405	HCCGIPHSIASEQDTYMAKEV WQWAHAHGIHWSYHVPFHLE AAGLIEQWNGLLMSQLQHOLG DNTLQGWGKVLQKVVVYALNQ RSIYGTSPPIARIHGSRNQGVEV EVALLTVPNDPL/GKY*LVPV TLHSDR
13082	43450	A	13162	138	387	
13083	43451	C	13163	184	297	
13084	43452	A	13164	1	430	
13085	43453	A	13165	1	867	
13086	43454	A	13166	35	601	CLSRRAASPVLASMSGRGKGTG G\KARAIAKAMSRSSSRAGRPSSQ VGRIVHRLLRKGHYS\AERVGIRR QPCCYLGG*CMEYLT*ESWS MAGINAARNNN\KKTRIIPRHLQ\Q LAIRNDEELNKLAWAALTIAQ GSR/VPNIQARCCGPR*TSATV GPKAPS\GEERA\TQASARSTK RARAAGRPSVPMPPQRF
13087	43455	C	13167	11	313	
13088	43456	B	13168	1	552	
13089	43457	A	13169	1	621	
13090	43458	A	13170	55	296	
13091	43459	A	13171	959	1182	WVYLF*PSCKGVIVY*AA\GFE\I FWWV\TINKNIDW\NYYNNQ QFMNYTRDAVKGIAEQLGTCNC QMAWENRIALDMILAERGVGC IMIKTECCAFIPNN\TAPNGSITK ALQQLTALSNELA\SSGGVNDPF TGWL\KWF\GKWK\G\TAS\ITL TAVMGVL\ILVGCCV\PCICGLV QRHRGPP\LVV\ETKPL\GLERLA GLPVG\HALKLGSGI\QATPQNGE NADR\REAFPAAS
13092	43460	A	13172	1	540	
13093	43461	A	13173	2	142	
13094	43462	A	13174	42	384	
13095	43463	A	13175	102	329	
13096	43464	A	13176	1	1257	
13097	43465	A	13177	1	378	
13098	43466	A	13178	1	1143	
13099	43467	A	13179	1	481	SDSE\LNRP\RVTMKFN\NPVTS\DR SKNRKRHFNAPSHV\RKIMSSP LSKELRQKYNVRSMPIRKTD\DEV QVVRG\HYKGQQ\GQGSPR\CTR KKYVIVYIERV\QREK\ANGTNCS TWGISP\KARWL\FT\RLKLDKDR KKI\ERKAKS\RVGKE\GKYK EELIEKMQE

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13100	43468	A	13180	39	556	AAAGYFAEDCEASCVCVKHP SVKKARCFLSL <sup>IK</sup> KP <sup>S</sup> GG <sup>S</sup> VT <sup>L</sup> SESTAIS <sup>H</sup> GTTG <sup>L</sup> VTW <sup>D</sup> AT <sup>L</sup> Y <sup>L</sup> AEWAIE <sup>N</sup> PAAF <sup>T</sup> NRT <sup>V</sup> LE <sup>G</sup> SG <sup>G</sup> AGLTG <sup>V</sup> AICKMYR <sup>P</sup> R <sup>A</sup> F <sup>I</sup> F <sup>S</sup> DC <sup>C</sup> HSR <sup>V</sup> LEQLRG <sup>N</sup> V <sup>V</sup> LLNG <sup>S</sup> LEAD <sup>D</sup> ITANLDSPRV <sup>T</sup> V <sup>V</sup> AQLDWDV <sup>V</sup> AT <sup>V</sup> VHQLSAFQ <sup>D</sup> V <sup>V</sup> IAADV <sup>L</sup> Y
13101	43469	A	13181	46	231	
13102	43470	A	13182	1	1503	
13103	43471	A	13183	3	340	FFFANTFYCVFNVLVNAPRLF <sup>L</sup> SLP <sup>S</sup> TQS <sup>L</sup> EAKL <sup>R</sup> DSS <sup>S</sup> DL <sup>R</sup> R <sup>D</sup> ILQKV <sup>R</sup> IP <sup>E</sup> SL <sup>G</sup> ML <sup>T</sup> LP <sup>P</sup> ESLR <sup>K</sup> T <sup>*</sup> EKNRRCACTL <sup>*</sup> K <sup>T</sup> TPV <sup>Q</sup> R <sup>T</sup> K <sup>P</sup> LSQHCRWV <sup>V</sup> W <sup>A</sup> PT <sup>P</sup> AP <sup>T</sup> AL <sup>S</sup> FSKT <sup>T</sup>
13104	43472	A	13184	2	594	
13105	43473	A	13185	1	1470	
13106	43474	B	13186	79	1355	
13107	43475	A	13187	248	540	
13108	43476	A	13188	386	1388	
13109	43477	A	13189	386	1334	
13110	43478	A	13190	3873	4070	
13111	43479	A	13191	146	510	PPCAVVCLLWIAAVYCLSTTF <sup>C</sup> APLCGQNTWLPKPCRHNRAA <sup>C</sup> SNASVSLSTVTLFSRLS* <sup>P</sup> RKG <sup>G</sup> SELLDSSGPLPASPSLPLCGVS <sup>G</sup> PRAGLGSAWPKIPFLGIREAKN <sup>K</sup> PRSENTRLTT <sup>T</sup>
13112	43480	A	13192	21	95	KCSSNGAPDAVHE*DLPWTPGP <sup>G</sup> AC <sup>G</sup>
13113	43481	B	13193	1	477	
13114	43482	A	13194	228	935	PLSSSMAAELEFAQIIIIVVVVTV <sup>V</sup> MVVIVCLLNHYKV <sup>V</sup> STRSFINR <sup>R</sup> PNQSR <sup>R</sup> REDGLPQIMHAPRSRD <sup>R</sup> RFTAPSFIQRDRFSRFQ <sup>P</sup> TYPYV <sup>V</sup> QHEIDLPTISLSDG <sup>E</sup> EP <sup>L</sup> LYQV <sup>V</sup> PCTLQLRDPEQQMELNRESVRA <sup>R</sup> PPNRTIFDS <sup>D</sup> L <sup>L</sup> DIAMYSGGCP <sup>C</sup> PSSNSG <sup>S</sup> ISASTCSSN <sup>S</sup> GRMEGPP <sup>P</sup> TYSEVMGH <sup>H</sup> PGASFLHHQRSN <sup>N</sup> AHRGSRLQFQQNNAESTIVPIK <sup>I</sup> GKDRKPGNLV <sup>V</sup>

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13115	43483	A	13195	526	1629	FYSFD SARGE PARPWR VRGLEG RVELGQQLG LTLGP APPG GLG GTQR VGLPGPAG PGAG EEG QA GPAE AGQV PVGGLADE AVE VH G VGDA VE AGE QEGE VVG VEN AL GEVAAGL PDA AHQQH VHV GQ EAG QEDD HGA EH QPL DLV LAA LLGAVAPAHGAQ DALV GRQQ QAD GEEE A/LPGS GS* WHA AM PGW GS A QSTRGAGS RPR * PPRA SGSRC WSA APW PR * PR RRP SGS GTGGS GRD GPQ PG SGP R/T MQQR KPTLM MFSY RR V RTPG RTG RRE TSCRA AART AAR RA SRC RRG RPPS GCTG T RPAR SG* SAGS IE VEG QAV G REAH HQ HG NID HRG QRL VDGM V DTA HRG VVC SDV PH
13116	43484	B	13196	2699	7361	
13117	43485	A	13197	67	1523	
13118	43486	A	13198	1	287	
13119	43487	A	13199	2	563	
13120	43488	A	13200	96	401	
13121	43489	B	13201	1	480	
13122	43490	A	13202	1	924	
13123	43491	B	13203	13	1512	
13124	43492	A	13204	1	402	
13125	43493	A	13205	609	803	RDPR HNPSSA /FQAGGI ALLMLI TRGEDLTGGV I H QY PPG GMNL WMQGTAGN QRR AENA AQQQ
13126	43494	A	13206	3	526	VTET AL TPYL VAKH GYFLP QD LAKR TET MNWLFW LQGA APFL GGGF GHF YHY APV KIE YAIN RF TMEAKR LL DVLDK QLAQ HKF V AGDEY TIADMAI WPW FGN VVL GGVY DAAEFL DAGSY KHV QR WAKE VGER PAV KRG RIV NPTN GPLNE QL HER HDPS DFT NT E NNR QG
13127	43495	A	13207	1	250	
13128	43496	A	13208	1	489	
13129	43497	A	13209	209	601	
13130	43498	A	13210	1	96	
13131	43499	A	13211	1	1110	
13132	43500	A	13212	1	595	
13133	43501	A	13213	1	240	
13134	43502	A	13214	1	675	
13135	43503	A	13215	1766	1957	
13136	43504	A	13216	1	426	
13137	43505	B	13217	94	3238	
13138	43506	A	13218	1	2370	

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13139	43507	A	13219	1	2796	
13140	43508	B	13220	43	566	
13141	43509	A	13221	1	903	
13142	43510	A	13222	3	110	
13143	43511	A	13223	2	755	
13144	43512	A	13224	1	1338	
13145	43513	A	13225	1	807	
13146	43514	A	13226	1	918	MARAD EPTVSVPMFMGLAAKPC WRDTEPNTGYRGPVHVRNIQLT HDPRLDYRSI/LIDINDIGQTFH ERLHPDAC\LSNAILVHNKKGP LADGIVITPSHNPPEDGGIKYNP PNNGGP\VP TSLKWWKTGPTH CWPMA*KA*SVSP\RRSDGIRSKN DVIDTSDDDM**QCLSRRSN\G HPGAKVANLVPKTTFIDGVQDT SFFLGTNGQSNRKAEHYFLNGK LAAVRMDEFKYHVLIQQPYAY TQSGYQGGFTGTVMOTAGSV FNLYTDPOQESDSIGVRHIPMGV PLQTEMHAYMEILKKYPPRAQI
13147	43515	A	13227	1475	2904	FWRAA APIPDCWRSGAVKKQH VEVTQLDWTPPGROYAGIPCS RRGYCPPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTTSFLGTINGQSNRKA EHYFLNGKLAAVRMD EFKYHV LIQQPYAYTQSGYQGGFTGTV MQTAGSSVFNLYTDPQESDSIG VRHIPMGVPLQTEMHAPGLPLA SSMKRWIRRATGFIFGKEQFED VVPVLGSKVNGVQFN AELVAD SLGISQIRCRAIFLTVVFFPV LH KQAFDLISLLLQQPGRNGGIDT AGHADDYFFCGFRIWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVVRPKGVVAFTT LVQGSLPELHQAWQAVDERPH ANRFLPPDEIEQSLSNNGVHYQHH IQPITLWFDDALSAMRSLSKGIG ATHLHEGRDPRILTRSQLQLRQ LAWPQQQGRYPLTYHFLGVI
13148	43516	A	13228	215	525	LAWARRCCRRLLA KATSLIRAPS SEMRASTPCRGQRRPSGYSWY GRSPRAVLEGLRVGAHLSRAN CPWPSSR/SQVVELIPDGFVFLD FTKIPGRDTQNEHIVLLH
13149	43517	A	13229	1	942	
13150	43518	B	13230	1	1201	
13151	43519	A	13231	685	921	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ~=possible nucleotide insertion)
13152	43520	A	13232	2	251	
13153	43521	A	13233	2	100	
13154	43522	A	13234	5	1093	
13155	43523	A	13235	2	482	
13156	43524	A	13236	1	2496	
13157	43525	A	13237	572	912	RCRPDKAFTPPhPAIGARCLMRR LRVLSCQLPLNVGWRRLRRIR QFSAPDEGAKCRVAILQ/DFDA QYGRFLEVTSQGAQQRFEQTD*K HAAALPFFFPSSAYSLAAISVVF GFR
13158	43526	C	13238	5	127	
13159	43527	A	13239	1	444	
13160	43528	A	13240	17	261	
13161	43529	A	13241	173	397	
13162	43530	A	13242	169	421	LKPKNLDEKLLPAssSSCRIWA TSPVHHLWQVLKKKILFGWNPT KSPRCLS/TRQAMFSLSKKASLP WTIAARSADQRCCRTRIAEL
13163	43531	A	13243	17	744	RPHQEQRIGCGVNAISSLRSA TAVGMIRRASVASG/DRAPIAG CGVNAISGLHRHFIEVTCHFL LVRYEGIAIFRGGKFRLHHFLN VVLHTLALGIGVCQVKHVEPH AVDTQCGDEELVHIRQLLLE AGNSFVVEVYLPPERARRAVISQ QFARIFRVDSLCKATRQFOIRRG RSHQTGQHMGIRRQVDAAHAD DRRTSGRVPPLIQVCPAHSSEA VVVVVDVVDVVDVVDVVGAV
13164	43532	A	13244	954	1104	
13165	43533	B	13245	54	1169	
13166	43534	A	13246	35	3066	VGHSTRPAASPGPAAGIGRSPA RLVQQPQRSLAKPLNRPQAQR GLLPQRRHPKRTRKRRKQAQN PQKRLPHRQPVRRRHRRHRL QKMRRPDKRQQRRAAPRRHPR RRQRLLAVRRLQLRAKVRRN RQRAPRQQLNGQRLILHPWRLR MQVRKRG*YSSAVRPTVRLK RWRQRQRQ*NQPMTMQRNV RKTRTALIYP/YKGCLNNINAV SKTDFADKRGMRVYVRVNAPAG ATSGKYYPPVVVMRSAGSFHI
13167	43535	A	13247	1	2919	

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13168	43536	A	13248	1	3211	MEFTSLTPDDLRLVLELYRTPFS DGYVFHSMQFHIFDLLKGQN VVLsapTSMGKSAIVDSLGMG TLKRLVLVVPPTVALADETRRRRL QERFGDRYQIIHHSSQVCHSDQ AVYVLTQERVNERDIDVIDLF VIDEFYKLAFRQLKSGDIDHQD ERVIELNIALSKLLKVSRQFYLT GPFVNISRGLEKLGYPTHTFVST DFNTVALDVKTASKRMTITKP SSKRWGKSRTCVDAHDHKNGI LHF GALP RALQQYT
13169	43537	A	13249	486	3882	LRLRGAEALPVASGCLANATDTP AGTTLWADTERHAVQ*+TCEA DTLGSCGYAAKPCLSPVAVWQ MLLTRLLEQHYGLTLNDTPFSD EPVLTAPIDAALRGIIEFGKFQL GNMVVGDIIECGSDVTDYAVG DSVCGYGPLSETVIINAVNNYK LRKMPQGSSWKNACVYDPAQF AMSGVRDANGARRGEFWWGGL GAIRVQLAFKWLNAAAGRLLPGG GLGGPIPYSAHRCIARRHGAD FCLNPIGTDVGKEITLTG
13170	43538	B	13250	1	1116	
13171	43539	A	13251	729	985	SAPPOLAPSLPDRATDPDTCP PG*RPVRYLPSRQIDCFNTRFRLL QRLTASQCAEAVDVAFFRLTV QQT PHFRCAQLRQRAFRID
13172	43540	A	13252	395	605	
13173	43541	A	13253	1	1140	MIYVFVTVKHRNDHFTKNTLA SYRGRPLLGLTLFGKVWVLYKD ETYLYQSGKGHTIQEVIRIVKGL NNPDLDAAVGEDLAQQLRDEL ELVKGASNEFDKELFLAGEITP VFFGTALGNFGVDHMLDGLV WAPAPMPRQTDTRVEASEDK FTGFVFKIQQANMDPKHRDRVA FMRVVSGKYEKGMKLQRQVRT AKDVVISDALTFMAGDRSH/AY PGDILGLHNNHGTIQIGDFTTQG EMMKFTGIPNFAPELFRRIIRLK DPLKQKQLLKGLVQLSEFGAV QVFRPISNNNDLIVGAVGVQLQFD VVVARLKSEYNVEAVYVESVNV ATARWVECADAKKFEEFKRKN ESQLALDGDNLAYIATSMVN LRLAQERYPDVQFHQTREH
13174	43542	A	13254	1	1495	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, -=possible nucleotide deletion,  =possible nucleotide insertion)
13175	43543	A	13255	372	1365	IRYPENRGLFAHCATRGQFPP HCILASYKCGEOPDSSSNHPRN LFVWRSNLGGSSKGKHEYMQ KYLLCTESGIQGEELGASDGKIP EEVEWQTAIEGKLDLLVTLDF RMSSTCLFSDIVLPTATWYEKD DMNTSDMHFPFIHPLSAAVDPA WERSRSDWEIYKGIAKAFSQVCV GHLGKETDVVLQPLHIDSPAEL SQPCEVLDWRKGECIDLIPGKTA PNIVAVERDYPATYERFTSLGP LMDKLGNGMDLTDYANMALSI PSANTDIWNLEQDTVGTRLTNS RHGLADNGGAWSYFFGNFN GDNGTINYDQDVNGIMVGVDT KIDGNDG
13176	43544	A	13256	3	1444	
13177	43545	A	13257	61	1058	LPYLIALLARAWFNGLLTSRTR LYIKGNGIVDPLKLQEMVADVS HHFPLRLPAPTPKALYSPCEIRH LAINVNLEYDPTAAFRNQVVF DFRKLDVFSFGENQNCVLGVNV DLYVRNSWNEVRTLHFNGEQS MIEALKTILGKMHQDAAPPDSV EVFCYSQHLRGLIIRTVQQQLVS ECIELRLSSTRQETGRFKALRVS GQTWGLFFERLNVSVQKLENAI EFYGAISHNKLHGLSVQVETNH VKLPAVVVDGFASEGIIQFFFET QDENGFNIYILDESNRVEVYHH CEGSKEELVRDVSRFYSSSHDR FTYGSSFINFNLQDPYLRARVSI
13178	43546	A	13258	1	1133	
13179	43547	A	13259	2	240	ISSARHFGALACTLELGKALTF GQNDLRQFAVTASAIAALL/SR HSPSFEMHMASDTLNFMPFEK GTILLAQDGEERFTVTH
13180	43548	A	13260	1	358	LPFLPSGLRGLAAENKIRPRHSA GSFLGPPCGLRLGKLV/ISAAALM STTIPISRVQGLLQFLNSKSPISR AERSWSTFGASAALFTTLASLL FLFPLLAISSSLANSFAKVFPPTC AGSP
13181	43549	A	13261	1	1635	
13182	43550	A	13262	1	1363	
13183	43551	A	13263	5	249	
13184	43552	A	13264	15	280	
13185	43553	A	13265	6	363	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
13186	43554	A	13266	78	346	TRYAMLTRHDNHLSKFYLARG RYRADFHAPETNTGERCYRYK PLPYWLE*RRGRNRYPALQ*TM FLPADGPARCLSQRQAAILKESV LPK
13187	43555	A	13267	568	831	ELQRHVLVVFAGFWIKVNSRN LFLVCRAEHKRSVVKGLLRQQ GQGFWFHFQDGFAVEVGNAN VIGSE*IVFGIVFPHRERCLVDK
13188	43556	A	13268	3	419	
13189	43557	A	13269	1	561	
13190	43558	A	13270	1	741	
13191	43559	A	13271	2	1040	
13192	43560	B	13272	1	1974	
13193	43561	A	13273	2111	2340	EVFIRDKLMERRNRRTRGTEKA /DRRTVRTWIGEAVAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPVKVLQSC1
13194	43562	A	13274	470	813	KTTSFPAKLFNACRISLLASAEV NPNSIAYLATWISQIPSCSCKRP SDFLIWSTNRYSIRF*SERLVG EAVA/AAAADGVTFSVPVTPHT FRHSYAMHMLYAGIPLKVLQSL LMGH
13195	43563	C	13275	440	1180	
13196	43564	A	13276	1	1290	
13197	43565	A	13277	1	1036	MKLMETLNQCIAGHEMKTAKI AIAQFNDDSPSPEARKitRRWRIG EAADLGVGVSSQAIRDAEKAGR LPHPDMMENSRRDRFEQRGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMSVLKNVVRRETDEVG KDPRPLPYLGHDEPYTFDINLS VNLKSMVVGTDGMQEPLKQ MGAWGPLSLKAMGFFIRGYG FFTFFGRRTLPLGFGSTPPFTPL LTKTIGVFIIDKLMERRNRRRTG RTEKARIWEVTDRTVRTWIGEA GAAAADGVTFSVSVTPHTFR HSYAMHMLYAGIPLKDLQSLM GHKSISSTEGYTKDFSLDVG1AR HRVQFAMPIESDAVAMLKQLF
13198	43566	A	13278	366	672	RNGTHIPRYIEAVPVWGLPAD/G VTFSVPV/TPHTFRHSYAMHML YAGIPLKVLQSLRQLRELQQAV HAGLPQQAKILFDGGSEIGKIPH IVLYKPVQCSLWAFVH
13199	43567	A	13279	2602	2976	
13200	43568	A	13280	982	1347	
13201	43569	A	13281	1	780	
13202	43570	A	13282	568	891	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=possible nucleotide deletion, !=possible nucleotide insertion)
13203	43571	A	13283	1	718	MKEKPSSPRQYSYSFLSSMILLGGGESWNLLRADQRQLFAKSWPRASRYQQGHQDQLFLRSRDLPSQVFIRDKLMERRNRRTGRTKEARIWEVTDRTRVTW1GEAVAAAADGVTFSVPVTPHTFRHSYAMHMLYAGIPLKVLQSLMGHKSI STEVYTKVFA LDVAAPAHPESTPVHLPRENKIPPPIMRIPCGLPTSPIEQKQKGKISATGTQWRRLKQETRLSSVSARLMSYVGVC
13204	43572	A	13284	1	496	AMFGFFIRGYGFFTPGRTLFPLGFGSTPPFTPLLTKT1GVFLDKLMERRNRRTGRTKEARIWEVTDRTRVTW1GEAGAAAADGVTFSVTPHTFRHSYAMHMLYAGIPLKDLQSLMGHKSISSTEGYTKDFSLDVGVARHRVQFAMPESDAVAMLKQLF
13205	43573	A	13285	2	545	
13206	43574	B	13286	1	735	
13207	43575	A	13287	1	1599	
13208	43576	A	13288	583	1005	
13209	43577	B	13289	31	1239	
13210	43578	A	13290	1	1023	
13211	43579	A	13291	1	933	
13212	43580	A	13292	1	1278	
13213	43581	A	13293	1	705	
13214	43582	A	13294	2	893	
13215	43583	A	13295	88	429	
13216	43584	B	13296	1	1419	
13217	43585	A	13297	1	2784	
13218	43586	A	13298	163	416	RNGTHPRYIEAVPWGALPAD/GVTFSVPV/TPHTFRHSYAMHMLYAGIPLKVLQSLRALKRELQQAVHAGLPOQAKILFDGGSEIGK1
13219	43587	A	13299	740	1431	CCQTLPVFHPPHPSHLGRPRCPPTH/HLSPEHRSLFLEAACHDSDSLEPLNLSSGSKTKSPSLPPKAKKPKGLEISA/RPAGALRHRHLHRPQQPSPLGLIPHPSLLATAQVFIRDKLMERRNRRTGRTKEARIWEVTDRTRVTW1GEAVAAAADGVTFSVTPHTFRHSYAMHMLYAGIPLKVLQSLMGHKSISSTEVYTKVFA LDVAARHRVQFAMPESDAVAMLKQLS
13220	43588	B	13300	1	858	
13221	43589	B	13301	1	1098	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13222	43590	A	13302	I	1047	MNRQLSDSYTEDTKEPSDVTTS ERTRSPPGSAKTTMIDLKKLQ DVLKTEDSKNPTKSAADLLEQ YVKATGPHEILQKATKTMEMI MIVEEKASDELQPDPELQQRYI HSVRKGPGLVKQRTQEIETRLR LAGLTVSSPLKRSHSLAKLGS TFSTEDLSSRPGPPPGPPGLHP GPPRPRPPPKLPPPAPPGCSVHC CHYPLHFVVSPLEGFYCSLMRI QIVFVTAFVHDSALLPLDASL APEALQNFORYTGQIVHRIGM AERMWCDRNRERHTVSSGGN RLPNPAPLPNPGVLSAPPNLIQR PKADDTSAAATIEKKATATISAK PQITNPKAET*NPVWQGSWI GEAVAAAAADGVTFSPVPTPH TFRHSYAMHMLYAGIPLKVLQ SLSRQ*SVRGKPGLVKQRTQEJ ETRLRLLAGLTVSSPLKRSHSLA KLGLSLTFSTEDLSSRPGPPGP PPGLHPGPPPRPPPKLPPPAPP GCSVHCCHYPLHFVVSPLEGFY CSLMRIQIVFVTAFVHDSALL PLDASLAPEALQNFORYTGQIH VHRIGMAERMWCDRNRERHT VSSGGNRNLPNAPLPNPGVLS APPNLIQRPKADDTSAAATIEKK ATATISAKPQITNPKAETRFCPL
13223	43591	B	13303	I	1185	
13224	43592	A	13304	529	774	
13225	43593	B	13305	I	1089	
13226	43594	A	13306	712	1024	GVESNLVVVVALCHRLIYLVW GTRTVRTWIGEAVAAAAADGV TFSVAVTPHTFRHSYAMHMLY AGIPLKVLQSIVVVALDVAARH RVQFAMPESDAVAMILKQLS
13227	43595	A	13307	556	1040	
13228	43596	A	13308	I	984	
13229	43597	A	13309	95	428	
13230	43598	C	13310	I	426	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, =Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13231	43599	A	13311	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEA/AAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIERYQLPQSYQLY YFELAIPVGYFPGSFSTASRL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIKLQCGG VVKQLSRRGNNNQHISSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIIARLTWVIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMSVLKNVVRRETDEVG KARLTWIGIGTINVVCAADVLIV PTPAELFDYTSALQFDDMLRDL LKNVDLKGFPDVRIILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVVRRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFAVDVAAR HRVQFAMPESDAVAMLKQLS
13232	43600	A	13312	1	1593	
13233	43601	A	13313	1	2536	
13234	43602	A	13314	887	1205	RPEKAR/IWGVTDRTVRTWIGR AVAAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEVYTKVFAVDVAAR HRVQFAMPESDAVAMLKQLS
13235	43603	A	13315	79	351	
13236	43604	A	13316	1	2320	
13237	43605	A	13317	187	798	
13238	43606	A	13318	2089	2610	
13239	43607	A	13319	1	1407	
13240	43608	B	13320	154	3682	
13241	43609	A	13321	1	1206	
13242	43610	A	13322	1	255	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13243	43611	A	13323	3058	3160	GSAA*LPPPLPAAFSGSCWLSQLRHPELHV*NEIYHLLH*KSFTSC*HNLSS*PRVPPYLSSERVLW*CLSFISIKI*SVTMP*SDLISLW*KLEPLTCRSTSHFRQKLAQ/RLP/AYQQGHQDLFLIRSDLPSQVFIRDKLMERRNRRRTGRTEKARIWEVTDRTVRTWIGEAAAAADGVTFSVVPVTPHTFRHSYAHMMLYA GIPLKVLQSLMGHKSISSTEVYT KVFALDVAARHRVQFAMPESD AVAMILKHYPEINALALYLKCG TEWIC
13244	43612	A	13324	1	1812	
13245	43613	B	13325	1	1776	
13246	43614	A	13326	583	751	
13247	43615	B	13327	826	2097	
13248	43616	A	13328	1810	4163	
13249	43617	A	13329	686	2939	
13250	43618	A	13330	1085	1690	SYFIMVKVGTSYVPINVSFSPKV GPGASRYQQGHQDLFLIRSDLP SQVFIRDKLMERRNRRRTGRUIYK ARIWEVITDRTVRIWICRGGL PAAAADGVTFISDPGPPIHTFRH SYAMHMMLYAR*YR*KFLQSLM GHKSHPINGKATPKVFPGPMG LARA/HRGAGWQWPKSDAVG\IMPKQLSLRINALGLYMETGKPE GIMLFFGC
13251	43619	A	13331	3	327	
13252	43620	A	13332	3	337	
13253	43621	C	13333	167	413	
13254	43622	A	13334	1	1256	
13255	43623	A	13335	1	1078	
13256	43624	A	13336	3	976	
13257	43625	A	13337	1	1004	
13258	43626	A	13338	2	291	WRKIYEANGKKRKQRLQS*SL MKQTLNQQRSKETKKASA/SM RIKYLGIQLTRDVKDLFKENYK PLLNIEKEDTNKWKNICPSWVG RINIVKMAIPPK
13259	43627	A	13339	1	2022	
13260	43628	A	13340	1	2262	
13261	43629	A	13341	5	283	
13262	43630	A	13342	1	1245	
13263	43631	A	13343	1	1203	
13264	43632	A	13344	1	687	
13265	43633	B	13345	1	1371	
13266	43634	A	13346	1	2241	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met. ind	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
13267	43635	A	13347	1	832	LKKCIKTPPEIPSKHVRNWVPKV LEQRQQGLETYLQVASITLIPKA DEDTPKKTTDKNSWITGTDAK VFNKILEIKFSSILKRLYWPVLE VLARAMRQEKEIKG^QLGKEEV KLSRFADDIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIRKYLGQ LTRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWGRINIVKM AILPKRYPFCQLCHQSIASTTKG VFTSILPLLMIEQLVSGRSCPSV AWSSMECTTV
13268	43636	A	13348	1	1314	
13269	43637	A	13349	1	843	
13270	43638	B	13350	1	1011	
13271	43639	A	13351	1	173	
13272	43640	A	13352	1	323	
13273	43641	A	13353	3	2020	
13274	43642	A	13354	1	1473	
13275	43643	B	13355	1	636	
13276	43644	B	13356	1	456	
13277	43645	A	13357	1	619	
13278	43646	A	13358	1	1293	
13279	43647	B	13359	79	1041	
13280	43648	A	13360	3	718	
13281	43649	A	13361	1	612	
13282	43650	A	13362	1	992	
13283	43651	A	13363	1	1236	
13284	43652	A	13364	1	1071	
13285	43653	A	13365	359	1250	KLPMGVAVVKLLHLPKVIIIVFW LASWMMSRWLHYPDWVTHIAQ QVLMNVVSVMQADCRMNLLEI FLRWLMLRKIFHVRLLPAVSTPP NCLNQLLLFLTPVNYLPGQVM HFKKPLQIKRNYLSSRHTLFMS RKKLGKVSG^YKIHVQKS^QAF^L SANSQTESQIMSELPEFTMASK RIKYLG^QLTRDVKDLFKEKYK SLLNEIKEDETNWKWNPCSWV GRINIMKMAILPKVIVRFNAIPI KLPMTTFFTELEKTTFKFIWNQK RAHIAKSNLSQLKNKAGGITLPD FKLYYKATVTKT
13286	43654	A	13366	1196	2132	
13287	43655	A	13367	1	2271	
13288	43656	A	13368	2	1105	
13289	43657	A	13369	1	2117	
13290	43658	A	13370	1	1447	
13291	43659	A	13371	1	1669	
13292	43660	A	13372	1	2823	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last a amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
13293	43661	A	13373	1089	2539	
13294	43662	A	13374	1	1787	
13295	43663	A	13375	1205	1207	
13296	43664	B	13376	1	2745	
13297	43665	A	13377	1	2063	
13298	43666	A	13378	1	4380	
13299	43667	A	13379	1	3347	MGDFNIPLSTLDRSTRQKVNKD TQELNSALHQADLIDSYRTLHP KSTETYTFSSAPHHTYSKIDHILG SKALLSKCKRTEIIITNYLSDHSA IKLELRKKNLTQNCSTTWKLN LLLNDYWVHNEMKAEIKMFF TNENKDTTYHNLWDAFKAVCR GKFIALNAHKRKQERSKIDLT SQLKELEKQEQTHSKASRRQEI TKRAELEKEIETQKTLQKINESR SWVFERINKIDRPLARLTKKKS EKNQIDAIKNDK
13300	43668	A	13380	1	2367	
13301	43669	A	13381	1	1116	
13302	43670	A	13382	1	1095	
13303	43671	A	13383	670	1500	QTESSSTSKSLSTMKWA SLWGWFNIRKSINVIOHKIGIQR QKPHDYLNRCKSL*QNSTTLH AKNSQ*IAQNLKKLISNFNKVS GYKINVQKSQAFLYTSNRQTES QIMSELPTIASKRKYQLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPKLPMTFTTELEK TTLKFIWNQKRAHIAKSILSQK NKAGGITLPDFKLYYYKATVTKT AWYWYQNMCYRSMEQNRLS YYVAYLQPSDL
13304	43672	A	13384	441	3131	
13305	43673	B	13385	1	5688	
13306	43674	B	13386	916	2165	
13307	43675	A	13387	1	1529	MDPPAGAARRLLCPALL*PLAG *PLRPRLAGAAPAPGTALLHER AMPL*LRPGLHDVHGPDL
13308	43676	A	13388	1	714	
13309	43677	A	13389	3	457	
13310	43678	A	13390	2	492	
13311	43679	A	13391	3	1201	
13312	43680	A	13392	1	309	
13313	43681	A	13393	2	1073	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
13314	43682	A	13394	3119	6984	CIVKHAAMRSAMTSLAARITVL NPTRATTPTNT/RVADDQGFLRQ WSKVAKERKLQRLVYIPEPSAEA VAAQMPD/LILISATGGDSALAL YDQLSIAPTLIINYDDKSWIHPR LSFNKADE/TTVFCGSKKSLAN GIPMANILFPTSVIATQQTQHFR FVDDFNAQFLRFASLDPAASPA ITISGKATLEIPGTELVFYAALE KKLNIKPGQTTFDGRFLILLPTC CLGNCDKGPNMMIDEDETHAHL TPEAIPELLER
13315	43683	A	13395	3	587	
13316	43684	A	13396	1	315	
13317	43685	A	13397	430	636	
13318	43686	A	13398	1	84	
13319	43687	A	13399	1	1647	
13320	43688	A	13400	1	2652	
13321	43689	B	13401	1	1494	
13322	43690	A	13402	1	750	
13323	43691	A	13403	1	513	
13324	43692	A	13404	1	2254	
13325	43693	A	13405	1	746	
13326	43694	A	13406	3	428	LGDDFVRAANIIILHCEGKVVVS GICKSGHIGKKIAATLASTGTPA FFVHPAEALHGDLGMIESRDV MLFISYSGGAKELDLIPRLEDK SIALIGKPTSPGLAAKAVLDIS VEREACPMHLAPTSSTVNTLM MGDALAMAV
13327	43695	A	13407	1	1431	
13328	43696	A	13408	943	2481	
13329	43697	B	13409	1	783	
13330	43698	A	13410	3	729	
13331	43699	A	13411	1	843	
13332	43700	A	13412	3	128	
13333	43701	A	13413	1	136	
13334	43702	A	13414	1	492	
13335	43703	A	13415	3	619	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13336	43704	A	13416	1	1600	GQACHASSPLKGSGRSPPNFEI LYGPIFEDSLAPD*PKVIAGQIT LRDAVTGPISSPNEAGKIYQLKP NPAVLICRVRGLHLPEKHWTV RGEAIPGSFLDFALYFFHINYQA LLAKGSGPYFYLPTKTSQWQEA AWWSEVFSYAEDRFNLPRTKIK ATLIELTLPAVFQMDIELHALR DHIVGLNCGRWDYIYSYIKTLK NYPDRVLPRQAVTMDKPLN AYSRLLIKTCRKRGAFAMGGM AAFIPSKEDEHHNNQVNLKVKA DKSLEANNGHDTWIAHPLGA DTAMAVFNDILGSRKNQLEV REQHAPITADQLLAPCDGERTE RKFNALMESEKGQSQNLWKFA VYSGLRHGEAALAWEDVDLE KGIVNVRRNLTIDMFGPPKTN AGIRTVTLLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPRVCNGKQKPYYSV SSLGARWNAAVKRAGIRRNP YHTRHTFACWLLTAGANPAFIA SQMGHETAQMVEIYGMWID DMSDEQIAMLNARVM
13337	43705	A	13417	2	278	
13338	43706	A	13418	3	662	GHLWIRIDLSQLSAVSHSVKELE NHTGVRLLDRTTREVVLTDAG QQALARLERLLDEINSTLRTDG RMGQQQLSGKVRVAASQTISAH LIPQCAESHRYYRDPDIQFVHLHDR PQQWVWMESIRQGDVDPFGIVIDP GPVGDLQCEAILEPFFLLCHRDS SALAVEDYVPAVPLPPEGSPVV KRITPVVERQLMLVRRKNRSL TAAEALWDVVRDQGNALMAA
13339	43707	A	13419	1	646	QQQLSGKIVRVAASQTISAH LIPQCAESHRYYRDPDIQFVHLDRPQ QWVMSIRQGDVDPFGIVIDPGP VGDLOCEAILEPFFLLCHRDS LAGGDYVWPWQALQGAKLVLQ DYASGSRPLIDAALARNGIQAN IVQEIGHPATLFPMVAAGIGISIL PALALPLPEGSPVVKRITPV RQLMLVRRKNRSLSTAAEALW DVVRDQGNALMA GRE
13340	43708	A	13420	1	1068	
13341	43709	A	13421	1	381	
13342	43710	A	13422	3	938	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13343	43711	A	13423	595	1630	CSWHDHRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSGG QAVKGNGQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGITIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLQESG QDFADFGITIKQDFRLLGQTSV DRLLQLSQGQAVKGQNLQPVLS LVKRKTTLAPNTQTA SLMQLARQVSRLQESGQDFADF GTTIKQDFRLLGQTSVDRLLQ SQGQAVKGNGQLLPVSLVKRK TLAPNTQTA SPRALADSLMQLA RQVSRLQESGHYDHYEFELGTR FRAVIKLCNGDSLRFHMTSVY ALVKCFHEGDPLHKTGCQHLLP KQQQNQEKYQVQPFQDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVEMLLREAGKAGFC RFRNHHQTFGSPAGANQRGPL AATLSGPQGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGNSYDHDYEFELGTHQ RLGAVARIVGDDLLNELRRDV VDARAGDVQHAAEKGDFR
13344	43712	A	13424	1	1395	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=possible nucleotide deletion, + =possible nucleotide insertion)
13345	43713	A	13425	1307	1992	DKLNPVAHQKAYLAQSSQCHP QNARLVQHTQIRILPISEPPSNRI FACWGKPAWTACCN/FSQGQA VKGNQQLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNNQLPVSLV KRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQLKHEVESPNRPI TSSEIQLVLIKSLPIKKSPGPDGFT AEFVERYKEELVPFLLKLFOTIE QERLLPNSFYEAISIILTSPKSRD ATKKDNFRPTSLMNIYAKILNK IGQTESSSTSLSLFSTIKSVSSPE CKAGSTYANQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQA VKGNQQLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQETTPWSPFSDPVLAFDY KVFMAFVYNVVRVSQRMVVA GCISAFNDKLLNDLICFPVAVPS SKQIFPSDVKAEPDHSCVSSY RIGSMAPNLTLSMPRHNYFPA GNVDHDNEFEL
13346	43714	A	13426	560	844	
13347	43715	B	13427	200	1519	
13348	43716	A	13428	950	1230	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNNQLLPV LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13349	43717	A	13429	695	1060	FRQRSAFPPPTVPNACSVRSR ERDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLQESG*AQR N*CRKHLRLSIPRK
13350	43718	A	13430	1	1558	MRDIFWVPDICKVMLYLVFFRS MGTPLRAVAMGLVITSWKIAQ KPRDFADFGTTINQDFRLLGQT SVDRLLQLSQGQAVKGNQLLP VSLKTDTAKAKNLYLTKAYGG GTNFRRKESQKLQLQSAKKRDA ELANGALGIIELNNNDYTLKKVM KPLITSNTGFADFGTTIKQDFRL LGQTSDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLQESG Q*AQRN
13351	43719	A	13431	391	1676	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLQESG*AQR N
13352	43720	B	13432	1	1638	
13353	43721	A	13433	1	2430	
13354	43722	B	13434	1	1282	
13355	43723	B	13435	1	1225	
13356	43724	A	13436	350	709	
13357	43725	A	13437	1	2236	
13358	43726	A	13438	548	1698	RSWLRSSSLGSGIPIATEISCTSCE ASTSS/VRDPGPKDLTFTQWHD RLIFAIARLLGRSACGVTFHKEQ LGTVKVLRGTTISQFARQRRAAG QLFTHFFGRHTALGAGNRH LRQQFSRLNVLVPQPKDQKGIFHH ARNECRALTRRETPAFRRIRAVF NSQLSQTQLHIFTTARPAGLAS KCRKPPQACYLWDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AVKGQNQLLPVSLVKRKTTLAP NTQTASPRALADSLMQLARQV SRLESGQNIESAKGLHVWDSW PLHNADGTDEYNGYHVVFAL AGSPKDADDTTSIYMFYQKVGD NSIDSWKNAGRVFKDSDKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGEHYG
13359	43727	B	13439	448	1116	
13360	43728	A	13440	97	1636	
13361	43729	A	13441	1	1296	
13362	43730	B	13442	1	2160	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
13363	43731	A	13443	485	865	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNNQLPV SLVKRKTTLAPNTQTASPRALA DSLMLQALARQVSRLQESGQS*NSS KTKNTKCLNSINQRKLKILSLOK DLMCGTAGCRCKTLTEQ
13364	43732	A	13444	816	1194	SLILFLRRRAVEKRGKVKWKS CPNGTTLTLSGAIFLFIIRDFAFD GTPITQDFRLLGQTSVDRLLHLS QGQAVKGNNQLLPVSLVKRKT LAPNTQTASPRALADSLMQLA RQVSRLQESGQ*AQRN
13365	43733	B	13445	1	2710	
13366	43734	A	13446	2027	2934	NPRILPISEPPSNRIFACWGKPA WTACCN/FSQQGQAVKGNNQLP VSLVKRKTTLAPNTQTASPRAL ADSLMLQALARQVSRLQESGQDF DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNNQLLPVSLVKR KTTLAPNTQTASPRALADSLMQL LARQVSRLQESGQSRVHSHSLGP LPITTTGSLINQKKGVGSGPG SKEQAEISCLKERKDLGLGILGS TVGILKVKHQGASTKQGHSDQ LIKILLSDTSLSTPAAPMVDSLIA RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPFSFLTGQ QTPAFGRRVSGVIEIADGSR KAAALTESDYRVLVGE MAALSRLGN RYASRLQY KIFHDEHG QTSVDRLLQLSQGQAVKGNNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMLQALARQVSRLQESGQ HSTD QKIRILPMAGRDP SSDL EHI RIQERALFK EQIQR TIVRALY 13367
13367	43735	A	13447	I	5240	
13368	43736	A	13448	4733	4753	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
13369	43737	A	13449	299	761	LNTFAITLCLLLREARKTLMTH QSTCFIKRDFADFGTTIKQDFRL LGQTTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESG Q*AQRN**PVPKERRRGRDRQE HQQPCCRNTETGTLARVWAARDQ
13370	43738	A	13450	3925	4190	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGQ*AQR N
13371	43739	A	13451	2	1040	
13372	43740	A	13452	58	350	HLASWWVVALVHWGCVVWTA ESSTSCTRSPFRARSWIGEAVA AAAADGVTFSVPVTPHTFRHSY AMHMLYAGIPLKVLAQSLMGH KSISSSTGVPPSSNS
13373	43741	A	13453	1	1290	
13374	43742	A	13454	289	1338	
13375	43743	A	13455	1	732	
13376	43744	A	13456	982	1347	
13377	43745	A	13457	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHNRNRTQFRLSETKE ITNPYAMRLYESLCOYRKPDGS CIVSLKIDWIHERYQLPQSYQLY YFELAIPVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIKLCQCGG VVKQLSRRGNNNQHISSTYDINR ADTQVRRAVNVYDIIVMSNSFN GQSEHQVWIARLTWVIGTINV CAADVLIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPEPDV RILLTKYNSNSNGSQSPWMEEQI RDAWGSMLKVNVRRETDEVG KARLTWVIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPEPDVRIILLTKYSN SNGSQSPWMEEQI RD A WGS MV LKNVVRRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLAQSLM GHKSISSTEVYTKVFA LDVAAR HRVQFAMPESDAVAMLKQLS
13378	43746	A	13458	1	780	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13379	43747	A	13459	116	396	SSVTGRTEKARIWEVTFDRTV/R RPWIGEAVAAAAGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHR
13380	43748	A	13460	3	514	
13381	43749	A	13461	2	545	
13382	43750	A	13462	1	1110	
13383	43751	A	13463	1	870	
13384	43752	A	13464	1	1422	
13385	43753	A	13465	1	1599	
13386	43754	A	13466	614	1236	TARVAAARRRCQCWGSGACGS ALTLPTRSSLTLTETPIVQQTRM VVRCPТАSLPSQWRSCPSSSTWA VPKTPPTWTCWRNSAISL/VF IRDKLMERRNRRTGRTEKARIW EVTDRTVRTWIGEAVAAAAD GVTFSPVPVPTPHTFRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13387	43755	A	13467	1	1023	
13388	43756	A	13468	1	699	
13389	43757	B	13469	1	1281	
13390	43758	B	13470	77	751	
13391	43759	A	13471	1	705	
13392	43760	A	13472	2	893	
13393	43761	A	13473	206	837	CAGAGGIARRRAEKEKALSAV NLDPPTSRLSSTSPLGAPPNPRV AAAGLSRRRPTPESAGRKS/GR WPRASRYQQGHQDLFILRSRSLP SQVFIIRDKLMERRNRRTGRTEK ARIWEVTDRTVRTWIGEAVAAA AAADGVTFSPVPVPTPHTFRHSYAMH LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13394	43762	A	13474	1	1416	
13395	43763	A	13475	1	765	
13396	43764	B	13476	1	519	
13397	43765	A	13477	1	2784	
13398	43766	A	13478	1	624	
13399	43767	A	13479	2089	2454	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met Ind	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13400	43768	A	13480	740	1431	CCQTLPVFHPPHPSPHLGPRCPPT TH/HLPSEHRSLFLEAACDSDS LEPLNLSSGSKTKSPSLPPKAKK PKGLEISA/RPAGALRHRRLRHR PQQPSPLGLIPHSLL\TAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAVAAAADG VTFSPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKHSSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13401	43769	A	13481	2	2309	
13402	43770	A	13482	1	603	
13403	43771	A	13483	1	762	MVPHSTGKSWNGCDPTSATLD QLVTFFMKLFSIGDARIPCLGP RSHSYRRSDYYSGTTIHSCRA DYWSGTTAHLYCRSDYHPVPS FILVTSTTNHQPLKPSISEASWN PLFASL/HHLQLITES/WYMSLA TTVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVRTWIGEAVAA AAADGVTFSVPVTPHTFRHSY MHMLYAGIPLKVLQSLMGHKHS ISSTEVYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13404	43772	A	13484	1	762	
13405	43773	A	13485	1	615	
13406	43774	A	13486	887	1203	RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKHSISSTEVYTKVFALDVA RHRVQFAMPESDAVAMLKQLS
13407	43775	A	13487	1	855	
13408	43776	A	13488	1	927	
13409	43777	A	13489	1	921	
13410	43778	A	13490	1	3216	
13411	43779	A	13491	1	1974	
13412	43780	A	13492	1	1221	
13413	43781	B	13493	1	2337	
13414	43782	A	13494	1	1273	
13415	43783	A	13495	1	1251	
13416	43784	A	13496	1999	3237	
13417	43785	A	13497	1	1773	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13418	43786	A	13498	1	633	AQALIATYGRDRDGPGRPLWLGSVKSIGHTQAAAGVAGVIKVMAMIRHGQLPRTLHVESPPEVFIRDKLMERRNRRTGRTEKARIWEVTDRVTWIGEAVAAAADAGVTFSVPVTPTHFRFSYAMHMLYAGIPL *VLQSLMGHKSISSTEVVTKVFAFLDVAAHRHRVQFAMPESDAGGPCTACSQQQGCRRGSSVSPGRQHPQPHVRV
13419	43787	A	13499	101	1943	
13420	43788	A	13500	686	3925	
13421	43789	A	13501	1	2084	
13422	43790	A	13502	734	834	
13423	43791	A	13503	1	1075	
13424	43792	A	13504	1	357	
13425	43793	A	13505	795	1273	SHPFSTDWSTDTGFRSKSIWC HRNCRW/RVAVVKLLHLPVII VFWLASWMMMSRWLHYPDWVTI IAQQVLMNVSVVMQADCRMN LLEIFLRWLWLMRKIFHVRLLPAV STPPNCNLNQLLLFFLTPVNYLPG QVMHFKKPLQIKRNLYLSSRHLT FMSRKKLG
13426	43794	A	13506	344	449	SHPFSTDWSTDTGFRSKSIWC HRNCRW/RVAVVKLLHLPVII VFWLASCMMSRCPHYPDWVTI IAQQVLTPLRKDVMQADCRMNL LEIFLRWLWLMRKIFHGFGM
13427	43795	A	13507	1197	1511	WHYREPLLLLRAQLTNPPSGQLV SITKYLQPVEY*AYVLE QAH HYQLKSVDQWPVQKQFSSGSD LYQLHPFHVQHFLEPCFPRHPE FAPPSTGTESHYYCCIW
13428	43796	B	13508	1	1494	
13429	43797	A	13509	1	554	MTARKARKITRRWRIGEAADL VGVSSQAIRDAEKAGRPLPD MEIRGRVQEVRVGYTIEQINHMR DVFGTRLRRAEDVFPPIVGVA HKGNPDQGTASMYHGWPVDSL HIIHAEDTLLPFYLGEEKDDVTY IPTCWPGLDIIPSCLALHRIETE LMGKFDEAQPNLGIGT/N*CRM CC*CADCSHAC
13430	43798	A	13510	1771	2068	DTYSWSWIGEA/AAAAAADGV FSVPVTPTHFRHSYAMHMLYA GIPLKVLQSQYPIFKLSYKNPVT QTAWF/WFPNRIFGVPVPIVSFS PKVPGPLGII
13431	43799	A	13511	65	277	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=possible nucleotide deletion,  =possible nucleotide insertion)
13432	43800	A	13512	327	748	VHQFHGSLHEGFCAGCGCPAPGTVCDAAGGFCRFRNHHQTFGPSPAGANQRGPLAATLSGPGEQQSAVARLTGEKKNHPGAAQYANRLSPRVGRFINAAGTTGFTPTGKRAKSIWCHRNCRW/RVAVVKKLLHLPKVIIFWLAS
13433	43801	A	13513	512	580	
13434	43802	A	13514	2096	2272	EWRNVCVTGTVENVTPSAAAQPPPQSRPFSWILRPF*RP*RKISTSFIRPLFTFLPA
13435	43803	A	13515	402	2784	RKNPFLH*LFR*TLRQTKPDNSAGKCVKI**HTQNQRSGRSQSDF*RRRKNIERSAAYR*RQLYIRRQPYAERPSHVEDKGHKYLVFEANTGTENGYQGEESLFNKAYYGGGTNFFRKESQKLQQSAKKRDAELANGALGIIELNNDYTLKVKMVKPLITSNTVTDEIERANVFKMNGKWLFLTDGRSGSKMTIDGINSNDIYMLGYVSNSLTGPYKPLNKTGLVLQMGGLDPNDVTFTYSHFAVPQAKGNNVVITSYMTNRGFFEDKKATFAPSFLMNIKGNKTSVVKNSILEQQQLTTLQVAKRAGLGGGQSGRTVLRLRPNYKNFKGTIQELQCNQYAVSGEIVFVVDRNTVEITELPVRTWTQVYKEQVLEPMLNGTDKTPALISDYKEYHTDTTVKFVVVKMTEEKLAQAEAGLHKVFKLQTTLTCNSMVLFDHMGCCKYETVQDILKEFFDLRLSYYGLRKEWLVGMGAESTKLNNQARFILEKIQGKTIENRSKKDLIQMLVQRGYEDPVKAWKEAQEKCDNLKTCHTSHGSVMAETAVINHKKRKNSPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHGDICEIHVAKYAEIFGLTSAAEASKDIRQA LKSFAGKEVVVFYRPEEDAGDEKGYESFPWFIRKAHSPSRGLYSVHINPYLIPFFIGLQNRFQTQRLS
13436	43804	A	13516	2	199	WRKKSSLDIPPLIIPNGIVKNLIRHFSQLLNVPITRPFSWILRPF*RP*RKISTSFIRPLFTFLPA
13437	43805	A	13517	1	1887	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
13438	43806	A	13518	125	828	ECRKHTKLKLQPTIWHVVKI/Y NSEKLLVYRKLLQVLTGLYKRS NLGVRLYACCGLLCPAYPQH FAHGVVDKIPGYPGRAGTLTG HPMQCDNLTKTCHTSHGVSMAE TAVINHKKRKNSPRIVQSNDLT EAAYSLSRDQKRMLYLFVDQIR KSDGTQLEHDGICEIHVAKYAE IFGLTSAEAILRYFIKHSADMEA ITNGMMNLRNQRHQLHLVALRHH FAHGENGGEEVVHIGHV
13439	43807	A	13519	504	755	EPCFPAAIPEFAPLSTGAESHIY CCIW*AKYVHQARTL*DQRS*A DHEAYRKTAVRRCSQTTQAW EQLVHQHQHILPSSCRYPG
13440	43808	B	13520	1	1980	
13441	43809	A	13521	923	1063	
13442	43810	B	13522	1	1932	
13443	43811	A	13523	383	1383	RKVFFIAALKRMPAMKKAMNLF LGLSNVRTVHPEGFTVYISTHIS FSPSLSGYKTRLRSFGLVKQKKS PILLEVLAIREIRQE/KEIKGQFG KEEVKLSSLFADDMIVYLENPIV SAQNLKLISNFSKVGQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRKYLGIQLTRDVKDL FKENYKPLNNEIKEDTNWKNI PCSWVGRINIVKMAILPKLSRM HGRPHQPPNAASTLPFPKRRSH YQQKSERLSRSQDNRKSHPECR HWQSCAKKSRLCAFTTRVVRT PRSAIYLTRTIELLESSALWHV QTQRIYAPLYETLDPGNRTHCE
13444	43812	B	13524	107	1000	
13445	43813	A	13525	1778	1897	
13446	43814	A	13526	273	421	SHPFFSTDWSTDTGVRSKSIWC HRNCRW/RVAVVVKLLHLPKVII VFWLASWMMSSRWLHYPDWVT IIAQVQLMNVSVVMQACRNM LLEIIFLRWLMLRIIFHVRLLPAVS TPTNCLNQLLFFLTPVNYLPG QSGTTVPLVSSV
13447	43815	A	13527	273	697	SHPFFSTDWSTDTGVRSKSIWC HRNCRW/RVAVVVKLLHLPKVII VFWLASWMMSSRWLHYPDWVT IIAQVQLMNVSVVMQACRNM LLEIIFLRWLMLRIIFHVRLLPAVS TPTNCLNQLLFFLTPVNYLPG QSGTTVPLVSSV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13448	43816	A	13528	273	688	SHPFFSTDWSTDGTGVRSKSIWC HRNCRW/RVAVVKKLHLPKVII VFWLASWMMMSRWLHYPDWVTT IIAQQLMNVGSVMPADCRMN LLEIFLRWLMLRKIFFTGRLRSFGL VKQKKSPIRMPCVYTNPCVSIV SRMGQASSL
13449	43817	B	13529	1	1053	
13450	43818	B	13530	1	1869	
13451	43819	A	13531	120	430	EDLSDTGVRKSIWCHRNCRW/ RVAVVKKLHLPKVIIIVFWLASW MMMSRWLHYPDWVTTIAQQVL MNVVSVMQADCRMLNLEIFLR WLMRKIFHSSLEDPRNWHL
13452	43820	B	13532	148	334	
13453	43821	A	13533	2	147	TSMDKGLQGALKKKI*DL*KK* L\KNIPVDKWITPREVFSGIVCK QNI
13454	43822	A	13534	151	325	KAICINTFSKPSMDKGL/LRRS KKEGFKTYKKNIYKNIPVDKWI TPREVFSGIVCKQNI
13455	43823	A	13535	283	406	HRTKISIVPEGIFKSFLPLAGIM TEQYFL*TLHRLRLIM
13456	43824	B	13536	1	1902	
13457	43825	A	13537	508	1041	LWREASKDIRQ\ALKSFAGKEV VFYRPEEDAGDEKGYESFPW/C YQTWHSPSRGLYSVHINPYLIP FFIGLQNRFTQFRLSETKEITNP YAMRLYESLCQYRKPDGSGIVS LKDIDIWIEERYQLPOSYQRMPDF RRRFLQVCVNEINSRTPMRLSYI EKKKGRQTTHIVFSFRDITSMTT
13458	43826	A	13538	1	1422	
13459	43827	B	13539	1	1002	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met #	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, #=possible nucleotide insertion)
13460	43828	A	13540	1	160	MVLIVAATVVVVVVVGLCWM AKSECERSAMRLSSLQVRIFTYLI GREAAFADNLKWMACANKES ALLDRIFLILLLCKEPWECHCL PLFKVAMPSKCDIPVICAHINIG FTLRQLRGFGPCNCISFEAKDS KNPQVVRVISQKHKALRCIWFIT CSICNPEFTEGALQGNKQRKRQ CLQWFRAKALESNEPGEFIGD KLLTQSCLFFPYTFLWLTGPHPS GSSYTDPCSSKADVTPSSTAVQ EHISSALELKTKIVSPITRQQHGF FTQISTLADVQENVMEYLHVL RPKVIDQEHDVWVTEAYIDSTV CRVKRRQQLLQQVPLTRKQQF LPAPYVQLLDSARTRTNKKQQQN PIIYTGSKQGSHVILFHGESWN LLRADQRLIFAKSWPRASRYQQ GHQDQLFILRSDLPSQVFI RDKL MERRNRRTRGRTKARIWEVTD RTVRTWIGEAVAAAADGVTF SVPVTPTHFRHSYAMHMLYAG IPLKVQLQSLMGHKSISSTEVYTK VFALDVAARHRVQFAMPESDA VAMLKQL*QPQWWWWWSW*D CAGWRKVNAACPVCCLPFRFA SSHTSLDERLRLQTI
13461	43829	A	13541	48	668	
13462	43830	A	13542	1	1278	
13463	43831	A	13543	100	157	
13464	43832	A	13544	1	1122	
13465	43833	B	13545	1	1131	
13466	43834	A	13546	273	812	SHPFSTDWSTDTGVRSKSIWC HRNCRWESPS*SC/WHLPKVIIV FWLASWMMSRWLNYPDWVTII AQQLVLMVVSVMQADC\KRIC WKYFCAG*CGKIFTYQ**TWN NTETSMSQKPCCKMKR\YSREE LAV*KMDHHSDLISLW*KLEPL TCRSTSHFRQKLAQQFPVSTGT PGFIYSAK
13467	43835	B	13547	1	987	

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13468	43836	A	13548	246	2065	LVGWLWGWLWGWLIVALPFM MIPWHSSIQPFTIHPFNWNFG* MPELCPOQGMDSWLAGWM/CWL DGWLWG*MAKLRKPV*PD KEGNEIWVDMYTVKPGSGWTVR TFDKPRKRFIAFFIAGILFRAIKN HFLPRETLQCLPYILTGFRRGQS EYFSIFSNMDLADTVMFLIVAL PFMMPWHSSIQPFTIHPFNWNFG
13469	43837	A	13549	2	118	
13470	43838	A	13550	397	729	THGIRIGDFFCFTKRKLRKPVL* PDKEGNEIWVDMYTVKPGSGW TVRTFDKPRKRFIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRRG QSEYFSIFSNMDLADTVMFL
13471	43839	A	13551	147	417	SSSWGRSSPQLVCGIFQTAGPQS LCKWNQ*VLAQTNKKTAGTSA DLYVPV*QL*RKAVVPLPTNAP WRFWRTRQEWFSSGRGSGYQS QET
13472	43840	A	13552	1	2418	
13473	43841	B	13553	1	1848	
13474	43842	A	13554	188	490	EWRNVCGVTGTEKVTPSAAAA ATASPIQVLTVLVTSQRAFSV LPVRRRLRRSMSLSRINTCVNRF CNPPIKKGMRYGLICPL*SLDGL CARLINQGKDS
13475	43843	A	13555	83	440	SLLFKCSGVIVLRRPLGYRQVM NVTRRCLLRTHWMISLLFY*L VNRHRSVEEYLVSYTLPMGV AVVKLLLHLPKNFVSLITPRGRL EKERAFLFQHMRISISTGLKIFV MHTSCPMVVC

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13476	43844	A	13556	1337	2583	QQRR*MCQNLMLTH\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRROPYAERPS\HVEDKGH KYLVFEANTGTENGYQQGEESLF NKAYYGGGTNFFRKESOKLQQ SAKKRDAELANGALGIIELNNND YTLKKVVMKPLITSNTVFI RDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAM\HMLYAG IPLKVLQSLMGHKSISSTEVQH VFAFLDAVAARIIRKSDGTLOEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAKEVVFYRPEE DAGDEKGYEESFPWFKRAHSPS RGLYSHINPYLIPFFIGLQNRF TQFRLSETKEITNPYAMRVTPN CVSIVCVNEINSRTPMRLSYIEK KKGRQTTTHIVFSFRDITSMITG
13477	43845	B	13557	1	696	
13478	43846	A	13558	326	1577	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRF*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHIRH
13479	43847	B	13559	1	3822	
13480	43848	A	13560	848	1476	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*SFELIPSIVF EPRESVNVYHLPFILKTAFRISS VTVFEVISGIFTTFNVS*SLFNSMI PRAPFANSASRFLALC*SFWLSS RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFYKVFMAFVNVV RVSQRMVVAGCIIAFIDKLLNV LICFSVSKNRFVIFHSVDFECV
13481	43849	A	13561	1	2196	
13482	43850	A	13562	326	3746	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRF*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHIRH*SCRYPS*ARCQ*LTC QIVHRGEKKEQQLI
13483	43851	A	13563	3802	4075	IRCFTVSPAPGYFPRFRAVIILK NGDSLRLHFMTS VYALQEAAAE VRHTLVTLRQLVTLYDPVDFQ RDDA*AIRAYD TDGIRINAWH TDW
13484	43852	A	13564	1708	3198	
13485	43853	A	13565	1	1401	
13486	43854	A	13566	1214	1357	NKINMFIAALFTIAKTVWNQPK\ CPTMIDWIKKRGSSRVASSSSPT RTR

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13487	43855	A	13567	3363	3852	SHPFFSTDWSSDTGVRRSKSIWC HRNCRW/RVAVVKKLHLPKVII VFWLASWMMSRWLHYPDWVT IAQQVLMNVVSVMQADCRMN LLEIFLRWLMRKIFHVRLPAV STPPNCNLQLLLFFLTPVNYLPG QGFAGFRNPPSNRIFACCWGKPA WTACCNSLRARR
13488	43856	B	13568	350	742	
13489	43857	A	13569	248	599	HRDSYKRMAVGVLVISVVLSR KLRKPV*PDKEGNEIWVWDMY TVKPGWTVRTFDKPKRKRIFAF FIAGILFRAIKNHFLPRETLQCLP YILTGFRRGQSEYFSIFSNSMDLA DTVMFL
13490	43858	B	13570	1	2148	
13491	43859	A	13571	3064	5069	RSDPDENCC*TGH*STLFNWCI WRNALSIWEPVCNEIFYRLIKPR WEIRWGKRAPVCPKHTLNTQPV EDTSLSTPAAPMVDSLARIARVGV MARGNAITLPVCGRDVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDADDDLIPSFLLTGQQT AFGRRVSGVIEIADGSSRRKAA ALTESDYRVLVGELDDEQMAA LSRLGNDYRPTSAYERGQRYAS RLQNEFAGNISALADAENISRKI ITRCINTAKLPKSVVVALFSIIPRQ APCMKSNNALIVILGTVTLDAV GIGLVMMPDLALKGLRVLLVEG NDPQGTASMYHGVPDLHIA EDTLLPFPYLGEKDDVTYA1KPT CWPGLDIIPSCLAHRIETELMG KFDEGKLPTDPHMLRLAIETV AHDYDVIVIDSAPNLIGITINV CAAHALIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEVDV RILLTKYSNSNGSQSPWIEEQIS DAWGSMVLKNVHAIVTGDAV GMDDIPQEARQYRHQAYAAYS IQGDGAEDDDERIVRFRHTRTV DSDTLASDAARLTCRIGLGNQ RNGGVLIEDKFECFFSLTAVFA TRAYYAVYHLTGARHSDIVVA HGYAGCNVRFVALLGTTLE TYLSNQGSNGFSCLHFGEDEVGQ

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13492	43860	A	13572	1408	5578	CSHLIIQLANQNTIITFGKCSSF TTATPIGNFYDTRYSSERRCLL TSQ*KRRDEIIQCVLSKQLRAR SLPDPTRKVFSTLSPRSTFRVNF TSRPHTGKVWAFFREPFLPPHL RKPDITDTGVLYKRMAYGSVIS/ ICFTKPKLKPVVL*PDKEGNEIW VDMYTVKPSGWTVRTEDPKRK RFIAFFIAGILFRAIKNHFLPRET LQCLPYIITGFRRGQSEYSFIFS NMDLADTVMFL
13493	43861	A	13573	2678	2884	SAPLQRNTARRFLLFLKACNSR FCYRWRHMTAIPSYNRSKLREI KGGLYHMGIFRRFLASKETPTF CY
13494	43862	B	13574	1	7903	
13495	43863	A	13575	1	880	
13496	43864	A	13576	1	996	
13497	43865	A	13577	763	778	NRCEPPV*GTRFSQQLLLAKA TLLIEELYALTIVHSWRPKW
13498	43866	A	13578	2	254	
13499	43867	A	13579	1	2358	
13500	43868	A	13580	206	382	
13501	43869	C	13581	1	1137	
13502	43870	A	13582	79	906	
13503	43871	A	13583	2	383	SPPEVVRGLYHPPRHGHQVHLF ASCRKGDVGRVRP*TRDPGSD LLPAQVPAGAARRGGTMPACV GTRSWYSTFWPMPEAARPTPS MVSAAASMGH*VTPSAGLYAIITS RSRLPAGGGITMTSCSGF
13504	43872	A	13584	1	1092	
13505	43873	A	13585	173	262	
13506	43874	A	13586	898	1391	QLGILRVNLLGIDLRTVGHQAA PPLHLLDLLQMH/SSPPCRPQ*A TSSPPPSLRCRAPHR*SLAAP*A PPPRPLSAGSPHRKGPPGPAPT GSWSSGNQAGLPCCLGWASVF LCPSHLPPHLPQSSASLAFHRV KHLIHLHNSVIDKMKYQLKFCL LLGEYLSV
13507	43875	A	13587	1	960	
13508	43876	A	13588	1318	1369	RDFHPK*HTIGIQYIWQQLEINQ CDTSIISMVLPVR*RDFHPKSHLL PGAAQIQ
13509	43877	A	13589	212	385	
13510	43878	A	13590	377	505	
13511	43879	A	13591	69	193	CSIRSLAQMLPFYPRRSICLSCL L**PHCCLWLAALRSESK
13512	43880	A	13592	1	230	
13513	43881	A	13593	2	341	

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13514	43882	A	13594	1	2421	
13515	43883	A	13595	1	623	
13516	43884	A	13596	1	906	
13517	43885	A	13597	1	568	
13518	43886	A	13598	107	199	
13519	43887	A	13599	42	328	GGASGVCSF*CSE/LSSFWWVR GLAGSGVKLQTATQEPSWLH PVDPVPGLOVELPASPAPCART PQPLGGRWDSAPWSRGRSSG AHGIDVALLP
13520	43888	A	13600	5	124	IWILWFFVSLT*RSRGPSQ*VLQ LIKAPHV DLLVTVTFC
13521	43889	A	13601	827	973	IHQSALCI*LKFYTSLLTHPVISLV VETLVWW*YLKM*KKLWSWI RGRG
13522	43890	A	13602	2	503	
13523	43891	A	13603	56	792	
13524	43892	A	13604	1	411	
13525	43893	A	13605	1	1554	
13526	43894	A	13606	1	363	
13527	43895	A	13607	1	966	
13528	43896	A	13608	932	1189	
13529	43897	A	13609	146	323	
13530	43898	A	13610	1	1827	
13531	43899	A	13611	2	412	
13532	43900	A	13612	1	2238	
13533	43901	A	13613	2	411	GATDCVCYYTGVGFNDTKTSAL HMVVGDSLAMDVSSVHINSTL LRYSVTLLGYGFGYGDIIKDSDK KRRGLARYDFLCIKTTFSHH* YEGETVFLPAQHTVGSPRDRKP CRAGCFCVCRQSKQQLEEEQKT ALYGLEL
13534	43902	A	13614	3	2185	
13535	43903	A	13615	206	1568	
13536	43904	A	13616	165	417	TWDYIRPNE*YM*MAKKMP MD\VVWCGNKNWRPAG\EFVDD G\TETHPSIGNHDCYIKA\VS GG RKEGIHTLIVDNREIPEIAS
13537	43905	A	13617	463	837	
13538	43906	A	13618	1	765	
13539	43907	A	13619	3	510	AGVHKIEFEHGTSGKRVVYV DGKEEIRKEWMFKLVGKETFVY VGAAKTKATINIDAIISGFAYEY TLEINGKSLKYMEDRSKTTNT WVLMHDGENFRIVLEKDAMD VWCHGKKIRRPAGEFVDDGTE TPLQYPPGPMTCYIKA\VS GG\KR KEGIIHTLIVDNREIPEIAS
13540	43908	A	13620	342	585	
13541	43909	A	13621	1	1119	

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13542	43910	B	13622	48	1104	
13543	43911	A	13623	656	916	GWRKYLQGAADMGIAEGGGS VWSSWASSSLISVPVR*LESTQ RSAPGWPLTGGCSESVALWL CVNDFEFQMRLMPSRDLSEPAC
13544	43912	A	13624	179	682	
13545	43913	A	13625	1	7511	
13546	43914	A	13626	56	8669	
13547	43915	A	13627	42	8716	
13548	43916	A	13628	1	2457	
13549	43917	A	13629	3	571	
13550	43918	A	13630	1	867	
13551	43919	A	13631	1	2238	
13552	43920	A	13632	171	396	
13553	43921	A	13633	1	3940	
13554	43922	A	13634	554	619	
13555	43923	A	13635	1	1359	
13556	43924	C	13636	208	359	
13557	43925	A	13637	2	513	PSHDHSKLGTRASGKVILHGEH AAVHGKVVALAVSMLNRLRTFLRL QPHSNKGDKLSPNIGKRAWD VARLQLSLDTSPFL/RWTKEDELEI NKWAFQGERMIHGNPSGVDNA VSTWGGAALRYHQGKISSLKRSP ALQILLTSTRGPRNIRALVGGG RNRLLEVPMGGPLLWSW
13558	43926	A	13638	3	1331	RVDDFVGELLRLRRGGAADVE AAAAAGFPGAMLSQVLLVSAP GKVLHGEHAVVHGKVVALAVS LNRLRTFLRLQPHSNKGKVDLNLPI NIGIMRAWDVARLHSLSDTSFLG ECKEEKPSEQGDVTTPTSEQVEK LKEVAGLPDDCAVTERLAVLA FLYLYLSICRKQRALPSLIDIVV WSELPPGAGGLGSSAAYSVCLA AALLTVCEEIPNPLKDDGDCVNR RWTKEDELELINKWAFQGER MIHGNPSGVDNAVQHLLGEGA LRLPSRGRFSFL*RGSPVFQ/LG LTNTKVPSAITRALVAGVRNRL LKFPEIVAPLLTSIDAISLECERV LGEMGEAPAPEQVLYLEELIDM NQHHHLNALGVGHASLDQLCQV TRARGLHSKLTGAGGGCGITL LKGLEQPEVATEKQALTSQCF DCLETSIGAPGVSIHSATSLDSR
13559	43927	A	13639	1	950	
13560	43928	A	13640	1	1653	
13561	43929	A	13641	1	2601	
13562	43930	A	13642	2	513	
13563	43931	A	13643	47	367	

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13564	43932	A	13644	1	633	
13565	43933	B	13645	1	1110	
13566	43934	A	13646	172	1095	
13567	43935	A	13647	1	855	
13568	43936	A	13648	3	440	
13569	43937	A	13649	2	230	
13570	43938	A	13650	2	606	AEEFDLCCSPCRRRLGGREEAGE EPTSPVTQYLOQPRSPPEECKMFA CAKLA <sup>CTP</sup> ISLIRAGSRVAYRPI SASVLSRPEASRTGEGGSTVFN A\QNGVSQ\LIPKGSFKTSAISKK TLDTA\AAKFIGAGAGNS*GVG WFLVAGIG\TVFWASLHWM ARKPFRWKQQL\FSY\A\ILGICL VLKAMGSPFVLMVAFLILFAHV TEITA
13571	43939	A	13651	200	2320	
13572	43940	A	13652	224	640	
13573	43941	A	13653	1	357	
13574	43942	A	13654	43	183	
13575	43943	A	13655	3	478	SSAGREPDPSDLPRRLCFTHRLP AARRWVQLCVHASPEPGQGV CPGRSERMVMIRVFIASSGFVAI KKKQQDVVRFLANKIEEVEED ITMSEEQRQWMYKNVPPDKP TQGNPLPPQIF\NGDRYCGDYD RLFESKESNTVFSFLGLKPRLAS KAEP
13576	43944	A	13656	2	428	CRDGKDVVSLVRA\TVWALSKR KLQPTRA\ALTPPSA\VN\KIKQF LKDKEPELVDVKGVRTRGNG LSVTVEYTKTKGSDEVIQDEA RVFIEKKAQ\LTPLGTEM\DYVED KLSSE\FMFN\NPT*TC\CCGAPGK L\VETLGLTEEM
13577	43945	A	13657	1	1377	
13578	43946	A	13658	1	1215	
13579	43947	A	13659	1	452	REAEAADLRSEAPGRRDGEDV GFLSSGQLSGLCSKRK\LQPTRA ALTLTPSAVN\KIKQ\LLKE*P\AC R\LKVGVRTRGNG\LSVTLEYT KTKGDSDEEV\QDGVRV\RFIEK\K AQLTLL*TEM\DYVED\KLSKG GVHSPNIKGTCGCGESFNI
13580	43948	A	13660	3	763	
13581	43949	A	13661	1	306	
13582	43950	A	13662	738	1022	GQHH\HPETKA\WQRH\NKKREF*T N\ILDEH*CKNPH*NTGKPNPAT HQKAYPP\SSGLHPWDARLVQ HTKINKCNPAYKQNQRQKPHD YLNCRKGL

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13583	43951	A	13663	2	516	QKIDLPEYQGEPDEISIQKQCQEAVRQVQGPVLVEDTCLCFNALGLPDPYIKWFLKLP <del>EGLHQ</del> FLAGVEGKSAYALCTFALSTGDPSQPVRLFRGRRTSGRIIVAPRACQDFGWDIPCFQPDGYEQTYAE <del>MPKAEKNAVISHR</del> FA <del>IL</del> LEI <del>Q</del> EYFGKFGQLDFCKLEAGPFR
13584	43952	A	13664	7	227	
13585	43953	A	13665	1	415	
13586	43954	A	13666	234	510	
13587	43955	A	13667	2	402	
13588	43956	B	13668	530	1544	
13589	43957	A	13669	1	603	
13590	43958	B	13670	1	1527	
13591	43959	A	13671	1	1179	
13592	43960	A	13672	2	413	
13593	43961	A	13673	100	374	KHISPALKALELPFERNLII/PLQ <del>LLKV</del> RILKEGEML/DI*HWFL**GMGTVQKGMPHKCYI <del>H</del> GKTRGVYNVYNVTQHAVIVVNKIQVKGKILA <del>K</del> IRN <del>V</del> RIEH <del>I</del> KHSKSPR*ASLK/RVLKENDQE <del>K</del> ERSPKKKGTWG <del>SNLKRHPAPPQK</del> H <del>T</del> L*RTNGKEPELLEPIPYEFHGHN
13594	43962	A	13674	1	1035	
13595	43963	A	13675	2	564	GPFGRNRHLPVIRQNDGPQRGKRRGTPKYVF*/RPFRK <del>H</del> GGGPLGPPY <del>M</del> IRYRKGDIVD <del>I</del> KGMG <del>I</del> TVQNGMPHKCYHGK <del>T</del> GRVYNVTQHAVIVVNKIQVKGKILA <del>K</del> IRN <del>V</del> RIEH <del>I</del> KHSKSPR*ASLK/RVLKENDQE <del>K</del> ERSPKKKGTWG <del>SNLKRHPAPPQK</del> H <del>T</del> L*RTNGKEPELLEPIPYEFHGHN
13596	43964	B	13676	68	391	
13597	43965	A	13677	1	404	PTRTWTRGRIPRLSAPS <del>R</del> GT <del>M</del> ADPRVRQ <del>I</del> KIK <del>T</del> GV <del>V</del> KRLV <del>I</del> KEV <del>V</del> LYKE <del>P</del> KQ <del>I</del> Q <del>E</del> E <del>I</del> K <del>M</del> RAEDGENYDIKKQAEILQESRMMIPDCQRRL <del>E</del> AY <del>L</del> DLQR <del>I</del> LENEKD <del>D</del> LE <del>E</del> A <del>E</del> EY <del>Y</del> KEARL <del>V</del> LDL <del>S</del> V <del>K</del> LEA
13598	43966	A	13678	1	436	LLLACRSMDCYLAIVHATR <del>T</del> LTQQRHLV <del>K</del> FICLGLRNLF <del>L</del> LLSLRILLFRRTF <del>P</del> SNVSP <del>V</del> CYEDMGNNTANWWM <del>L</del> LR <del>L</del> PQ <del>S</del> FGFIVPL/LIMLFCYR <del>F</del> TLH <del>T</del> LFKAHM <del>G</del> QKHWTM <del>V</del> IFADV <del>L</del> LLCWL <del>P</del> YNLVLLAD <del>T</del> IMGT
13599	43967	A	13679	1	705	
13600	43968	A	13680	292	1489	
13601	43969	A	13681	434	1205	
13602	43970	A	13682	1	390	

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13603	43971	A	13683	21	479	TYPEAWKLYYRSR*SRDLRKY HAHSVSP*QDQRYTS*KILKCD EHIQKLGSCITDPGNRETSQNT MHTVFRDKTKDTTHPESCCSSE KGGQLPLPWFHRKNVPQFAEP TETLFGPDGSKGAKSLVELLDE SECTSDEEIFISQDEIQSFMANN QSFSYNSRQEYRQHLKEEKFNKY CRLNDHKRPICSGVWDNGWEA
13604	43972	B	13684	32	438	
13605	43973	A	13685	533	1226	
13606	43974	A	13686	1	1566	
13607	43975	A	13687	215	453	
13608	43976	A	13688	1	553	RRPARAAVIKQPPAGASQHAA TPTQTPLCTPARPLPPMAHVQQ LEGRWRLVDS\KGF**NTMKE\  GVTIALRKMGRNAQAQICIIITS DG*NPSPLKTESTLKT\TQFSCT/\ LWGEKFEETTA\DGQKKLTNCL STFPDGALWQHQEWGDERKS TITKKN*KDGEISWLECVMNN \ VTCTPDSMKK
13609	43977	C	13689	11	106	
13610	43978	A	13690	3	155	LCELQKAIDLFTDA\KLNPRLA LYAKRASVFVKLQKPNAAIRD CDRAIEINPDSAQPYKWRGKAH R*ILAWPFCMGRGPVSSSYRS QMLPSETVTEPLK
13611	43979	A	13691	1	1732	
13612	43980	B	13692	95	1715	
13613	43981	A	13693	1	446	
13614	43982	A	13694	1	786	
13615	43983	A	13695	88	828	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13616	43984	A	13696	157	1515	RREKMAELKYISGFNGNECSSED PRCPGSLPEGQNNPQVCVPNLY AEQLSGSAFTCPRSTNKRSLWY RILPSVSHKPFESIDEGHVTHNW DEVDPDPNQLRWPFEIPKASQ KKVDFVSGLHHTLCGAGDIKS NGLAIHIFLCTNSMENRCYFVNS DGDFLIVPQKGNILLIYTEFGK LVQPNEICVIQRGMRFSIDVFE TRGVILEVYGVHFEPLDCPIG ANGLANPRDFLPIA\WYEDRQV PGGYTVINKYQGKLFAAKQDV SPFNVVAWHGNYTPYKYNLK\ NFMVINSVAFDHADPSIFTVLT AKSVRPGVIAADFVIFPPRWGV ADKTSGPYYHRI\NCMKRME LIRGQEQQKQGWFLPGGR/SL HSTMTPHGP\ADACFEKASKVK LALKRIADGTM\AFMF\*SSFLNA GPKWGLQAP\RVLDKNYPKCW EPLKSPF\TPNSRNPAEPN
13617	43985	A	13697	1	156	
13618	43986	A	13698	8	306	
13619	43987	C	13699	1	1143	
13620	43988	A	13700	1	1551	MRKDSCASSMHQQVSRSSKRA GQKTPPEDQEGGQRALRSSHIR LGQFLLIEDCKTPSPSSLLGADAI AKQRKTSVAAASVATIPIR VQGPTVVGSWARGVSAASGP RGTGPKGKARSEKGCSLSHGPO TNKPLVVQKGQKMEQANHPV GLVISVVVKDILKKIVQRETSHP LIHVRYAEAITGRRTAPEDKGS LGRDMLAKAGAJYMMGNKL PIWCHLLEEGIYLEVWALEGQF GRAKNACPVQIRLKDPPTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVVKCSCPNTPILGVQKP NGQWSLVQDLRLISEAVIPLYP VVPNPYTLLSQIPEEEAWFPVVL DLKDAFFCIPLHYDSDHSQFLF AFEDPTDHTSQLJWTVLPGQFR DSPHLFGQALAOQLGHFSSPGT LVLQYVDDLLLATSEASCCQA TLDLLNFLANQGYKASRSKAQ LCLQQVKYGLLILARGTRTLGK ERIQPILA\YHPKTLKQLWGFL QIT\GFCQLWIPR\*SKI
13621	43989	A	13701	188	688	

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13622	43990	A	13702	636	2628	SNDRTEDDCGKHPFMSSPP/TEP WVCLIEGQEIDFLLDTGTTSV LIPCLGRLLSSRSVTIQQLGQPVTT RYFSHLLSCNWTLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPLICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDP SFYFQRQYPLRPEAHKGQLQDIV KHLKAQDSDVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLSSQVPEEAEW FTVLDLKD
13623	43991	B	13703	302	619	
13624	43992	A	13704	1	5172	
13625	43993	A	13705	1	2091	
13626	43994	A	13706	1	1754	GPRGTGPKGKARSEKGCSLSHG PQTNKPVLVQKGQKMEQANHP VGLVISVYKDOIKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIYIMMGN KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPPTIFP YQRQYPLRPEAHKGQLQDIVKH VKAQGLVKKCSSPCNTPILGVQ KPNGQWSLVQDQLRILEAVIPL YPVVNPVYTLLSQIPEEAEWFP VLDLKDAAFFCIPHYDSDHSQF LFAFEDPTDHTSQLIWTVLPQG FRDSPHLFGQALAQDGLGHFSSP GTLVLQYVDDLLLATSEASCG QATLDDLNFLANQGYKASRSK AQCLCLQQVKYLGILILARGTRTL GKERIQPILAYPHPKTLKQLWG FLEITGFC*LWIPGYSKIAKPPLYT LIKETQRANTHLVEWESEAETA FKTLKQALVQAPGLSLPTGQNF SLYVTTERAGIALGVLTQTRGTT PQPVAHLSKETDVVAKGWPHC LRVVAAVAVLVSEAIKIQGKD LIVWTTHEVNGIL/AGKGSWL SDKRFLRYQALCLEGLVLQIRT SCGSHLAVTRLWALYF
13627	43995	A	13707	2	887	

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13628	43996	A	13708	3	1750	GWAVPRPGPRGLTVATEAAA AAAAAAAIISSRTRAPQAPEGR NRRLEKMMADDIEAMLEAPY KKDENKLSSANGHEERSKKRK KSKSRSRSRERKRSKSKERKRS RDREKKSKSRSRERKRSKRSKERR RSRSRSRDRRFRGRYRSPYSGP KFNSAIRGKIGLPHSIKLSSRRS RSKSPFRKDKSPVREPIDNLTPE ERDARTVFCMQLAARIPRDRDLE EFFSTVGKVRDVRMISDRNSRR SKGIAYVEFVDVSSVPLAIGLTG QRVLGVPIIVQASQAECNRAA AMANNLQKGSAQPMRLYVGSS HFNITEDMLRGIFEPFGRIESIQL MMDSETGRSKGYGFITFSDEC AKKALEQLNGFELAGRPMKVG HVTERTDASSASSFLDSDELER TGIDLGTTGRLQLMVARLAEG TGLQIPPAQQALQMSGSLAF GAVGRNLFCYRFAKQDFSHQT ETSALSAASAVQPLATQCFQLS NMFNPQTEKEVGVWDTEIKDDV IEECNKHGGVIIHYVDKNSAQG NVYVKCPSIAEAIAAVNALHGR WFAGKMITAAVYPLPTYHNLF PDSMTATQLVPSRK
13629	43997	A	13709	141	343	LHEGLL*RGHALLSGALHG*C VGSCLFSTPRCLTSSTACGYPSS CTPGSCTAWCPASRRLSCWT
13630	43998	A	13710	5	426	
13631	43999	A	13711	1	1188	
13632	44000	A	13712	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEEDP NCHEQHLSNTATHLGTQDEAVI DGRRKPEESRTTSHICRCRS
13633	44001	A	13713	1	700	
13634	44002	A	13714	3	483	
13635	44003	A	13715	2	361	RRFRAGAGYVVESTGVFTTME KAGAHLQGGAKRVIISAPSADT PMFVMGVNHEKYDNSLKIISNA SCTTNCLA/PASTGAAKAVGK VIEPLNGKLTGMAFRVPTANVS VVDLTCSRLEKPA
13636	44004	A	13716	2	249	SADAPMFDMGVNHEKYDNSL NIISVMKAGPVEKRPWAHPMD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIIHDNFGIVEGLMV

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13637	44005	A	13717	1	1079	GTRRQSAASSFASPAEPRHSDT MGKVKGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFDLNLYM VYMFQYDSTHGKFHGTVKAE GKLVINGNPITIFQER^YPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPSADAPM FVMGVNHEKYDNLKIIUSNA^S CTTNCLT^PLAKVHNDNGIVEG LMTTVHAITATQKTVDPGSKL WRDGRGALQNIIPASTGAAKA VGKVIPELANGKLTGMAFRVPT ANVSVVDLTCRLEKPAKYDDI KKVVKQ^A^SEGPLKGILGYTEH QVVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13638	44006	A	13718	3	483	
13639	44007	A	13719	2	361	RRFRAGAGYVVESTGVFTTME KAGAHFLQGGAKRVIISAPSADT PMFVMGVNHEKYDNLKIIUSNA SCTTNCLA/PPASTGAAKAVGK VIPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13640	44008	A	13720	2	249	SADAPMFDMGVNHEKYDNL NII/SVMKAGPVEKRPAPWPM TLP^LAPRSFLCSNASCTTNCL EPLAKVHNDNGIVEGLMV
13641	44009	A	13721	1	1079	GTRRQSAASSFASPAEPRHSDT MGKVKGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFDLNLYM VYMFQYDSTHGKFHGTVKAE GKLVINGNPITIFQER^YPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPSADAPM FVMGVNHEKYDNLKIIUSNA^S CTTNCLT^PLAKVHNDNGIVEG LMTTVHAITATQKTVDPGSKL WRDGRGALQNIIPASTGAAKA VGKVIPELANGKLTGMAFRVPT ANVSVVDLTCRLEKPAKYDDI KKVVKQ^A^SEGPLKGILGYTEH QVVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13642	44010	C	13722	40	243	
13643	44011	A	13723	2	2972	
13644	44012	A	13724	1	602	

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13645	44013	A	13725	1	325	MGRNQSRKAENTKNESASSPP KDRNNSPVRQSWTENEFDELT EVGFRKLVITNFSELKEHVLTD HKEAKNLEKS LEVVAAREISQE KEIKVFN*EKRKSNCPCLQMT
13646	44014	A	13726	1	981	
13647	44015	A	13727	1	739	MGRNQSRKAENSKNQSTSSPPK DCSSSPAREQNWTKNEFDELTE VGFRRLSIANFSKLKECVLTHR KEAKNLEKSDRENGTLKENTL QDIIQENFPNLLARQANIQEIQI RIPQORYSLRRATPRHIIIVRFTKV EMKEKMSRAAREKGRVTHKG KPIRLTADLSAENLQARREWGP VFNILK NFQPRIPYPAKLSFISG GEIKSFTDKQMLRDFFTTRPAL QELLKEALNMERNNNQYKPLQK HAKW
13648	44016	A	13728	1	1277	MKEQNGGGGREEDHKDKGIRQ LPSLPSAGEAKSDKPEHHINRY RKEIASFEDEKRAMGVAKMAE QEQLQSAAPSMTNAEVGTAHG GRAEAGRVDSPGKRVLGDF PFLAKGSRDRLPKGAGHSLPKY YAFTKVLATGRQERNNSINISKK VIYTKTTSTGHQHQRPKIDKTT KMGRNQSRKAENSKNESTSSPP KGHSSSPATEQSGTENDFDELT EVGFRRSVTTNFYELKEDVQTH RKEAKNLEKRLDKWLTRINSV EKTLSDMMELKTMARELRTDC SSFKSRENFQVEERVSVIDPIYE LSREDKVDRDKKVRNQKQLQEI WDYVKRPNLRLIGVPPESDGEN GTKLENMLQDIIQENFPNLARQ ANIQIQEIQRTPORYSSRRATPR HIIIVRFTKVEMKQKVLAAREK GPVTHKGNGSGLS
13649	44017	A	13729	1	1584	
13650	44018	A	13730	493	575	SHLPMNPANTRSRNQRPDKKKQ KKNVC/DNIRELEQQMEDAYR GTKRKMLPSSSSRMRSDGFDEE SQRYYWRPKNEISGTLLEDDFLK AKSWNRKFYDYEANMPDRWGQ QVAIKSYTLKNLQTVVVISKILP TGRKHLPR*SHLPMNPANTRSQ RNPTKKQKKNVCQ
13651	44019	A	13731	1	655	
13652	44020	A	13732	2	1664	
13653	44021	A	13733	1	2364	
13654	44022	A	13734	1	224	

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13655	44023	A	13735	1033	7511	
13656	44024	A	13736	56	8669	
13657	44025	A	13737	42	8716	
13658	44026	A	13738	1	5046	
13659	44027	A	13739	1	2298	
13660	44028	A	13740	1	2362	
13661	44029	A	13741	1	2046	
13662	44030	A	13742	1	1503	
13663	44031	A	13743	1	813	
13664	44032	A	13744	185	735	
13665	44033	B	13745	317	910	
13666	44034	A	13746	1	867	
13667	44035	B	13747	1	2325	
13668	44036	A	13748	1	430	
13669	44037	A	13749	1	867	
13670	44038	A	13750	35	518	CLSRRASPVYLASMGSRGKTG GKARAKAKSRSSRAGLQFPVG RVHRLLRKGHYAERVGAGAPV VLAAVLVEAQPLRVLELAGN AA\RSNKKTRIIPRHLQLAIRND EEL*KLPGP*RIAQQGSR/VLPNI QA\VLVPKIKTSATVGPKAPSG GKKATQASQEY
13671	44039	A	13751	1	937	
13672	44040	A	13752	1	1096	
13673	44041	A	13753	85	1512	
13674	44042	A	13754	3	2377	
13675	44043	A	13755	1	1134	
13676	44044	A	13756	49	408	
13677	44045	A	13757	47	2603	
13678	44046	A	13758	1	378	
13679	44047	A	13759	1	696	
13680	44048	A	13760	3	401	
13681	44049	A	13761	882	1106	KLHPYTTRQYCHFRI*TDVMAK RSRNAVKGLSALVWCALSDFA AGFTPDDGCTRATFTGGWRK RDCRGAVAGG
13682	44050	A	13762	688	1100	
13683	44051	A	13763	476	552	
13684	44052	B	13764	178	1107	
13685	44053	A	13765	1	198	
13686	44054	B	13766	94	625	
13687	44055	A	13767	1	732	
13688	44056	A	13768	1	4443	
13689	44057	A	13769	216	575	PGAGDRYVGKPVSAAGVTAVSC GVWSSMPDATLJASQAYTSH VGRIRRSPRR/INTARADYPAL TALPFNNFRTHNRFGNAASVL ASIGIGSSLICAARISAHSGAEH KPREPKAANIK

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13690	44058	A	13770	1018	1489	KLPGQRRFVQTPSHVLHHTLSYPTAPAQSSYPAPLSPSQDRAPTLAHQTT*FSASYTANAQWQRVAADHLKSVRETYAHVRQFSPALGNAPPDLQPLS*ASCVPKSGARYSSVIRQNRRDFFRATDHMYVTVPTRPQKMWNPVNTQMNSFRADTCER
13691	44059	A	13771	1013	1755	GSPGLRPGGAAGKALAPSGCTGNSHRAPM*PGAAQATRPEKW A*QRP/HVSTGARGARVRALAA VAAAEQRAGAAVRAAALHT RAAVSAGAARAAVVQVVLALARTEAGAAAAAAQGVVAQVQAE S AIAAWLQAAPVHPLLTVGALE TGWAVADVGRVRVCTPDTQA AVEAGSICTHCPAHLTPQVPEP TRAGAFKGPGCLTTAASIGTRV PVTGPRPRDKASGGSRGRAPGA EAAAGGDRDRAEGSSPAL
13692	44060	A	13772	1	1236	
13693	44061	A	13773	1	456	
13694	44062	A	13774	1	219	
13695	44063	A	13775	1707	1853	
13696	44064	A	13776	1	615	QLATFFFGGGLPGGSAPWDPDGG EACLWVLVRLPGRTVWVQFVQLRSFAPPFAHNGRASSGRVS VHYGIAQTAEWAEEICVGAR KIRELAIAIFHQNTIMHFANGG/N PTRRSAVLSSM0GSLPGGCIDA VDHIPVARIVEALENPGGAYQH NGMNRHFPDIRFIWWAGGANF THHQD'TNRLIRA WQNDSYFRKGRIKAKMGPKLF
13697	44065	A	13777	407	661	ANWIKWRWHRAMHSSSSMWQTANSLASFISAPVTSSSACRSTLPATRYWC1*WRSSAIWKWVILSGPVATRICKATIWIQLICN
13698	44066	A	13778	1	2448	
13699	44067	A	13779	3	1612	
13700	44068	A	13780	1	1626	
13701	44069	A	13781	3	118	
13702	44070	A	13782	1175	1396	
13703	44071	A	13783	197	933	
13704	44072	A	13784	2	64	IILLNSAPAWM*TFKLGPGVDV NYMLHTQNK
13705	44073	A	13785	1	855	
13706	44074	B	13786	1	1605	
13707	44075	A	13787	1	588	
13708	44076	A	13788	1	2769	
13709	44077	A	13789	813	1341	

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13710	44078	B	13790	1	999	
13711	44079	A	13791	1	281	
13712	44080	A	13792	1	1332	
13713	44081	A	13793	1	1384	MPITLRRSVEKEQLIEANTIMPF GKYKGRRLLDLPEEYLLWFARK DEPPAEARYTHIDLHVPAPLLV MFTLDDRQSAACDRNPHLPIHVC SSWTSPKCAPRLWTRALLPRT TPPYATGTTGSRASWVFVTFPD ASFYRKAPRQEFTSLQGRSL YVRQRSTANPTEITRRTLHKM VEVNACLQLDNKDIADYEIHN QLMRRRLRQLIAQSWHTDEIRKL RPSPEAIMTEQEKTSAVVEETR EAVDTTSQPVAT
13714	44082	A	13794	1	2004	MTQQITLKDILSNDNYFTLHN TYDLTRKDGEVIRHKREVYDR GNGATILLYNTKKKTVVLRQF RVATWVNGNESGQLIESCAGL LDNDEPEVCIKEAIEETGYEV GEVRLKFELYMPSPGGVTELIH FIAEYSDNQRANARGGVEDEDI EVLELVQCQGQIGVPDTVLAVF ATGIGFLAMSVTKPRINAQYP MPWRNLAQIYEHINRTRIHRNL QFTDAFKRRLIDNICRKNNIIGT HTGQSKFSQGTQOIFGEIPQVVP ASELAAAMKQIKELQRLLGKK TMENELLKEAVEYGRAKKWIA HAPLLPGDGERTDDWMGDGRSS RHTDDTDVLLRIHVIGELPTY GYRRVWALLRRAELDGMPAI NAKRVYRIMRQNALLLERKPA VPPSKRAHTGRVAVKESNQRW CSDGFECDCDNGERLRTVTFALD CCDRLSSRGRNAAKRQRDDP LRWKFLRPLSGGTKLLMPLDQQ APARFAFPVTCTLILCGTGHV VYTILPIIYDVIAKNNIRPERPM AASSIGAQMGIIASPVSVAVSSL VAMLGNTFDRHLEFLDLLAI TIPSTLIGILAIGIFSWFRLKDLD KDEEFQKFISVPENREYVVGDT ATLLDKKLPKSNWLAMWIFLG AIAVIALLGADSDLRSSF/GGKP

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13715	44083	A	13795	3	918	DKTRKRRIRQ*IPNATSFLYQNS PNGLSE*LPAGTWFAGNAPASS CGFRDRYLIVCNSHQTPHVPGQI TVAAPPDARAQAILRIVRQLQRF FHRFEGGHIRQHRAKNLLEHP HIVLTQNRNRFEEADALQPDPA WQQGTLSNGLQWQVLTTPQRP SDRVEIRLLVNTGSLAESTQQS GYSHAIPRIALTSQSGGLDAAQAA RSLWQQGIDPKRPMPPVIVSYD TTLFNLSLPNNRNNDLKEALSY LANATGKLTITPETINHALQSHI DMVATLVFRYLLKKGGWWYRL KGSTLLSHDPAHPLKQPVEAEK
13716	44084	A	13796	1	1368	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASIK NEVFRSGMIAIVAVYGIAMWA ETMFAPACYYGYYILPTYPSDLA AIQFDRSGTTTIGRFRVNHFSILP GLIGVSVCVFGWIFAAIKRDA AAGRAKENVIFHHFFPQSVKAD IATNPFKRPGGAFIRITQTFRTV QTFRLSA YRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNVPLDSSVLSSSLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLCIVQAQGVY TVVAIAAVGICIPPLGMGLATL GRKNFSAEERETGKAALVMGC VGVTGEAIPFAAADPLR/PSFGG KPLSMVLVIQMFMLLTGALIIIL TKTNPASISKNEVFRSGMIAIV VYGIAMWAE TMFAPACYGVYI LPTYPSDLAAIQFDRSGTTTIGR FVINHFSILPGLIGVSVCVFGW FAAIKRDAAAGRAKENVIFHHF PFQSVKADIA TNPKRPGGAFIR ITQTFRTVQTFRLSA YRLDFAG DRLRISTPRAKMRTAFKKDHLR QRRRCIRQRAPPARHNLVGA ALPATVAGVNFTFSNVPLDSSV LSSLTDFSTAVGSIVMLAVIM GLMLA FDMGGPVNKVAYAF LICVAQGVYTVVIAIAVGICIPP LGMGLATLIGRKNFSAEERETG
13717	44085	A	13797	3	2185	
13718	44086	A	13798	1	920	

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13719	44087	A	13799	251	479	TQRVDWRSRSSISPGLDHLA <sup>F</sup> AFGKEGGKMLDRLRERRDVK <sup>T</sup> LQQSGSAAGAEFALAGAH <sup>P</sup> H <sup>T</sup> GTTA* <sup>IQ</sup> QAINV
13720	44088	A	13800	1	939	
13721	44089	A	13801	1	386	
13722	44090	A	13802	3	524	
13723	44091	A	13803	1	548	
13724	44092	B	13804	67	1144	
13725	44093	A	13805	811	974	VSRRRIKLDVTEEFARAGDNKRC ICQ*RHGLAERDIARLLVEIVVI WCDIGVIQA
13726	44094	A	13806	1164	1262	
13727	44095	A	13807	2	894	
13728	44096	A	13808	1	1587	MVK <sup>E</sup> GTFREDLFYRLNVHLIL PPLRDRREDISLLANHFLQKFSS ENQRDIIDIDPMAMSLTAWSW PGNI <sup>R</sup> ELSNVIERAVVMNSGP <sup>I</sup> FSEDLPPQIRQPVCNA <sup>G</sup> EVKTA PVGERNLKEEIKRVEKRIIMEVL EQQEGRTRTALMLG <sup>I</sup> SRRAL MYKLQ <sup>E</sup> YDATGFFRDGMTIMV GGFMGIGTPSLV <sup>E</sup> ALLEL <sup>E</sup> SGVR DLTLIANDTAFVDTGIGPLIVNG RVRKVIASHIGTNPETGR <sup>M</sup> ISG EMDVVLVPQGTLIEQIRC <sup>G</sup> GAG LGGFLNPTGVGT <sup>E</sup> VERQTSID TSTRKRPFELGRPSRNNDK <sup>I</sup> R <sup>P</sup> NDQALDRKNIRE/ALHDSLKRLQ TDYLDLYQVHWPLRPFYC <sup>F</sup> GK LGYSWTD <sup>S</sup> APAVSQLDTLDAL AEYQRAGKIRY <sup>I</sup> GVSN <sup>E</sup> TA <sup>F</sup> GV MRYLHLADKHDL <sup>P</sup> RTVIQNPY SLLNRSPFVG <sup>L</sup> AEVSQY <sup>E</sup> VEL LAYSCLGF <sup>G</sup> T <sup>L</sup> TKYLN <sup>G</sup> AKP AGARNTLFSRFTRYSGEQTOKA VAAYV <sup>I</sup> ARRHGLDPAQMALA FVRRQPFVASTL <sup>L</sup> LGATTMDQL
13729	44097	A	13809	1	618	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13730	44098	A	13810	80	952	RPGIVALNAILPLSRTQRSKPTR LKKRAIANCAPTWKKRFVALV YRTA*RFPSITLSVAVT*PASAK NKAIKMTQKIEQSQRQERVAA WNRRAECDLAQFNQSPKQTYQ AEKARDRKL CANLEEAI RSSGL QDGMTVFSFHAFRGQDLTVN MVMDVIAKMGFKNLTASSL SDCHAPLVEHIRQGVVTRIYTS GLRGPLAEEISRAYCADSHHGP FAMVNNMTDLTAQEPAWQTR DHLDPPVIGELRNRCFGDAFTV QATRTGVPVVWIKREQQLLEV DFLKKLPKPYVMLFDLHGMDE RLRTHREGLPAADFVSFVYHLISI DRNRDMLKVALAENDLHVP FTKLFPNANWYERETWDLFGIT FDGHPNLRWIP
13731	44099	A	13811	92	735	RLLRLPLQPRRSSVLPGLTTFHAS STSETRQSKPTRLKKRAIANCA PTWKKRKFVALVYRTA*RFPSIT LSVAVT*PCVNIITIGCQVKVT TIATAQIQRTRFNHFQRFQYFR NSPKQTYQAEKARDRKL CANL EEAIRRSGLQDGMTVFSFHAFR GGDLTVNMVMDVIAKMGFKN LTASSLSDCHAPLVEHIRQG VVTRIYTSGLRGPLAEEISRG AEPVQIHSHGGRVHLVQNGEL NIDVAFLGVPSDEFGNANGY GKACCGSLGYAIVDADNAKQV VMLTEELLPYTDNPEA
13732	44100	A	13812	I	1113	
13733	44101	A	13813	5121	6228	LRRDSGRLRSCWHPRSPSTMGS LGQREDLQDEDRNSGADPGQR GRCSIHLEGPQQPCQLQRAVQG EGDPVLAKEEIQDQCHPHGQV QLLLVPAAEPVRAVPPRVPQPV PHHHHPAELSGIREE*GNQND EN*TISTTRTGSLESSR*M/SILP LSRTRQSKPTRLKKRAIANCAP TWKKRFVALVYRTA*RFPSITL SVAVT*PYWSGAPGGPCRRPYC HFRHRGARGSGAPGDDGEAPP AAAFLGGDVGFGL
13734	44102	A	13814	56	196	CRGDGGKLIHQCRQRRMGI*PCG* LRQRKAELFQHLPLC*FWRPEI GTVCSSGSDRLLR
13735	44103	B	13815	64	2373	
13736	44104	A	13816	3	403	
13737	44105	B	13817	55	1040	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ~*possible nucleotide insertion)
13738	44106	A	13818	587	1533	VILLTAKFFPSMYSPIKTAGGPA ST*VL*MIISIDAEKAFDIKIHQPF MLKALNKSENKIPRNPTYNGCE GPLQGELOTTAQGNKRGYKQT QQHDMHMSTKNQYHENHTA QGMKGITQPSAFIPTAESNSFQP QVKTLPSPIDAKQQIQRKIQKK QQEQKLQSPPLGESAAKKSESA TSNGVTNLPGNPSILSPQPIGV VAAVPSPIPQVQTRQLVTPSP MSSSDGKVPLPLNVQSHQNCW WTRFMNSSLNVKMTTISLTPS NSNTPLKHASFISATGTTESR SVPQINKGSVVSQSPGSRSSA GGTSAVEVKVEPETSSDEHPVQ CQENSDDEAKAPQTSPSALLGQKS NTDGALQKPSNEGVIIEKATKE RRSSPATEQSWMENVIEEQREE GFRRSNHSQIREDSQTKGKEEK RLKELMELKTKVRELREECRSL RSRCDQLEERVSAMDDEMNEM KREGNFREKRIKRNEQSLQEIW DYVKRPNLRLIGVPESDGENGT KLENTLQDIIQENFPNLARQANI QIQEIQRTP
13739	44107	A	13819	590	817	
13740	44108	A	13820	107	410	KGRNIQLNGPSSRVLWRSLYF LNLTGGLPC*IGEVLLDNLQSV FQLGSILPITFRYTNQT*1WSFI VVPYFLEALLISFYSSFSKLPFLH FIHFIFHR
13741	44109	B	13821	I	3735	
13742	44110	A	13822	922	1137	HFFLHFNFGESENQYVWSFSSR GVSLWRSLYFVLNLNVGLPC*IG EVLLDNLQSVFQLGSILHITFR YTNQT
13743	44111	B	13823	I	954	
13744	44112	A	13824	3	156	
13745	44113	A	13825	683	972	SHRLLRLHSSRSSPGLVSSSISS FKHFSQLVILFTLMIVSFAVQKL FSLIRSHLSILALVIAFGVLVM KSLPTPMSSMVLSR/SFF*GFYG FRSYI
13746	44114	C	13826	I	895	
13747	44115	C	13827	372	1727	
13748	44116	A	13828	705	1072	LALLVELIPLPLCNGLLCLF*SL LV*SLFYQRQLGLQPLPFFVFHLL GRSSSILLF*AYV*LFWHDFAA AGTGCSPCFLALPSGALVGQAA WW*QKSLSICLSVKDFISPLSM KLSLAGYEILG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13749	44117	A	13829	1	1136	
13750	44118	A	13830	547	675	
13751	44119	B	13831	144	1877	
13752	44120	A	13832	1	441	
13753	44121	A	13833	27	344	
13754	44122	A	13834	287	600	GPGSLQSSPLLSPPWPRASSPLL LRPSVRGWHLGEP*NCFPSPLA AS/EQAPKRSS*PQCNHR*RETA ARGLAYPPDRPLPSMLSCEPSE TPAKAGPGRERGCEKC
13755	44123	A	13835	2	226	
13756	44124	A	13836	2	226	
13757	44125	B	13837	45	518	
13758	44126	B	13838	1	699	
13759	44127	A	13839	3	362	
13760	44128	A	13840	2	130	
13761	44129	A	13841	3	96	
13762	44130	A	13842	1	545	
13763	44131	A	13843	2	144	
13764	44132	A	13844	2	91	
13765	44133	A	13845	1	370	
13766	44134	C	13846	1	214	
13767	44135	A	13847	215	310	
13768	44136	A	13848	2	91	
13769	44137	A	13849	1	289	
13770	44138	A	13850	1	997	
13771	44139	A	13851	1	192	
13772	44140	A	13852	2	267	
13773	44141	A	13853	2	181	
13774	44142	A	13854	1	171	MESYAAIKNDEFMSFVGTWMK LETILSLSKLSQGQKTKHCMFSL TDVIARRRSWTSI
13775	44143	A	13855	92	244	KRRRRRGQIRKMKEEEGNRRT WMKLETIILSKL*QRQTKHRM FLLIGGN
13776	44144	A	13856	146	382	
13777	44145	B	13857	124	1215	
13778	44146	B	13858	1	628	
13779	44147	A	13859	377	484	
13780	44148	A	13860	2	220	WARTSCLKHQKQWQQKPKLA NGI*LN*RASAQQKKLPEWTG TWMKLETIILSKLLQQGQKTKHR MFSLIGGN
13781	44149	A	13861	965	1150	GVDQRAVCSSRIW*SHLFHFS VVVHLPLWAGTWMKLETIILSK LSQQGQKTRHRMFSLIGGN
13782	44150	A	13862	254	571	YSYKLEIIGKQPEIYRDPYCRP AV*SQTAVLAISEAPWA*DLP QVSDTISWWTVCA*AHWKSABL GWE*PGFPGTWMKLETVSLSK LSQQGQKTKHHMFSLIGGN

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
13783	44151	A	13863	62	214	
13784	44152	A	13864	274	435	
13785	44153	A	13865	1	294	ASTAGVSYYVAQAGLKLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSLIYIYFFLDEFM YFAGTWMKLETIILSKLSQQK TKHRMFLSUVGGN
13786	44154	A	13866	663	1266	PPLTCQCSHLCVTLVGH/WIKLE TIIISKLSQLQGKTKHVRVFLJGG AGALAKECMMSLYPGCKITVFDI PEVVWTAQHFSFQEEQIDFQ EGDFFKDPLPEADLYILARVLH DWADGKCSHLLEIYHTCKPG GGILVIESLLDEDRRGPLLTQLY SLNMLVQTEGQERTPTHYHML LSSAGFRDFQFKKTGATYDAIL
13787	44155	A	13867	1	681	
13788	44156	A	13868	1	247	
13789	44157	A	13869	2	178	
13790	44158	B	13870	1	2042	
13791	44159	A	13871	1	378	
13792	44160	A	13872	1	683	
13793	44161	A	13873	1	972	
13794	44162	A	13874	308	406	
13795	44163	C	13875	177	653	
13796	44164	A	13876	1	465	
13797	44165	A	13877	3	1175	FFSSQAALLVVLGSSHTLQRA RKHSAPGLPDTCALLQPPAASA AAAPMSGPDVETPSAIQICRIM RPDDANVAGNVHGGTILKMIC EAGAIISTRHCNSQNGERCVA LARVERTDFLSPMCIGEVAHVS AEITYTSKHSVEVQNVMSENI LTGAKKLTNKAATLWVYVPLSLK NVDKLEVPPVVYSRQEQQEEE GRKRYEAQKLERMETKWRNG DIVQPVN.NPEPNTVSYSSQLIH LVGSPDCTLHGFWHGVTMKL MDEVAGIVAARHCKTNIVTAS VDAINFHDKIRKGCVTISGRMT FTSNINSMRFKVLLDAPVVD FQKRYGRQCLSS*VSLSQER QV/PLPVQLVP/ETEDEKKRFE EGKGRYLQMK\AKR\QGHAEPQ
13798	44166	A	13878	121	36I	SLELENRSKFSVATAQLVPSR RLSINCIRRAFITSSNGFPLWFCL HQKGPVDCCVAVY*CGTEDGS WAPTHPGVGPSP
13799	44167	A	13879	1	462	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
13800	44168	A	13880	3	287	PCSLSSDCASNQRDSVGIGPSE PRVGVNILVIRFLSPSEKRSRPRV GVTRFSSAWEPSQLAGILPISEP PSNRIFACWGKPAWTACCNLSLR ARR
13801	44169	A	13881	1	1332	
13802	44170	A	13882	1	753	
13803	44171	A	13883	1	516	
13804	44172	A	13884	71	277	IYFNTQESFCPPRPLK/LCDRG CHKGL*NAFKAFSPFWPLALG SFLLMQISAACLNNSPENGLFFS TT
13805	44173	B	13885	1	1095	
13806	44174	A	13886	1	741	
13807	44175	A	13887	264	2880	WLLQKHKLHVSR*LGLPDTSTW ILPSRPDAGGRFPIRTPCPVLVV HKPSRHCREWTANTVLPKGAL AKWLLEPKADLQGWHLPA QYTKPSISYNIKLYINCYNRTVT TAAQHQVQQRKHGASIFLAEN VAVRIEKDKEERKVTRAPTEQA WTAGSWIETAYREIKGVGQES VCITVMHLEELVYELAWIJMSA VVEAFDPVAPSSKCRNLNPDPD YCCTPYTLHTSPPPPSCTPYT LHTGPPPQTPFCCTPYTLDTSPS PQTHSCCTPYTLHTVPTFHLP AHPHLHHTPPPQTQGGQFVSED EYLEISDIKRDQSGEYECALND VAAPDVRKVKITVNYPPYISKA KNTGVSVGQKGLSCEASAVP MAEFQWFKEETRLATGLDGM IENKGRMSILTFFNVSEKDYGN YTCVATNKLGNTNASITLV HIVGSKALLSKCRTEIITNLS DHSIAKLELRIKNLTNHSTTW KLNNPLLNDYWVHNEMKAEIK MFETTNKNDTTVQNLWDAFK AVCRGKFIALNAHKRKQERSKI DTLTSQLEKELEKQEQTHSKANR RQEITKRAELKEIETQKTLQKI NESRSWFFERINKIDRLLARLIK KKREKNQIDAIKNDKGDIITYP TEIQTTIREYYKHYANKLENL EEMDKFLDTYTLPRLNQEEVES QNRPITGSEIIVAINSLPTKKSPG

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13808	44176	A	13888	1	629	AMAGSPPPASLLPC\LISDCCAS NQRDSVGVPGPSEPGVGYSLVV RRFLSPSEKRSIRVGVTFRSRCR PSPL-SLTQKGNSL\TSWASQVLT PAPEKQPDNKL\PLPRRGSRDPT EYFHGQEVRDKSDEHVDHVSQ IHSFRDEVKRLGAEDSSNAETP TELHEOFNTGGVYRPPNSTSVIQP LDQGVIRTFKPCYTKEYSLEKIVS AVEENPDRT
13809	44177	A	13889	1	1452	
13810	44178	A	13890	167	309	
13811	44179	A	13891	3	386	SVGALQKQQGWHQRRCISLHF PSFLCVFSLAKSRRADHNQDPR ASRMAFSLTSSPLARSAASAVA AFGCCTSGNGRFSVP*AYRQV FQRIAIAVYGPLMRDR*AHPVK TPDAIDCRIRQPAIPRLQ
13812	44180	B	13892	121	298	
13813	44181	A	13893	473	1826	
13814	44182	A	13894	1	270	
13815	44183	A	13895	3	3706	
13816	44184	A	13896	1	1464	
13817	44185	B	13897	591	729	
13818	44186	A	13898	1	1326	
13819	44187	A	13899	1	1152	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13820	44188	A	13900	1	2524	MREEFAHRWLARAGEKTPPDALEKLTDPLMFAAAMVSAGKADVCIAGNLSSSTANVLRAGLRIGLQPGCKTLSSIFLMLPQYSGPALGFADC SVVVPQPTAAQLADIALASAETWRAITGEEPRVAMLSFSSNGSARHPCVANVQQATEIVRERAPKLVVDGELQFDAAFPVPEAAQKAPASPLQGKANVMVFPSENLEAGNIGYKIAQRLGYRAVGP LIQGLAAPMHDLSPCAATDAGSAAAQRIQDVLVSVHVIPRPHVDLEQVPIGLKAYTATCNPVSLRFTIKSSSDRIKLSNQTLQSKNLFIMRFYCFSLCLSLSAFYHCRGVIVNIQAVFWLQKGTEAADILTTCAQLWIMMYALLSVFSLLDVILNLAQKFPAA SQLPLKGIFQGIKLIGAILVGILMISLLIGQSPAILISGLGAMAAV LMLVFKDPILGLVAVRNWDTNTTTPTWSLVSDFKNWSGMSASGGRRIKRSISIDVTSIRFLDEDEMQRLNKAHLLKPYLTSRHQEINEWNRQQGSTESVNLRRMTNIGTFRAYLNEYLRNHPRIRKD MTLMRVQLAPGDNGLP LEIYAFNTVVWLEYESIQADIFDHIFAIIEEEFGLRLHQSPGTGNDI RSLAGVTINKAPGDDIELKNTVDFVFSFYASRCASAEMNANSSAANVVKS LRNPLQVSDWG WGIDPLGLRITMNNMMYDRYQK
13821	44189	A	13901	1	2370	
13822	44190	A	13902	1	282	
13823	44191	A	13903	1	714	
13824	44192	A	13904	3	506	
13825	44193	A	13905	459	551	
13826	44194	A	13906	401	492	
13827	44195	B	13907	479	702	
13828	44196	A	13908	120	256	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13829	44197	A	13909	16	1249	SKSGAIEIAIRLAGRVHGVVVQITSEIGPLTLLTANFAFSAS*STA WKATSMGDGEVLS*YTSASAS AERQSTHQ*TGFAPLCLR*PLPMI /VAQRADDVGFSFEVHGQVRV RPVAQHAQTDKVFALTIVNLGR RVFAALGAEELGGGARSARVPP ECYAVRETALLQKIFPIRQCEN SVYRNRSRPLCQLQYQIGRCLGPC VEGLVSEEEYAAQVEYVRLFLS GKDDQVLTQLISRMETASQNLE FEEAARIRDQIQA VRVTEKQF VSNTGDDLDVIGVAFDAGMAC VHVLFIQGKVLGSRSYFPKVP GGTTELSEV VETFVGQFYLQGSQ MRTLPGEIILDFNLNSDKTLAD SLSLAGRQINVQT KPRGDRAR YLKLARTYAATALTNSFRSIYR SPATDRACQRVETAGNER
13830	44198	A	13910	1	438	
13831	44199	A	13911	1	1200	
13832	44200	A	13912	1	300	
13833	44201	A	13913	1	431	
13834	44202	A	13914	2	1465	
13835	44203	A	13915	1	513	
13836	44204	A	13916	3	535	RDKILVFKDENFWMIRGYAVLP DYPKSIHTLGFPGRVKKIDA AV CDKTRRKTYFFVGIWCWRFDE MTQTM/EKGFPQRVVKHFPGISI RVDAAFQYKGFFFFSRGSKQFE YDIKTKNITRIMRTNTWFQCKE PKNSSFGFDINKEKAHSGGKIL YHKSLSLFIFGIVHLLKNTSIYQ
13837	44205	A	13917	I	876	
13838	44206	A	13918	23	414	
13839	44207	A	13919	2	425	QERGPHQV QRKECLEREYSPVV S*AKGTGVAVGQKGTLQCEAS AVSSAEFH/WYKDDKRLIEGNK GVVKVENRPFLSKLIFFNVSEHD YGNYSCTVASNKLGHHTNASIML FFPGA VSEVSNNGTSRRAVCWV LLPLLVLRLLLKF
13840	44208	A	13920	1025	1270	
13841	44209	A	13921	370	701	
13842	44210	B	13922	I	660	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, .=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
13843	44211	A	13923	1	432	RFSRVDDFVLTMDGPPRRAR GDLTHSGLWRVCCIEGIYKGHC FRINHFPEDNDYDHDSSEYLLRIV VRASSVFPILSTILLGGLCIGA GRIYSRKNNIVLISAGILFVAAGL SNIVGIVIYVYISSNTGDPDSKRDE DK*NHYN
13844	44212	A	13924	1	1093	
13845	44213	A	13925	1	1203	
13846	44214	A	13926	1	1353	
13847	44215	A	13927	2	445	
13848	44216	A	13928	1	227	
13849	44217	A	13929	1	840	
13850	44218	C	13930	120	356	
13851	44219	A	13931	40	342	
13852	44220	B	13932	403	473	
13853	44221	A	13933	70	2169	
13854	44222	A	13934	1428	1905	RCAATSGYGERVQRTV/PTHTV W*ASLSQSSAHRVV/AINSIAK RSSMPPKSWATVALTSTKLKCR FMAKVRNKSFSVLHNV*MTISI/ SPWVILSSGVDEKLFPRAVRVA MTAGASGFLAGRAVWASVVG LPDNEMLRDVCAPKLQLQLGDI VDEMMAKRR
13855	44223	A	13935	227	342	VHSWQRYSGR*RGY*PQNQSA TDQTRRWQSLKTAGAVA
13856	44224	A	13936	480	928	FFADLQQPVCA DYSYPLLVQMK LAPHKS*NA WLWQRSATKS FSV I/AQQLNDH INMPWV ILSSGV D EKLFPRA RVAMTAGAS GFLA GRA V WASV V GLP DNE MLRD VCAP KLQLQ LGDI V DEM MAK R R F I P L R W V D A L T R W L I T V S K R V Q A R L Q L C H K R F Q R H T S V R E Q I V T V L S G I R D N H V H F Q T L T G D G V G N Q R Q L V Q
13857	44225	A	13937	564	1185	WLHASAALLRW*YQLPGQPHH RRCRSADGSHVPSLCAAVPQDR /PLITVRRIGMQAMTTSTTGDRQ RSWQIA MDGSQKLPQRMLDSV RWHLAH DSKF D LL ALGVAGW MRYVGG V DEQ GN PIE ISD P L LN RMAANRF V H I T Q LP V IY RA FRN SFT Q V A R L Q L C H K R F Q R H T S V R E Q I V T V L S G I R D N H V H F Q T L T G D G V G N Q R Q L V Q
13858	44226	A	13938	228	424	HRFCPAARH/R SWSGLREMAVS ISMPRI JNSGRYCA ICWYKRRS RCARNML IFPV ARST PIP GPGS
13859	44227	B	13939	128	1670	
13860	44228	A	13940	2	2367	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, ~=possible nucleotide insertion)
13861	44229	A	13941	1	921	ELPASPAPCARTPQPLGGRWEAARRKERVLCLFDVDGTLTPAR/QGRTLKGSSHRECHADTPEAE CGVCSVTEVRAKWRSGTC*P ECYASPLPP*KIDPEVAFLQKL RSSYLPVGSQTSWHTLSSSCPLC DPEVIGRDTVPVSGSGSPGHAQ SPVFLGQTIONHLGGARFEE RA/CGSLWLPALPHHRRGTFIEF RNGNCVPSQGLAHSRSSELPSA PSPLQKEQAALLALSAPPRE* QSPPLPTGGMISFDVFPPEGWDK QVRSSQCGEGLHLNIPPLPILCV QGGNDFEIFADPRTVGHIS
13862	44230	A	13942	105	416	HSVLEVGPWWEVFGSWGQILH SLVSSHVHRHWLLPSPSAMTES SLTFQQKPSRCQHHASCKAYHS HQLLLVPTAGRLEDRSHH*IPC KHSPAPAWSLAAPVGN
13863	44231	A	13943	191	573	SSSGGYQQQLMRVIGTRDTAV NKASNVPSFGA*I/PSGRGQQAK LIALTRALTLAKELHVNIYADC KYAFHILHQHDVIWAERGFLTV QGSSSIINASLIKTLKATLLPKE AGVIHYKGHQKASAPIA
13864	44232	A	13944	1	1065	
13865	44233	A	13945	321	537	
13866	44234	A	13946	346	1260	GGPARAEFSRHLGCKGHHLPLPK DVASEVPAGSSTS VSSLLIRNTGC PGLGSWEPP*FFSENKRLSTLMS FTLRDKSMFSPQSGLFLGCSAG EHSLARLDPPTASGLPGTASGVRP GR/RQRVGS DIEASTQGESKPCI LSI*TLPNA*LKTKTLPLEIAAC TNPHSFSITARIGPAHLLAAPPV TPAAGRRGARAPGR*CAAARPPP ASQ*VSGSPAPGGGPSTYAPAAR TS*PSSLLPAGAKRLRFSRVATFC CSFLAWSSSSNKAFC*EHMSL LSSWIQSLEKVASCCPCEQFDS WKRLENILLFS
13867	44235	B	13947	1	459	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hind	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, <=possible nucleotide insertion)
13868	44236	A	13948	63	1263	VEAAKKAHHAACKEEKLAIRESANSKADPSLRPQAHTYALSPFLTAMPSPV*QGEHVIVYTRVRHS DQVSESSGKPLSLPPLLEPGIWAF EAAQVPPRWDQVRSLEPTTEWEAPGLKKRRLVSQGLNGNEPLCAWIFL*TKEKYEKSLELDQGT PQYMEMENMEQVFEQQQQEEKRLGWDKG*LAPAF*KSHVSL*FS YKAIYHDLQESIRAAADE/DRRGFRK**TFGFSPSAPVA*EWSADLNRTLSRREKKKATDCQDPHGPLQSWDPLKALSLHSTLNVP SNPQSAQSQQSYNPRGPHTLCRPVLRALWPPLSCSVSSYEKTQSYPTDWSDESNNPFSSTDANGDSNPFDDDATSGTEVLCSPPSVSYLSWRRRLPLCLAGDELTKMEDEDEQGWCK
13869	44237	A	13949	2	485	AAAFGTRLSRRGRGCGVGTSGGGRRRVPAAPRRPRSPQPHQ/P PRRPSRRTPGCGSGRGA/PSRGRRLVPPPPEPRAAQQRARHHRTRPAAQPPRPPAQPQRCSPRRVRPTPAWSPPGRRGPRRSRRRRRGGRARARRPRRRGQVPRPQSATGAGHAR
13870	44238	A	13950	1	207	
13871	44239	B	13951	1	5297	
13872	44240	B	13952	1206	1360	
13873	44241	A	13953	46	369	NEGKNAKGSQRERSGYPQREAHQTNSSGLGRNPTSQRKVGANIQHS*RKEFSTQHFISSQTKLHK*RRNKLILYRQANAERFCHHQEGSTKHGKEQPVPAAKSCQNVK
13874	44242	A	13954	476	868	KYDCCISSTCRALVHFSRTTFQVNSPLSPNISAFGYMPLKYSIYFLHHLRPNII*AAASYFLKYKGTLKLPALRGCLS*STRCWCKIHCIC*ND/ECLQFLGPWFENEFCFLPSTSQFVEFLDILVLQNEP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13875	44243	A	13955	1770	3003	PANIIIMTGS\NSHITLTLNVNG\LNAPI*RHRPAIA/S/WLKSQDPSVVCICQETHLTCRDTHRLIEKGWRNIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKKEGHYIMAKGSIQQEEELTILNIYAPNTGAPRFI KQVLSLDLQRDLDHAHTIIMGDFN TPLSTLDRSTRQKVNVKLDIQLEDSALHQADLIDIVRTLHPKSEYTE TFFSAPHHTYSKTDHIVGSKALLSKCKRTETITNCLSDHSIAKLELRKKLTQNSATWKLNSLLNDYWVHNKMKAEIKMFFETNENKDTAVQNLWDTFKAVCRGKFI ALNAHKRKQERSKIDILTSQQLKE LKKQEQTNNSKATRQEITKIRAELKEIETQKTLQKKQPNKDPM EKNNKTDRVLARLIKKREKNEFSAHILYKFSKQNGS
13876	44244	A	13956	105	392	RSRKPRGNPKSHPEDTDPTKAP RKRQISSRGHRSHR*EPGPQSAAPGFREQRRRGQMG*IWYLTPTP PGGQPQSSAASPRGFPPTNNSSLPAEPE
13877	44245	A	13957	55	403	SEGMMSGKASEKQEAFACPRLT RAVDGPS*SGLLGSRLPPSCSPGKEAPGGS ELYCLMRGLQTL*A RSGTGLR/PNPAEIR*EPGPQSAAPGFREQRGGQMG*IWYLTPTP PPGQ
13878	44246	A	13958	217	444	RSRKPRGNPKSHPEDTDPTKAP RKRQISSRGHQSCHR*EPGPQSAAPGFREQRGGQMG*I*TPCRP ALPKSKPRPL
13879	44247	A	13959	309	670	PCPRASSQGLKATH\GQR*SSEPGASFPGLQDGRRREPRPD*D GPSTGLVRCLGHANVGDPCLKVFVFFKNLSPTYLARSAEQTLPLLLPHLHGCLHQPLHLGFTAA WAQLTFWEASQ
13880	44248	C	13960	392	760	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met ind	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
13881	44249	A	13961	24	915	HAGRARGSLFPGARPSETRAH CVRTPNCKEEDTPMVRGKN SGGEHCTWGPSLAAGG*GIGDP GGLPGTIPHPGQLLHHGFAGP HMASLCCGVSSPAGVRQWP* GSGNH!QVKSWLGLPKNV*AP SML*NPKMQRQLMKAQPHGRCE VRRGRVCSALGP/GMSGKASE KQE*A*DEGHPHLHAPGT*QDQ VDGPS*SGILGSRLPPSCSGPK APGGSELYLCLMGRQLT*ARS GTGLRANPAEIR*EPGPOSAAP GFRREQRRGQMG*IWYLTPTPP GGQRPSSAASPRGFPLV
13882	44250	A	13962	397	612	RPQHHTFCCDGRVMMARQKG FYLTFLIILGTCTLFFAE/CSFG *VELPDYGYFGSRGRTCFGLSG GLVLG
13883	44251	A	13963	125	1298	FQSWAQPLFLSCNRKTHFGTR IPIMSMVMVVRKKVTRKWEKLP GRNTFCCDGRGMMARQKG!F YLTFLIILGTCTLFFAE/CGRYL AVQLSPAIPVFAAMLFLFSM!AT L!LRTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQQGQRPPIRK NFQINNQIVKLKYWYTKIFRA SRASHCSICDNCVERFDHICPW VGNCVGRNRYRFYLFLISL LTIYVFAFNIVVYALKSLKIGFL ETLKETPGTVLEVLCFFTILWSV VGLTGHTFLVALNQTNNEDIK GSWTGKNRVQNPYSHGNIVKN CCEVLCGPLPPSVLDRGILPLE ESGSRPPTQETSSLLPQSPAPT EHLNSNEMPEDSSTPEMPPPEP PEPPQEAAEAEK
13884	44252	A	13964	44	647	DYSAQHGKASQKHVARLISSGT FQGATVSRPFQQLSTSSSSFCSSSS SISSSSSSSSLLILSCSSSEVFLS LSFFFCSFEASFLPFCCSRLYASRA SFNGVTRWNSISSMAESTSLA FSVFRPFIAKLLAQDVAYSTKT LAAREIGAPGLLGDVDTVRERL GDRG*AKLPFQHLLPSCPFRVPP RAAHLRLDDPGDGHGIGQV
13885	44253	B	13965	158	1075	

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13886	44254	A	13966	125	1297	FQSWAQPFLLSCNRKTHFGTR IPIMSVMVVRKKVTRKWEKLP GRNTFCCDGRGMARQKGIF^ YLTLEFLILGTCTLFFAFAE/CGRYL AVQLSPAIPVFAAMLFLFSM^AT LILRTSFSDPGVIPRALDEAAFI EMEIEATNGA^PQQGRRPPRIK NFQINNQIVKLKYWYTCKIFRA SRASHCSICDNCVERFDHHCPW VGNCVGRNRYFYLFLISLSL LTIYVFAFNIVYVALSKLKGFL ETLKETPGTVLEVLICFFTLWSV VGLTGHTFLVALNQTTNEDIK GSWTGKRNVRQNPYSHIGNVKN CCEVLCGPI.PPSVL.DRGRILPLE ESGSRPPSTQETSSLLPQSPAPT EHLNSNEMPEDSSTPEMPPEP PEPPQEAAEAEK
13887	44255	A	13967	247	850	DYSAQHGKASQKHVARLISSGT FQGATVSRPFQLSTSSSSFCSSSS SLSSSSSLSSSSLLSCSSESVFLS LSFFFCEASFLPFCSRILYASRA SFNGVTNRWNSISSMAESTSLA FSVFRFPFIAKLLAQDVAYSTKT LAAREIGAPGLLGDVDTVRELR GDRG^AKLPFQHLLPSCPVRPP RAAHRLLDPPGDHGIGQV
13888	44256	B	13968	298	380	
13889	44257	A	13969	48	252	QRAGSPHSPRSLSAPPPELPLW RHLRSPSAHRTCTVGAPFWDGQ G/LEPAPSAALAAFPRSRARDLQ LA
13890	44258	B	13970	1	447	
13891	44259	A	13971	236	559	MWLEPMQMGFLHMMEKMAA RTSAILD^GTLK^FHFTLTTSLK ALSSHTPIFPGTGELOQLPVSPSV CLDQGMQLKPKSTSSHLLKTVKP RMKRSQLLHMKQSFPEKIYL
13892	44260	A	13972	1	645	MKPQTLTVSVTAKFVAHLEFVP SDVQMCSEFLPSGGFVVSLASG VKLQTTAVSFTAHKSSVDPKNS EAQLASPSGFCTRAADGAACQS LPCTCTPQPLGGRWDWALWS RGW/LVVEEA^AAQEPTEELRE RALALASPERGSHSAAVGQRAP QVPPKWEPRQRRRRERARARAVR TASTLSPLNPPSKQDTLTVGN LADDHSSYFLLDRGEEGALQL
13893	44261	A	13973	28	322	
13894	44262	A	13974	1760	4426	
13895	44263	B	13975	942	3414	

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13896	44264	A	13976	1	274	
13897	44265	A	13977	545	1150	RISGPAGAVLLPVMPALWRLRHR MFSLTTKK*HLPahrsllaEGYLL YQPQLDTLKLARL\QKYQELQV LFEAYQIKKTLDRQSSASLET LLALLQAEAGAKIEEDTENMAEK FLDGELPLDSFIDVYQSKRKLA HMRRVKEKLQEMVLKGQRL/S TRPWPCPPGCPNWHLPPFP LPQSQWASCRCTSAHPPPTPG AAGRL
13898	44266	B	13978	213	611	
13899	44267	A	13979	1	639	MEAVTVVPVGTEEGMEEEQD SGTTTGCGLPSVEKMLATNPKG TPISLLQKYGTRIGKTPVYLL KAEGHQPNTFWVVGNTSCT AQGPRRKVVVKHKAEEVALRHL KVESMLEPAPEDSSSSFPLDSSL PEDFPVFTAATPVSSVFLT RSTPMEKQPPLP/QQSECIPVG ALQKLVVKQKGWWLPEHTVT*E SRPDQHEELT*RVERFT
13900	44268	A	13980	361	894	AFFPMSTAGVCGNVEGEPETP WSLPLSQQVFPSPNA/CPQGTLGR S*AGVAGAPGPGVPGRSPAA/GI PEPAAARPGRPALSRLPGLGGAG ARSGAA*G*GSRPGG/PLPAAADP VQSWG*EAPSHP*PGTSAADSP PSGVSGATGDCLWGSGRAELF GFATTTSAAPFPGLPTFFFIPVSP
13901	44269	B	13981	1	3842	
13902	44270	A	13982	3	407	DAWAAAARPGRSCALPPIGA/PE EPGHVPGAA*G*GSRPGGRFQL PDPVQSWG*EAPSHP*PRNFQ TRRHLGVVKQHGCSQSPHGSRA SQAHPGISGLF/GPHHPGPPLFIH GPRCCCAQATASNHLFACGTSS DP
13903	44271	C	13983	127	297	
13904	44272	A	13984	3	1920	

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13905	44273	A	13985	3	2271	GQGRRTAGGGGGGGAGVGAG AGAMEAERGPERRPAERSPGQ TPEEGAQALAEFAALHWVSGE GIVGVSPAHTPADGNSGPQVFD AGEVF GimQVEEVEEDEEAR EVRKQQPNNPLAPPTSLCPMPTR QPHIVACARSIFLIDHAWTCRV EHARQLQQVPGPLLHRMANL MGIEFHGELPIWVPEGSSGW MGEREVPVVLCLQTAEEKMPV WYIMDEFGSRSQHADVPASFATA ^PLEEGPQPSPVSPPLMGTH/DL GTEEVTRDFAYGETDPLIRKCM LPLSSSHRGMETPCVHTSASL PLQACELPSWSLNLINEPPRPAF PSLP*PHLYFRCVSF^AIPGLVLE SRLDTWEPGSPSSGSPHRVYTD VQQVASSLTHPALPVRSRASR PPLELAHLLPPPCRQLSQRPGV LNQFPCENLLTVKDCLASIARR AGGPEGPPWVVLGWHHLGTQ APGAPQTALLPRGEDDNHWICK PNWLGLCVLGSPRGLCPGHQR ACTCVLQVVSKYIESPVLFRE DVGKVKFDIYIVGGTSLAGR PLKNPYVSAHLSSRAFAQGRRG RGGPTWSGWLLARDPARV^DL LSSLVHSVERCPMQWALSEWQ LHHLSTWSSGLCGLAG**VFQM HRTPTPP**QACSRPSGGLYR A*WALCLLPGAADPLLRGCSEQ AS*LRLPGPQAEIIFRATFELFQV
13906	44274	A	13986	1	600	MEEQRVQFTLWLHFSPHGICQF ESGRQEAKKLKGSGQQPLKTGEI KTGIQKYREALLQHYLGPASL AGRSKALTGTAEERSCSSGDSSI FTLCVNYNDRSAIMKTLAAIGT GFDCASKEAIQLVQILGMPPER FMYANSCKQMSQIKYTANNGV QMMIFGNEVKLMSVARTHSKQ P/CHISVKSGAMLKASRLLE*A KEL
13907	44275	B	13987	1	2040	
13908	44276	A	13988	205	438	LYFLETGVFCVQVPAQQC*CSV PGSCRRLPLEAGWRGLGLSRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, - =possible nucleotide deletion, + =possible nucleotide insertion)
13909	44277	A	13989	284	632	KTGVFCVPGPRPTVLM*CSFG GKKNQYCLTDAGCLQEKHSL GPAGVHLEEAQWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRGKVTRWLSPHQVQRQAD AGTCSPFEP
13910	44278	A	13990	594	1003	VRKGHHAVRGLCGRAQFRCIS GDPGKRPLG/LPGGNAPKSGSL ARRPQPVIPGSRPQ/RGSVSHL GPAGVH*R/RAGWRLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRGKVTRWLSPHQVQRQAD AGTCSPFEP
13911	44279	A	13991	1	1500	VRVAHIPIAAEIAIPDRGGH SVGKRKLTFWFFYGVLPFRDV AIEFSPEEWCLDSAQQHLHRD AMLENYGNLVSLAAGDQSLPG DAAASAVCRQLSPSACGAILGL PPVNGVAPVRLRGEIVTYWSQ LTGLALALSKDAGGLRRLTRP TRRAPPAALLLAPQTAEARWRG KCDPRHGGGCALALQGWTLYP RESPRESKELGGLWSRADLD SRRQGFEEQWYPRPLRELRGRG GRRPEARRWEGGSPGPCCRLLPL SAPELAPYRKLKVNGLRGAGL GDGETGGTGEGRGRRKRCC RTLSRDEGFNDICQDWLRQF VGWVLYEQEVTLPEQWTQHLR TRVVLRIASAHSYATVVAARS RQGRGIGGLIYTLGMPFFLSGW QVPEPHAAQYVRECLIAGPLLM P/TTCCPILLISPVSAVGEWGRHA RA*GADSSSLVQNTDFDFNNYA GLQRISVLLYTTLTYYIDDITTT GVEHDSAEIPIFPEYLRVNTGN
13912	44280	A	13992	2	307	
13913	44281	A	13993	220	427	MSTLPFPSLQMFRRPPYGPSPST RSQDNRSYSRVTEELQERRRW NSGDAN*DQSPEARRQPRHIE EAA

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13914	44282	A	13994	1	2832	MGKYTTQGDKVLMPLAIQVH HAVCDGFHVRMLNEQQYC DEWQQGAYPKGYFVQNTDFDF FNYAGLQLRSVLLYTIPITYIIDD TITTGVEHDSAAAPMVDSLIAR VGVMARGNAITLPVCGRDVF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRVSGVIEIADGSRRR KAAALTESDYRVLVGEELDEQ MAALSLRLGNDYRPTSAAYERGQ RYASRLQNENFAGNISALADA
13915	44283	A	13995	1	2934	MITFDFMSHIQVTLMQEVSFHG LGQLRPCGFAGYSPPGCFHRL ASSVCSFSRCTVQAAVDLDPFWG LEGTSPPLAASLGSAPVGTLCG GSDPTFPSWTALADLVHEEGBT PASNFCRLNLAGEASQSWRKE GLGTPRPTASSTEELQTLNEDSR LMTSPHNLEETRDCTELPKKS LGWKEIRVYGGQNKTLGFWLQA QILLICDGNNLRMFRLLPYGSPS TCRSQDNRGYGGVTEELMERK RWNSTDGFHIQGVLE
13916	44284	A	13996	68	425	SHILPGAPGAPAWWTRWPPLP EPFPGRGRGSPAGTSPISRPGLVQ SS*ASRGSDSRLPV/GPASCQAS GPGPDSRPPPCTPA/GPHH GSL PSAGRVGASAAAAGPPSPAVPL PPAERPAP
13917	44285	A	13997	324	723	TAFSLNFQGGVGEVWAGTRA ARGACAGERGLGGSRTRSGW/P GTAGPGQAGHGTCSLPCSLPP AMGSCVSEPRQAPPAPWRLV PSTAQGLRSVGTQCGTGGSSAC GPC\GDPGF*THQSAPCQNGPIS SL
13918	44286	A	14000	39	383	

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13919	44287	A	14001	181	1446	EDLLQEAQALAEVTAQKGGLG QVRSLDSLEACAGSPPLQLVD LQDRPRLTSLPSSAANRGKLG EKAQSNPCGHRHQAAGLKLPG LFSAQAPQGQPTPAAPRFRAATR KPGTAQSHIAPLWSPAMSFFPEL YFNVDNGYLEGLVRGGLK/ALGE LSQADYLNLVQCETILEDLKHLH QSTDYGNFLANEASPLTVSVID DRLKEKMKV/VEFRPEGHTMPY EPTSPSF*TSITLQFT*FDNVI/L WLHHRARLHQRSIAELVPQVAH PLG SFEQMEAIVNIAQTPAELY NAILVDTPLAAFFQDQISEQDLD EMNIEIIRNTLYKAYLESFYKFC TLLGGTTADAMCP LEFEA NR RAFINT NFFG TKTVPKKDRCP AFFPH/CGAGFPPEGPAAMGFG LNNLLTGAKKRGPY NFPVQL AFLRGDG
13920	44288	A	14002	1	1182	
13921	44289	A	14003	26	342	ARFLAGP*LPSSRTGLRDLQPA MPEPPPTPWAPVRPEPPRRAAPP PAPRRPVPSTGKEQTTQGLRSA GAGHRDWQAAPPAAPVRDPLG EASWAPESGGDVESLYV
13922	44290	A	14004	66	463	
13923	44291	A	14005	3	1446	
13924	44292	A	14006	221	852	NSFLMVGFFPFFSL/CAAFDTKT GLRAVAKKLSRPFRLPDGYYTE FNIYLLFNFY LTSSA V*VVLSH SVVIECLLSIRHCSRVRFKSSED KNFLRGSRLLCNFSLISRYLVTH LMGADLNIV*RYR*YK**FFK MNSPFLPLPVGGELIMHHKVDP VCFVFSLPSKSKS*QFCVSSSAL *ILDFGLARHTDDEMATAKGQPE CFVRWACAS
13925	44293	A	14007	55	784	RHIQDPASQRLTWNKSPKSVLV IKKMRDASLLQPFKELCTHLME ARGAGGGHDARS TAPVSR PPCRRVGSAAGMSRLALCFQEN MIVYVEKKVLEDPAIASDESFG AVKKKFCTFREDYDDISNQIDFI ICLGGDGTLLYASSLF/QGNA VVLRSRLKVRVVKELRGKKTA VHNGLGEKGSQAAGLDMDV KQAMQYQVLNEVVIDRGPSYY LSNVDVYLDGHLITTVQGDGV VSTPTG

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13926	44294	A	14008	155	1592	PESRHQCFSDRSANFLTMEMEQ EKMTMNKELSPDAAACCSAC HGDETSYHNPPIRAKRSRL SASPALGSTKEIRRTSLHGPCP VTTFGPKACVQLQNPQTIMHIQD PASQLRLHVEQRPPRTVLVIKKM RDASLLQPFKELCTHLMEEENMI VYVEKKVLEDPAIASDEISFGA VKKKFCTFREDYDDISNQIDFII CLGVDTGLLYASSLPGQGPSPP VMAFHGLGSLGLFTTPISFENFQS QVTQVIEGNASCSSGSRKKGQ GW^RSLRGKKTAIHNGLGEK GISQACRPCTMDVGKA/QAMQ VPRS*NEVVIDRGPPSYLSNVD VYLDGHLITTVQGDGKARSTV LGP^ASL GRE^RLRLSLSGVIVS TPTGSTAYAAAAGASMIHPNVP AIMITPIRSVLPTAGGPHLSSL DPQIMLSPEARNAAGGPFWKP WLRLLLSSRPSIISITSCYPLPSIC VRDPVSDWFESLAQCLHWN
13927	44295	A	14009	327	466	
13928	44296	A	14010	2	196	
13929	44297	A	14011	923	1776	WRKCGCETAGSASATRAAATE KMEAPRNKMCRDQENSAWRN AVPGP^*RQPEEFPTTTSILAEPTVLSRKCRPSEKRGSATEKFG ATSAVTENPPLGAAGERANKTL GAATVTPTLGRPRMEKGGR CPSTL^PSVQERQEPSPSGNHPE TQKIEFAGRRVTFQIRWATTLR TRISGTGASPRDRSAFFGFPWC G/AAQPSDEESTPATQEEAQAGQ AGVAAAASSEEPGHCAPRPPHA PRSALIFEDWSREPERSSDDGDLSCCRRPATEPWRPPGSAWRLPCA A
13930	44298	A	14012	568	1223	SARGLLPGSGPLSHAGPQLQVE WFGLCLPPDSTLELVVCGTVAI SRVRMSAVCVLRTWSRNAGIQ L^ICFTVQPCNSVHVL/KGPNY VCFFGYPSFKYSHPHNFKLTI NAVCGQILVQFRFPDTEEGIRK VTV/KCYVKEGDTVSQFDNIGK VQSDKASVTIASPYDGVI/RKL^ HSLDDIAYVGKPLVNIETEALK GTVNLFYQIDYCPPFVIGSQLK

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13931	44299	A	14013	5	296	LFSRVP SKGPP RYHHTSSRG*TRAD*LISSGNS*AH CIP SGLQGM LNLLPTP RAP VRPEPP RAPPA PRRPVFDH PRAC GTGRQLHLQ PRCGIH
13932	44300	A	14014	1	376	MQAVLLTVLQKHNQSVIYWY MKYIYYEGLVIMDDYDVYIMD YMTMETEKSHDLQAGGGPKPV VQFQFKPKIQLQASRONGVKSWS KSKGLRTRCANA VQQQENREGP AKHSPFLCLFVLFGSSTGRMIPN HTGDTSKVIA GTEERGVPKKVT LKFDACAAIDRPWAHQLDCTY HFKGSDNDEHDSRLHTNAG*^L C/RLWIT* LWRLRNPMICRLEA QESQWYFSSSPKSCPKPVEAMA LSPGPSPKA*EPGVLMMSKGRKI GRAQLSIHLSSAFLFSAPQQVE
13933	44301	A	14015	1638	2289	VEKKKKPMSAPALRRLPDLT KLF TLYVSETKKM A VRVLTQTVGP WPRPVALLSKQLDEVSKRWP P CPKSLV A I A L L A Q E A D K L T L R Q N L N I K S P C A V V I L I N T K G H H *L M N A R L A R Y Q S L L C E H P R I T L G S L Q H L N P A T F L P V S E S P V K H N C V E V L D S V Y S V Y G P N H R D H P L N I S R L G A V T W M G S S F H Q P L Q S D T L K K T T S P G S S H T R K L T G P R T A E A
13934	44302	A	14016	1	675	MAPPLRPLARLRRPGMLRALL LLLIISPLPGLREGIEGITPIGT SLPDLDPARRRWE GGIGR V GSE VADLC PGKEGGK VPEAEKEGV WCFSELSFVKEPQDVTVTRKDP VVLDCQAHGEVPIKVTWLKNG AKMSENKRIEVLSNGSLYISEV EGRRGEQSDEGFYQCLAMNKIF *AILNQKAHI.ALSRIGST*RRRP DRP*EDEAFVMTTHCFQDL LTS
13935	44303	C	14017	18	329	
13936	44304	A	14018	391	895	WASSDTPTGFTQRWRPDWAGG GGG EERG DGTGVV WEGEV KVY RFR RVTGSSFP SPA VLV RAPN TGMPKLT V I QT*GPL G E R G K E P VPPN VPTLPQTFGGLN A S V VRK TEIPSPSPPPV CYL RASAER Q/PA GGSPQAK W RRA A S S P P P L P P V H L P P P P P R P P P P P P P P P
13937	44305	B	14019	1	1110	

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13938	44306	A	14020	282	710	YPEPQGWRVAHTVQYPIHQPL KPGPRGR*SIMDIQVPPKEGGV LILKNSSRLLNSWTQGCLQISA FSPFTSS*LPGTPWSNVGPYKIAPI ITSFGE*PFIKVQLPWSWISHIQ V/SHK*QIHRHSVLDIGWSPGQEC GPKGCFV
13939	44307	A	14021	I	1416	MILIDAEKAFKDQIQQPFMLKTL SKLGTGTYLKIIIRAIYDKPTAN IILNGQKLEAFPLKTKTQRQGCP SPLLNFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMMIVYL ENPIVSAQNLKLISNSFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRKRYLGLIQLTRD VKDLFKENYKPLLKEIKEDETNK WKNIPCSWVGRINIVKMAILP DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWGKDSLFLHKWC WENWLA VCRKLKLDPLFTPTY KINSRWIKDLNIRPKTIKTLEEN LGITIQLDIGVGKDFMSKAPKAM ATKAKIDKWDLILKLSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSSLAIREMDIKTTMR YHLPVRMAIKKSGNNRCWR GCGEIGTL
13940	44308	A	14022	I	3450	
13941	44309	B	14023	I	3171	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Motif	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, -=possible nucleotide deletion, !=possible nucleotide insertion)
13942	44310	A	14024	1	2433	MRTKTQHTRISGTHSKPVCRGK FIALNAHKRKQEKSICKTLTSQ LKELEKQEQTHSKASRRQEITK RAELKEIDTQKTLQKINESRSW FFERINKIDRPLARLIKKREKN QTDTIKNCKGDTTDPTEIQTII REYYKHLYANKLENLEMDK LNTYTLPRLNQEEVESLNRPITG AEIVAAISSLPTKESRTGWHHSRI LPEVQGGTEKEGILPNPSFYEASII LIPKPGRDATDKKENFPRISLMNI DAKILNKILAKRIQHKKLIIH DQVGFIQPGMKGWFWIRKSNV QHINRTKDKNHMIISDAEKA DKIQQRFLLKLTLNKLGDGT KIIIRAYDKPTANIIILNGQKLEAF PLKTGTRQGCPSPPLNFIVLEV LARAIRQEKEIKGIGLQGKEEV SLFADDMMIVYLENPVSAQNLL KLISNFSKVSGYKINVQKSQAF LYTNNTQTESQIMSELPTFIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKDDTNKWKNIPCS RINIVKMAILPKWNKK WNQKRAHITKSILSQKNKAGGI TLPDFKLYYKATVTKTA WYQNRDIDQWNRTEPE SIEMLH TYNYLIFDKPEK NPKNQWKG KDSL FWK CWE NWL AICR K L DP LT PYTK K NS W K I D LN V R P K T K I K T E E N L G N T I Q D I G M D K D F T S K T P K A M A T K A I D K W D I I K L K S F C T A K E T T I R V N R Q P T W E K I F A I Y S S D K G L I S R I Y N E L K Q I Y K K K S N N P I K K W A K D M N R H F S K E D I Y A A K R H M
13943	44311	A	14025	1	1023	MGAIYDKPTANII LNGQKLEAF PLKTGTRQGCP SLLNFIVLEV LARAIRQE KEIKGIGLQG KEEV LSLFADD MMIVYLE NPVSAQNLL KLISNFS KVSGYKIN VQKSQAF LYTNNTQ TESQIM SELPTFI ASK RIKYL GIQLTRD V K DL F KENYK PLL KEIK DDTN K W K N I P C S W V G R I N I V K M A I L P K A I C R K L K L D P F L T P Y T K I N S R W I K D L N V R P K T K I K T E E N L G N T I Q D I G M D K D F T S K T P K A M A T K A I D K W D I I K L K S F C T A K E T T I R V N R Q P T W E K I F A I Y S S D K G L I S R I Y N E L K Q I Y K K K S N N P I K K W A K D M N R H F S K E D I Y A A K R H M
13944	44312	B	14026	1	2206	
13945	44313	A	14027	1	1689	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
13946	44314	A	14028	1	2523	MKQFLYLDESNALGKKFIIQDI DDTHVFPVIAELVNVLQERCHTR LGYTEFLVAWRVTFGLCVAEV TLHLKYQILRGLLEMMMSFSDA DILKQLPVTPGLFPASLSPSSL LGNSPPSWLRHNSESKVSAVSS PSATKTLSTGIGKLDPGHKEMA EESELLKNKMQAPPLSRCPEQ KCQHQQLRLHHWKPSPVRHQVKR RSPAVLRSAMPADCPAVLEAT TATHPEKGTLALKLHPSDSDSMS LKVDVEALENSPGATYIWKG KVTRDSQPKEQGKGDLLKKKK GKLKPNYDPKLTPDPERWLP QECSFYQGRKKGGKKKDQMGK GTQGATAGASSELDAKTVSSP PTSPPRGSAAATLSAASTSNIIPPRH QRPAAGAPATKKKQQQKKKKG GKGFPVLREITVVVKVDTLVVFQ ILEERLSVFIQYDTSYPFSTVDI EDHECAVVWLLLRKSKSDDKTT RLEAVREMSETHHWHDAEKA DKIQQPFMLKTLNKFVGVDGTY LKIIRAIYDKPTANIIHNGQKLE AFPLKTGTRQGCPPLSPLLFNTV LEVLARAIRQEKEIKGIGQLGKEE VKLSLFLAGDIIVYIENSIVSAPKL LKLISNFSKVSEYKINVQKSQAF LYTNNRHTESQIMSKLPPFTIATK RIKYLGIQLTRDVKDLFKENYK PLLENIKEDETNNEWKNIPCSWSVG RINIMKMAILPKVIYRFNAISIKL
13947	44315	A	14029	1	2868	
13948	44316	A	14030	1	3099	MGEPLITPLSTLDRSTRQKVNKD TQEELNSALHQGDLIDLYRTLHP KSTETYTFSSAPHHTYSKIDHILG SKALLSKCKRTEIITNLYLSDHSA IKLELRINKNLTQNRSSTFWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDDTYQNLWDAFKAVCR GKFIALNAHKKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELEKIEETQKTLQKINESR SWFFERINKIDRPLARLIKKRE KNQDITKNDK
13949	44317	A	14031	2	3419	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, -=possible nucleotide deletion, !=possible nucleotide insertion)
13950	44318	A	14032	I	2685	MGDFNPTLSTLDRSTRQVNK DTQELNSAPHQADLIDLYRTLH PKSTEYTFPSAPHHTYSKTDHIL GSKALLSECKRTEHITNYLSDDS AIKLELRINKLTQNRSSTTWKLN NLLDDYVVHNEMAEIKMF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQKLEKEQEQTHSKASRRQ EITKIRAELEKEIETQKTVQKINES RSWFFERINKIDRQLARLIKKR EKNLIDAICNKGDDITTDPTIEQ TTIREYYKHLHYANKLENLEEM DKFLDTYTLPRLNQEVEVSLNR PITGSEIVAIINSLLTCKSPGPDG FTAEEFYQRAIRQEKEIKGIGQLGK EEVKLSSLFADDMMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPTFIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDETNKWNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFTELKTTLNFIWNQK RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWWYQ RDTDQWNRTEPSEIMPRIYNL JFDKPEKNKQWKGDSLWNKWC WKNWLAICRKLKLDPLPTY KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLILKLKSCTAKE TTNRVRQPTKWEKIFATYSSD
13951	44319	A	14033	845	1616	ARAEVKLSSLFADDMMIVYLENPII *ARAEVKLSSLFADDMMIVYLENPII IIAQNLKLKLSIKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDETNKWNKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFPIPYTKINSRWIKD LNVRPKTMKTELESQNTIQDI GIGKDFMTKTPKAMATKA/KKS FCTAKETTIRVNQRQPTWEKIF AIYPSDKGLIS

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met ind	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
13952	44320	A	14034	707	2878	TLMQKSSIKYWQNESSSTS <span style="font-variant: small-caps;">K</span> SL STMIK <span style="font-variant: small-caps;">W</span> ASSLGCKAWFNIRK <span style="font-variant: small-caps;">S</span> I KV <span style="font-variant: small-caps;">I</span> QHINRAKDKN <span style="font-variant: small-caps;">H</span> MI <span style="font-variant: small-caps;">I</span> DAEK AFDKIQQPFMLKTLNKL <span style="font-variant: small-caps;">G</span> LDG <span style="font-variant: small-caps;">T</span> YFKII <span style="font-variant: small-caps;">R</span> AIY <span style="font-variant: small-caps;">D</span> KPTANII <span style="font-variant: small-caps;">I</span> LN <span style="font-variant: small-caps;">G</span> QK <span style="font-variant: small-caps;">L</span> AFPLKTGTRQQG <span style="font-variant: small-caps;">P</span> LSP <span style="font-variant: small-caps;">I</span> LLFNIVL EV <span style="font-variant: small-caps;">L</span> ARAIR <span style="font-variant: small-caps;">Q</span> E <span style="font-variant: small-caps;">K</span> E <span style="font-variant: small-caps;">I</span> KG <span style="font-variant: small-caps;">I</span> QLG <span style="font-variant: small-caps;">K</span> EEV KLSLF <span style="font-variant: small-caps;">A</span> DDMIVY <span style="font-variant: small-caps;">L</span> ENP <span style="font-variant: small-caps;">I</span> VAQN LLK <span style="font-variant: small-caps;">L</span> IRNF <span style="font-variant: small-caps;">S</span> KV <span style="font-variant: small-caps;">G</span> Y <span style="font-variant: small-caps;">K</span> IN <span style="font-variant: small-caps;">V</span> QES <span style="font-variant: small-caps;">I</span> AFLY <span style="font-variant: small-caps;">T</span> INR <span style="font-variant: small-caps;">Q</span> TES <span style="font-variant: small-caps;">S</span> IM <span style="font-variant: small-caps;">A</span> LP <span style="font-variant: small-caps;">T</span> IA SKRI <span style="font-variant: small-caps;">Y</span> LG <span style="font-variant: small-caps;">I</span> QL <span style="font-variant: small-caps;">T</span> RD <span style="font-variant: small-caps;">V</span> K <span style="font-variant: small-caps;">L</span> DF <span style="font-variant: small-caps;">K</span> EN YK <span style="font-variant: small-caps;">P</span> LL <span style="font-variant: small-caps;">K</span> E <span style="font-variant: small-caps;">I</span> DE <span style="font-variant: small-caps;">T</span> NK <span style="font-variant: small-caps;">W</span> KN <span style="font-variant: small-caps;">I</span> PCS G <span style="font-variant: small-caps;">E</span> GRIN <span style="font-variant: small-caps;">I</span> V <span style="font-variant: small-caps;">K</span> MAIL <span style="font-variant: small-caps;">P</span> KN <span style="font-variant: small-caps;">W</span> KK <span style="font-variant: small-caps;">T</span> TF R <span style="font-variant: small-caps;">F</span> I <span style="font-variant: small-caps;">I</span> WNH <span style="font-variant: small-caps;">K</span> RACIA <span style="font-variant: small-caps;">T</span> LS <span style="font-variant: small-caps;">Q</span> KN <span style="font-variant: small-caps;">K</span> A GGITLPDFKLYYY <span style="font-variant: small-caps;">K</span> ATV <span style="font-variant: small-caps;">T</span> KTAW YWY <span style="font-variant: small-caps;">Q</span> N <span style="font-variant: small-caps;">I</span> D <span style="font-variant: small-caps;">I</span> D <span style="font-variant: small-caps;">Q</span> WNR <span style="font-variant: small-caps;">T</span> EP <span style="font-variant: small-caps;">S</span> K <span style="font-variant: small-caps;">I</span> PR <span style="font-variant: small-caps;">I</span> YNN <span style="font-variant: small-caps;">N</span> LF <span style="font-variant: small-caps;">D</span> K <span style="font-variant: small-caps;">P</span> DK <span style="font-variant: small-caps;">N</span> KK <span style="font-variant: small-caps;">W</span> GK <span style="font-variant: small-caps;">Y</span> SLF NK <span style="font-variant: small-caps;">W</span> CLEN <span style="font-variant: small-caps;">W</span> LA <span style="font-variant: small-caps;">I</span> CR <span style="font-variant: small-caps;">K</span> KL <span style="font-variant: small-caps;">D</span> PF <span style="font-variant: small-caps;">L</span> TSY <span style="font-variant: small-caps;">T</span> K <span style="font-variant: small-caps;">I</span> NSR <span style="font-variant: small-caps;">W</span> I <span style="font-variant: small-caps;">K</span> DLN <span style="font-variant: small-caps;">V</span> R <span style="font-variant: small-caps;">P</span> K <span style="font-variant: small-caps;">T</span> KT <span style="font-variant: small-caps;">I</span> LEGNL <span style="font-variant: small-caps;">G</span> NT <span style="font-variant: small-caps;">I</span> Q <span style="font-variant: small-caps;">D</span> IGM <span style="font-variant: small-caps;">G</span> K <span style="font-variant: small-caps;">R</span> DF <span style="font-variant: small-caps;">M</span> SK <span style="font-variant: small-caps;">T</span> PKAMAT <span style="font-variant: small-caps;">K</span> A <span style="font-variant: small-caps;">K</span> ID <span style="font-variant: small-caps;">K</span> W <span style="font-variant: small-caps;">D</span> LN <span style="font-variant: small-caps;">N</span> LN <span style="font-variant: small-caps;">L</span> KSF CTAKETT <span style="font-variant: small-caps;">I</span> R <span style="font-variant: small-caps;">V</span> N <span style="font-variant: small-caps;">M</span> Q <span style="font-variant: small-caps;">P</span> T <span style="font-variant: small-caps;">E</span> WE <span style="font-variant: small-caps;">K</span> IF <span style="font-variant: small-caps;">A</span> IYPSDK <span style="font-variant: small-caps;">G</span> LI <span style="font-variant: small-caps;">S</span> RI <span style="font-variant: small-caps;">Y</span> NE <span style="font-variant: small-caps;">L</span> K <span style="font-variant: small-caps;">Q</span> Y <span style="font-variant: small-caps;">I</span> Y <span style="font-variant: small-caps;">K</span> KK TTN <span style="font-variant: small-caps;">P</span> IK <span style="font-variant: small-caps;">K</span> W <span style="font-variant: small-caps;">A</span> K <span style="font-variant: small-caps;">D</span> M <span style="font-variant: small-caps;">N</span> R <span style="font-variant: small-caps;">H</span> FS <span style="font-variant: small-caps;">K</span> EDI YAA <span style="font-variant: small-caps;">A</span> KK <span style="font-variant: small-caps;">H</span> M <span style="font-variant: small-caps;">M</span> K <span style="font-variant: small-caps;">C</span> SS <span style="font-variant: small-caps;">L</span> A <span style="font-variant: small-caps;">I</span> RE <span style="font-variant: small-caps;">M</span> Q <span style="font-variant: small-caps;">I</span> KTTMRY <span style="font-variant: small-caps;">H</span> LT <span style="font-variant: small-caps;">P</span> V <span style="font-variant: small-caps;">R</span> MA <span style="font-variant: small-caps;">I</span> KK <span style="font-variant: small-caps;">S</span> GN <span style="font-variant: small-caps;">N</span> RCWRGCGE <span style="font-variant: small-caps;">I</span> G <span style="font-variant: small-caps;">T</span> LL <span style="font-variant: small-caps;">H</span> C <span style="font-variant: small-caps;">W</span> LD <span style="font-variant: small-caps;">C</span> KL VQPLW <span style="font-variant: small-caps;">K</span> S <span style="font-variant: small-caps;">V</span> V <span style="font-variant: small-caps;">W</span> *FLRN <span style="font-variant: small-caps;">L</span> E <span style="font-variant: small-caps;">I</span> P <span style="font-variant: small-caps;">F</span> D PAIPL <span style="font-variant: small-caps;">G</span> I <span style="font-variant: small-caps;">Y</span> P <span style="font-variant: small-caps;">N</span> D <span style="font-variant: small-caps;">Y</span> K <span style="font-variant: small-caps;">S</span> CC <span style="font-variant: small-caps;">Y</span> K <span style="font-variant: small-caps;">D</span> T <span style="font-variant: small-caps;">C</span> T RMFIA <span style="font-variant: small-caps;">A</span> LT <span style="font-variant: small-caps;">I</span> AK <span style="font-variant: small-caps;">T</span> W <span style="font-variant: small-caps;">N</span> Q <span style="font-variant: small-caps;">P</span> K <span style="font-variant: small-caps;">C</span> PT <span style="font-variant: small-caps;">I</span> DW <span style="font-variant: small-caps;">I</span> KK <span style="font-variant: small-caps;">M</span> W <span style="font-variant: small-caps;">H</span> Y <span style="font-variant: small-caps;">I</span> T <span style="font-variant: small-caps;">M</span> EE <span style="font-variant: small-caps;">Y</span> AA <span style="font-variant: small-caps;">I</span> K <span style="font-variant: small-caps;">N</span> D EFV <span style="font-variant: small-caps;">S</span> F <span style="font-variant: small-caps;">V</span> G <span style="font-variant: small-caps;">T</span> W <span style="font-variant: small-caps;">M</span> K <span style="font-variant: small-caps;">L</span> I <span style="font-variant: small-caps;">I</span> LS <span style="font-variant: small-caps;">L</span> SK <span style="font-variant: small-caps;">S</span> QE
13953	44321	A	14035	869	3869	RHKKP <span style="font-variant: small-caps;">F</span> KKLTNP <span style="font-variant: small-caps;">G</span> AE <span style="font-variant: small-caps;">I</span> QTT <span style="font-variant: small-caps;">I</span> REY YKHLY <span style="font-variant: small-caps;">A</span> NKLEN <span style="font-variant: small-caps;">L</span> E <span style="font-variant: small-caps;">E</span> MDK <span style="font-variant: small-caps;">F</span> LNT YTL <span style="font-variant: small-caps;">P</span> R <span style="font-variant: small-caps;">L</span> NQ <span style="font-variant: small-caps;">E</span> E <span style="font-variant: small-caps;">V</span> SLN <span style="font-variant: small-caps;">R</span> TT <span style="font-variant: small-caps;">I</span> GT <span style="font-variant: small-caps;">S</span> E <span style="font-variant: small-caps;">I</span> EARINS <span style="font-variant: small-caps;">L</span> PT <span style="font-variant: small-caps;">K</span> SP <span style="font-variant: small-caps;">G</span> PD <span style="font-variant: small-caps;">G</span> FT <span style="font-variant: small-caps;">A</span> E <span style="font-variant: small-caps;">F</span> QRYKEEM <span style="font-variant: small-caps;">V</span> P <span style="font-variant: small-caps;">F</span> LL <span style="font-variant: small-caps;">K</span> L <span style="font-variant: small-caps;">F</span> Q <span style="font-variant: small-caps;">S</span> E <span style="font-variant: small-caps;">I</span> KE <span style="font-variant: small-caps;">G</span> LPNSF <span style="font-variant: small-caps;">Y</span> E <span style="font-variant: small-caps;">A</span> SH <span style="font-variant: small-caps;">I</span> L <span style="font-variant: small-caps;">P</span> K <span style="font-variant: small-caps;">G</span> R <span style="font-variant: small-caps;">D</span> TT <span style="font-variant: small-caps;">K</span> KE NFRPI <span style="font-variant: small-caps;">L</span> MN <span style="font-variant: small-caps;">I</span> D <span style="font-variant: small-caps;">A</span> K <span style="font-variant: small-caps;">I</span> N <span style="font-variant: small-caps;">K</span> L <span style="font-variant: small-caps;">A</span> N <span style="font-variant: small-caps;">Q</span> I QQH <span style="font-variant: small-caps;">I</span> KN <span style="font-variant: small-caps;">L</span> I <span style="font-variant: small-caps;">I</span> HH <span style="font-variant: small-caps;">D</span> Q <span style="font-variant: small-caps;">V</span> G <span style="font-variant: small-caps;">F</span> IP <span style="font-variant: small-caps;">G</span> MQ <span style="font-variant: small-caps;">G</span> WFNICK <span style="font-variant: small-caps;">S</span> V <span style="font-variant: small-caps;">N</span> V <span style="font-variant: small-caps;">I</span> Q <span style="font-variant: small-caps;">H</span> IN <span style="font-variant: small-caps;">R</span> TK <span style="font-variant: small-caps;">D</span> K <span style="font-variant: small-caps;">N</span> H MIF <span style="font-variant: small-caps;">S</span> IDA <span style="font-variant: small-caps;">E</span> K <span style="font-variant: small-caps;">A</span> FD <span style="font-variant: small-caps;">K</span> F <span style="font-variant: small-caps;">Q</span> QL <span style="font-variant: small-caps;">F</span> M <span style="font-variant: small-caps;">L</span> K <span style="font-variant: small-caps;">T</span> LN <span style="font-variant: small-caps;">K</span> LG <span style="font-variant: small-caps;">I</span> D <span style="font-variant: small-caps;">G</span> ML <span style="font-variant: small-caps;">K</span> I <span style="font-variant: small-caps;">I</span> R <span style="font-variant: small-caps;">A</span> I <span style="font-variant: small-caps;">Y</span> D <span style="font-variant: small-caps;">K</span> L <span style="font-variant: small-caps;">T</span> AN <span style="font-variant: small-caps;">I</span> I <span style="font-variant: small-caps;">L</span> NG <span style="font-variant: small-caps;">Q</span>
13954	44322	A	14036	2	99	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, ^=possible nucleotide deletion, V=possible nucleotide insertion)
13955	44323	A	14037	1	914	TVTVIHTVARVGNLDIQQRKSELFLSLVCEAIKNEMNVMLKSSPVDLVTTADQKVEMQLISSIKEKYPSHSFGEESVAAGEKSLTDNPTWIIDPDTGTTNFVHFRPFVAVSIGFAVNKKKKVDETYLGLVKETCFPLQIEFGVVYSCVEGKMYTARKGKGAFNCNGQKLQVSQQEDITKSLLVTELGSSRTPETVRMVLNSMEKLFCIPVHGIURSGVTAAVNMCLVATGGAGAIDAYYEIGHICWDVAGAGIIVTEAGGVLMDDVTGGPFDLMSRRVIAANNRILAERIAKEIQIVPLQRLDDED
13956	44324	B	14038	91	1959	
13957	44325	A	14039	28	152	LPSPSSKD'TDS/AASCCAPGRAGKGVSNSRSLSFPPSSVPLP
13958	44326	A	14040	35	879	GSQCSSPPASRCGSCSSAPSRA CPCRDPEAVAGLARTPVLLTKTNPSPPARTGLNAPSMGTSLI/PA LCCCFPLYQGSTELQCKAP**LP SPSSKD'TDS/AASCCAPYFLVLLKVLSVDNSSIWCAGGPAQS/S SLYTIPMSSMSAKNCVLSRGTWASFTCS*GSQRVSLGTPALG TEDHTSRSLGHSHVCHVDSLPA TACSCSFQTASSEVSPPATACSCSFQTASSE VSPAATACSCFTSFFFVCALWF GICPSCSAAVLST
13959	44327	A	14041	3	159	EHQCENPQ*NTGTPNPAAHQKAYPP*SSGLHPWDNQRQKPHDYLNRCKGL
13960	44328	A	14042	54	245	GGGGGEAEADRLEREPETEKALSSSL/RRAPDQC/RALIMQLFQAHCFFLST/QATAALQAHYAHIFPSK
13961	44329	A	14043	903	1205	WDVSQNNKSYL*QTHSQYHTEWAKTGSIPFENWHKTGMPSLTTPIQHSGVGSSGQGNQTNREPNHE*TPIHNCFKENKIPRNPTYKGCGPLQGELQTTAQ
13962	44330	B	14044	1	339	
13963	44331	B	14045	1	1547	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13964	44332	A	14046	807	1440	NTGKPNPA AHRKAYPPRSSRLH P*DLQQTPTDLQLSDLTPRGKTNKQKGIA SPSTKRTSTPKPHLQ ANAQRFCHHQACVTRVPKGST KHGKEQLVPATAKTCQIVKNIN AMKKLHLQLTEIQTIREYHKHL YANKLKNLEEMDKFLDTYTLPLRKQEEVESLNRPIMGSEIEAIIINSLPTKSPGP DGTAKFYERYK EELVVFLLKLFSIEKEGLPNSF YEASIIIPKPGRDTTKKENRQRPISLKNIDAKILNKILANRQPIEK LIHHHDQVGFIPEMKGWFKKCKS INVIHHINQTNDKNHMIIISIDAE KAFDKTQQQPQFMLKTLNKLGTIR QKKEIKGIGQLGKEEVVKLSSLFAD DMIVYLENSIVSAQNLKKLISNF SKVSRYKINLQKSQAFLYTNNR HMESQITSELFPFTIDTKRKYLGQFTRDVVKDLFKENYKLLLNEIK EDTNWKWKNIPCSWIEESIS
13965	44333	A	14047	603	764	LPLFLIEYPLFLSLA*LPWPKLPTLC*IVVREGIPVLCCFSKGMLPVFAHSV
13966	44334	A	14048	1566	1865	MQSIRKTIGIHAKYDKACRNEDICLRENTSAADTQAKRV*SGP PANSRNPAAEGPDC*KEN*OTE RTSTPKPHLYVTIHKDQRGTQLLTNNGTKLDR
13967	44335	B	14049	I	1932	
13968	44336	A	14050	711	1575	TRKFRRNG*IP*HIHPPPTKSGRSRIFNRPITGSEIEAIIINSLPTKKS PGPDGFTAEFYQRYKEELTNILDEHRCKILNKILANGIQHDIKKLIIHDDQVGFI PGMQGWFNIRKSNVIQHVNRTRDKNHMIIISIDAEKAFDKIQQPQFMLKTLNKLGDGMYLKIRAMYDKPTANILNGQRLEAFPLKTGTRQGCPLSPLLFNIVLEVILARAIGQEKEIKGIGQLGK EEVKLISLSADDMIVYLEKPIASAQNLFKLISNFSKVSDTKMSYKNNHKHSYTPITDKQRACKS

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13969	44337	A	14051	1	1579	MQGWFNVRKSLNIIHHINRNNDKNHIISIDA EAKFDKIQQPFLMLKTLNELGIDGTYLN IIRTYDRPAAANIILNVQKLEAFPLKTGTRQ GCPPLPLFNIMLEVLA RAIRQE KEMKGIGQLGKEEIKFSFL FADDII VYLENPIFSAPNFLKLISNLSKFS GYKINVQKSQAFLYI UNRQTESQIMSELRTIATKRIKYLGH LTR DVKDFNENYKPLL NIEKEDTN KWKNIPCSWTGSIN VKTAILPK VIYRFNAIPIKLQLT FTELEKTA LKFMWIQGYSNQN NSMVLTLV IPRKMRSA VELQQT STDQLR D LTVRK KTNKR KATAST SQKG LHQN PICRSP TSK TKEV GFR RSV ITNF SELK EDV RTYH KEAK NLE NRL DEWL TRINS VEK TLNDL KE LKT MARDL H D ACTSF NRR FDQ VEER VT TED QIN E ND G EN GT KLE NTP QDII QEN FPN L A S RPT F KFR KYRE HYK DTP PRE EQP QD *L SDSP RLK *R K C *R Q PER K VE LPT KGSP D
13970	44338	A	14052	50	1105	TRKSRRNG*IPGH IYPPKTK QE EGESLN RNP ITGSE IEAI NNLPTK KSPG PDG FTAK FYQ STNN KHN MII SIDA EAK FHK IQQ PFL MLK KTL NKL GIDG TYL KII RAI YD KPT AN IIL NGQ KLEAF PLKT GTRQ GCP PL FNIV LEV LARA IRQE KEIN C IQL HNEEV KLSPF ADD MAYL EN PIV SAQ NLL KLIS NFS KVSG Y KIN VQK SQA FLY TIN RQ TESQ I MSEL PTIAT KRI KYL G IQL TRD VK YLF KENY K P L N E K ED TNK W KYI PCSW IGR INI VK MAIL PKV I YRF NAI PIK LPM TL SSN W KKT TLK FIW NQ KR A RI AK S L SK KK N KAG SIM LPDF KL
13971	44339	A	14053	1	764	MQGWFNVRKSLNIIHHINRNNDKNHIISIDA EAKFDKIQQPFLMLKTLNELGIDGTYLN IIRTYDRPAAANIILNVQKLEAFPLKTGTRQ GCPPLPLFNIMLEVLA RAIRQE KEMKGIGQLGKEEIKFSFL FADDII VYLENPIFSAPNFLKLISNLSKFS GYK I*FPL FLIE YPS FLSLA *LPW PAL PTLC

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13972	44340	A	14054	1	344	MGINQRRKAENSKNQSASSPTK DCSSSPAKEQSWTENDFEELTE VGFRRQANAERFCHIQVCPRK APEESTKHGKKQ/RSISHCKNM PNCKDHRCYEETASTIDSLAETQ QQKREF
13973	44341	A	14055	301	370	DDGVF*IDNHVICKQRQFDLFLS
13974	44342	A	14056	1	1418	MVREGFPPEEVTFELKNELEISK GQQMGKNI PDTGASSAKALGE RELGTLIDKMKMNNSPDGSKKD  THRKEAKNLKRLDEWLRTRANS VEKTLNDLMLQQLKTMARELHDA CTSFNSQFDQVEERINKIDVRLA RLICKKREKNQIDAIKNKDQDIS TDPTEQTTIREYKKHYANKL ENLEEMDKFLDTYTLPRLNQEE FESLNRP IIGSE EA VSNSLPTKK SPGPDGFTA EFYQRYKEELVPF LLKL FQSI KEGILPNAFYEA I  LIPKPORDTTK KENFRPVSLMNI DAKILNKILANR IQHQH KKF HH DQV SFIPRMQGWFNICKS NIIHH HINRTNDKNHMII S DAEKA FDR  QQPFMLN TLNKL GIDGMYL KII RTIYDKPTAN IILNGQKLEA FPL KTGTRQGCP LS ATPVQHSVGS SDQGSQ ARERNK GYSIRK*GSQ  VSVC *HDCIFRKPHRLSPKSP
13975	44343	A	14057	1240	1596	CYSFLFVRCPSDSQVPLQLQVC/C EFAGGPL QTVFAWVSPAEVVE MFLQG*RKPFYMSY/TSFEMAL MKVWTMVR TSASPVGDVFGR GWSP PPTSTVG ALT VFGVSPGS CRSSPL PSE RLWV
13976	44344	A	14058	507	971	PANQKKSRT RR HSQ ILPEAQR GAGT SP TIPINGKRG NPKL L *SQH HPDTKA WQRHNRKREFY TD P DDH*CKNPQ*NTG KP NPA AHQKAYPPRSSWLHLW DARL V QRTQISKRNSSYKQ NQRQKPHD YLSRCRKGL QQNSA LHAKNS
13977	44345	A	14059	561	758	
13978	44346	A	14060	2364	2663	DGQLTLV SILNHYS LAQSCEY* DGE CFCLHCSASPFL*EGAQST ACTA PPEC FASDLGAV*LPQHS WC STLL LEGAPWP G T LGT TAPQF QHRKLG TNLAG

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13979	44347	A	14061	1	64	MPIGKVGEYYIKGTLRATKESE QQSSALELSSDRVYLNKEPGD QPWNAAFVFRGCVGALALRPP HLGWGEPRWAGFRGAFGFPFS TLNPSNWSTLIIQGCKQEGFYS PSMRPRVVPKRGSAPKVRAEEN AALPSRCPPGPLPVAQP/TGPAD GGSCEQCPSCCGGCCQLPPLP WFPR*TPCDKRV
13980	44348	A	14062	1	774	MFVWSNVEGHSVAMPFWPSIP FLNPPCSHTRPSNLPVTQWPPTR ENNLPSWQLLLTSIIQAFQLSA LHKEQGSSSEKDGRSPNKWDK DHIRCPMSAVMIFSKRHQAL/V RAHQGHPNQDNWTVSQMLSK WWYTLGPNERQKYHELAFAQAT AALQAHYVHIFPSKGRWELLH GSQRLDWGRCQLKLLGQQGQ DVLHTNLGKEENSSCWGYKME CEEGFGPGQGDGCGLGGVHAPL LSPEGLDSEQNTLIMGDIFHCA KKL.P
13981	44349	B	14063	1	753	
13982	44350	A	14064	2	1457	YPRRRPSRAGVLAGPAVLAGPP SSPGRPRRAAFFAEPFPSARRS PRRAAVLAVPPSPRPRRAA VLAAPRVLAAAPPSSPRRRP PSSPRRRPRRAAAGSLPAGELP QSSRLAAHLAAD*PDS*IAAGA VPRGWEGLTIMAEGKEEQVT YVDGSRQRAYAEKPPVVKTIRS CTV/SGHSRHNSSSGM/*SSPNSP /IPFQFTFQIPSSLQAAALWLCL*V TWHFFV*PVLSRHCFSPGGLF SLSLQSAGCPAGSLQAEFVALP PGGQSRLHRTAS*VPGAFQEK CPLERVWPFHPSKQHPRNGLAF PLP*APORTQPAEDTLPRHPEM GLILSQGTAG/PGRECQATQLPA QHSHAEVLHFGGAMSGQLSLV GPQDSKRTARLTDQ:HLSPT* QPPGLTEGTSLEQQ**S*MGWM VGVIAGAPSGWGSQSGPSEGTP LFSSPA*LPWPELPTLC*IGVVR EGIPVLCQFSKGMLPVAFAHSA
13983	44351	B	14065	72	1235	
13984	44352	B	14066	1	2715	

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13985	44353	A	14067	50	1304	TRKFRNRNG*IP*HIHPPKTKSGRSR FNRPITGSEIEAIINSLPTKSPGPDGFTAEFYQRYKEELTNILDEHRCKILNKILANGIQLQHDIKKLIHDDQVGFIPIGMQGWFNIRKSNVIOHVNRTRDKNHNMIISIDAEKAFDKIQQQPFMLKTLNKLGIDGMYLKIRAMYDKPTANILNGQRLEAFLPLKTGTRQGCPPLSLFNIVLEVLRAlGQKEKEIGIQLGKEEVKLSSLADDMIVYLEKPPIASAQNLFKLISNFSKLSGYKINVQKSQAFLYTNNRQTESQIMSELPTIATKRVKYLG QLTRDVKDLFKE NYKPLLNEIKEDTNWKNPICSWIGRINIVKMAILPKCKTVGLLS NISTHKS A V A H A L V E A G G I P S L I N L L V C D E P E V H S R C A V I L Y D I A Q C E N K D V I A K Y
13986	44354	A	14068	1	1155	MFVWRNVEGHSAVFPWYSIPFLTPPCSHMRPSKLPVTQWPPTRENNLPSWQLLLMSVHQASLSALRKEQDSSSEKDGRSPNWKDKDHIWWPMS AVIIFSKQHQAL/VRAHQHPNQDNRTISQMLS EQWYTLGPNEQMKYDIAFQNEARIRY/CHRPRKRARFLSHASPPWRQLPAAGAEASGAWNLPA GGG*HDYNRCSVPVFRTEVSTRPRPSEICGLTQE*TLLSAKSQVGNTFGFAHTISDITTPCGLCTSKAAIEVPEADTLPHICSWHKGEECGLRGPEPSSPPRPSLAARVSA GRGLALRRRRPEVPP/ SRAPRSAATATPANEQRRAVADVGQWARARGGRVRAAGRSGIJJ.RVKKMMKMKTVMIHFLMKDEYIFSS
13987	44355	A	14069	1331	1584	SLQRKAARFASSTVPPRPGQGILPIISFSNVPGSRRLKAPLVFIGP G*ITLNRIPYLPHSAA RD PFTWN TFSFLLPCEEVPST
13988	44356	B	14070	1	1248	
13989	44357	B	14071	1	459	

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13990	44358	A	14072	1	2156	MGKKQSRKTGNNSKNQSASPPP KERSSPAMEQSWMENDFDDL REEGFRQSNSYSELKEEVRTHGK EVKNLEKKLDEWL'TRITNAEKS LKDLMEKKTTARELHDECTSLK RVSVTEDQMNEMKREEKFREK RJKRNEQSI.QFIWDYVKRPNLH LIGVPESDRENGTKLENTLQDII QENFPNLVRQANIQIQQEIQRQTPQ RYSSRRATPRHIIIVRFTKVEMK EKMLRAAREKGGRVTHKGKPIR LTADLLAETLQARREWGPPIFNI LKEKNFQPRISYPAKLSFIDRST RQKVNKNDTQELNSALHQADLJ DIYRTLHPKSTEYTFSPAPHHTY SKIDHIVGSKALLSKCKRTEIIIT NCLSDHSAIKLELRKKLTRNHS TTWKLNLLNLLNDYWHNEMK AEIKMFFETNENKDKTYQNLW DTFKTVCRGKFIALNAHKRKQE RSKIDTLLTSQLKGLEKQEQTHS KASRRQEITKIRAELEKIEQTKT LQKINESRSWFFEKINKIDRPLA RLIKNKREENQIDAINDKGDT TDPTEIQTAISEYYKHLYANKL ENLEEMDKFLDTYTLPRLNQEE VESLNRPITGSEIEAIINSLPTKK SPGPDMF/RRILPEGQGGAGTI PSETVPINRKRGNPP*/PHFM/SA SIMLIPKPGRDTTKKENFRPISL MNIDAKI/RQ*NTGKPNPAAHQ KAYPP*SSGLHPWDARLVQLTQ

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
13991	44359	A	14073	3	1794	AMLPMELGCGPLPEPLPVGCSR FSLFK*QTCISTVP/GYMVTAQS MSSTPPPPSPSTLPPSPSPPPPLPQ PLPPPPSPPTLSSLSSPSPPPRPLP VSPSTLPLSPQPSPQPLLPPSSPP SLPSPPPSPLPLSPSPSAIPSLPPP SPQPLPPPPSPPPPSLPSPLLPPP PLSSSPSPLSPLSPSPPPSPLSPPS PPSPPPPPQQPSPPSPLSSPP LSSSQPSLPLPSLSSLPLPSSPSL LPLSLPLSISPP*SLSSLPLPSPS LPSSSFQST*TIGQCFLSVMH VAPCTYLALAGNTLMAWPLMS ASSKAASGGVSMFVWRNVEPCS VAVFSWYSVPFLTPPCSVRPS NLVTQWPPTRAKNLPSRQLL TSVHQASQSLSALCKEQDSSSEK DGRSPNKWDKDHIWWPMMSG HDLQQAAPGPGRAHQGHPYQD NWTISQILSERWYTLGPNEMQK YHDLAFQHMAGEDIASDEEHM VIHEEEGVMVSSLMTALAPLTL ISSSRIFGKVYGPPTSSSYTYSD ASSSTLAPTSFLLGPGFAKQES GEEAEDGLRELETEKALSSSL/R RALDQ*/LALIMQLFQAHCFFLS T
13992	44360	A	14074	1	2496	MLLSIDAEEKAFDKIQQQPFMLKT LNKLGHGYEQQHHLHTNDVDE EDLSDAASKGDDFASEQSDQ AHFLQPEAYGLGEGAEATGT AHQGNHVRVEECGRSLCCGVP LVLHPLDPDSLQPHEAQQPASH SVACNQRKQPAKLPAVAHERP PGGTGSVDPGRPPGATCPESPG PATPHTLGVVEPGKSSPPMTEE EPWAPQGSPCWTAQKSLSLRK EQDSSSEKDGRSNKWDKDHI WWPMSVALMIFSKRHQAL/V
13993	44361	A	14075	4317	5099	KMFVFLCISAQLSLQCFRGSFHF IKIYDFSFQLFLFLELPYLLLN HFKMLELVLQQGHPNQNDWNT VSQMLSKWWYTLGPNERQKY HELAQFVKVAHICNKD**KFKSS EAKPTSQGLAGVGNKGSWEWS MSETGTATAPGVSELLSVAAQ TLQSSDTKSSFCGAEWGH*GI GCDDVIADDGFSTTDTLKFKE WVTDVESGDNGSCEEPEGNKGFG GKVFAPVIPSSFT/HCRPLLDPE/ PPGSPDPPAAGFKVYGPPTLSSS

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13994	44362	A	14076	1	637	MSRVGSCRWVCGLADFKNGAT DLCDKSLHNRELSAERPLNEQI AEAEEDKIKKTYPPENKPGQSN YSFVDNLNLKAITEKEKIEKER QSIRSSPLDNKLNV/EKDVFDFNQ EFGKLIDGYDSTKEWDWVHKF QDIPNVLVGTAFNVDDGNGGF VVHWLNNKEFHTSSTEVMFH QLRKLSDKQVDHENDDADRED EEHSQEDRERGLHMKLDH
13995	44363	A	14077	448	464	KKRA*GSVSQRFPAET*LAD*VI NTGSQEAKRREQR
13996	44364	A	14078	179	382	NTPNQRSVASNRFVKCTIIHQHS VKCTQSALCKMHQSAGFLKVD NHRED*KKGHSDRAKTEHGRG QIRE
13997	44365	A	14079	697	1654	PKPSVRGMGFLGTGTWILVLV LPIQAFPKPG\GSQ\DKSLI\H**ED LSAERPFPFELNRLLEAEGTRFK KTYPPENKPGIQSNSYFV\DNL NLLRAITEKEKIEKERQSIRSSP LDNKLNVEDVDSTKNRKLIDD YDSTKSGLDHKFQ\NETADNSF SQEEEPVVAGEDLPPPSQESD VQPVQPEEVSA\RFQLRQLDQI KLSTQAAKKLKEESSSLERME ETSLSP\PTKRW\DT\RLIGAF YRVLIGAFYRVL\MGAFYKPIAS YRALIGFVYR\ALMGAFY\NPLV RQKSSPRPHSTQEVQLASPLTN TQIYYVIFTV
13998	44366	A	14080	72	1117	I\LENHLSDRVAEGGPLQGLRLG VQGEAVPPGLVHQRGGLGLD GELIGSVGQQVSDVEGAGSHR G*RHTGRTPAVSAGPAA*SATH TAPMWLAGW\YEP\QPGPVLV SPPTPGQTRQASWC\*ARCA GSWWH*HQT\PGGA*RVAAPAP SWSRSCP*RPTRS\AA\APPAPSR PGRAVGLATGAGHPAQHG\HGR AVPTG\PRAAAGAGSW\SELCP\SS CAGTSRGR*AGTRR*AA\PA\GSG RPGPGAWAGPRCSRSTY\AAA CGRGGA*AGADSGPRSGTHAG HCGARCRSS\PLV\PA\AGH\LPP PGPGR\TGD\CPASSCPG\PG\PHG CSLSGSWGE\GWVSA\RRQ\GLP WAVA
13999	44367	A	14081	2	269	
14000	44368	A	14082	1	591	
14001	44369	A	14083	2	477	

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14002	44370	B	14084	237	419	
14003	44371	A	14085	2	1220	LPPGFVMAAAARWNHVVVG TETGILKGVNLQRKQAAFTA GGQPRREEAVSALCWGTTGGET QMLVGCADRTVKHFSTEDGIF QGSETLPG\GEGLMFRGLAQTQDG TLITCVDSGIL.RVWHDKDKDTS F*PTPGTESGPWGVGCAKTAQ HPHVVCRLGKRMLLKIWDLQ GSVNLCKAKNVRNDWLDR VPIWDQDIQFLPGQSQKLVTCTG YHQVRYVD\ASPQRPPVLETT YEEYPLTAMTLPGGNSIVGN THGQLAEIDLRQGRLLGCLKGL AGSVRGVAVHPSKPLT*PPVRL DRVLRIHRIQNPRLGEHKVYKL VSIE/RALLLSGRDNLGG*APEP SKTQTRCP*EDTEDR*TLGDPW RQLPSGKLFVGWSSPKELSKR GERRSGLGPAPPADAPVPTL
14004	44372	B	14086	96	592	
14005	44373	A	14087	102	612	HCAGSPHSPRSLSGTPLPGLPL WRHLRSPSAHRTCVGAPFWAG QDRSQLP*LAGRCGGRGPGSGNP GCA\PACGPAVGPGGRGLGPP TRSSQPALPAGPNEGLSTRASG CRGRTGSPSSASPLGLSCLPAG QGWGP/GSPPCVSLPPTWAPV RPEPPG*AAPPAPRPPV
14006	44374	C	14088	1	636	
14007	44375	B	14089	31	612	
14008	44376	A	14090	234	504	SFYHLGAGE*PGKSRVPIPQFQS PWGPYCQGRARGGEVCHLQAV PPRGAGAARTLSGHPLGSPEQL PQPGAAELPGGVVPSTPPCP
14009	44377	B	14091	1	924	
14010	44378	A	14092	11	354	RLSTSPPDSGAQLASPSSGHTRA AGGAACQCSRAVRS/PFSPSPWVV DGTGCGGAGGGARWGGSGCT GAHGVGGR/PGMAGI*GPEPCP EGRQLRPLAPVGCGQ*REP/G*K NSMGETT
14011	44379	A	14093	147	513	GSASGVVRLSRWARGLAGFRS EAADLRGECYSS*GSASGVVRL SRWARGLAGFRSEAADLRGEC YSS*KQRGPKELRSPAGFT*WIP /LPGLQVELPASPAPCAPTPQPL SG*WDGRRGAGGGARRGGSG RTGALGVG/GGSGMAGCRSRA LPPREGS

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14012	44380	A	14094	418	1026	WNPHQGCRWSCLPVPVRHALAF LSPWVIDGTGRHGAGGGALWG GSGRTGAHGVGGGS*GMAGCR SRALPHGKAAKAR*EIERSASG/ TGTAGGPSTPSAATGPGAKSLI ARGQQGWPAAPSGAPAKPTPT GNSSWPASAAGSSGSCSRLS/SP HLPAS*GSGLQPWPAAQKGAPTV QQQAEGLIPRPLPEEWSLPLFLG HQGEHSGMA
14013	44381	A	14095	897	2111	PPLLQSSPNFFLICYLPHWNSHE NTHRTGRRGAGGGARRGGSGR TGAHGVGGRLRHGGLQVSPA PWEGS*GPARNRAQRRTYHCSGP GLQSGLPHYSGYHT*PDEKEKN GREGOKLER
14014	44382	A	14096	1304	1922	KLNIGVYSSIEIPD5GAQLASP GSGTRAAGGAACQSCALRHSS ALGWSMG/PGRRGAGGGARW GGLGRTGAHGVGGRLRHGGLQ VPSAPREGS*GSVRNPAQRWR AGTAGGPSTPSAATGPGAKSLI TRGQQGWPAAPSGAPAKPTPT NSSWPASAARSPGSRSR/RLPPH LPAS*GSGLQPWPAAHYFEFFLPI GQNAQTEVSY
14015	44383	A	14097	318	533	MVCFDADCPVVVDGTGRRG AGGGAHRRGSGRTGAREAGGR LRHGGLQVSPSPARREGS*GPAS PAGCLAHL
14016	44384	A	14098	346	957	ARYTLHPTRLGSPAGFTQWIPH RGCWRSCLPVPVRRAALFLSPW VVCSFPVDGTGRRGAGGGARR GGSRTGAHGVGGRPGMAGC RSRALPRGKAAKARREIERSAG G/TGTAAGPSTPSAAGPGAKS PFARG/LAGPAAPSARPAKPTST RNSSWPASAARSPGSRSWKMS LYMKKSASGQSQAQWIAKMW KSPRFKPLWLTS
14017	44385	A	14099	124	663	SCLPVIRRALTFLSPVVVNGTG RRGVGGGARRGGSGRTGAHGV GGRIPGMAGCRSRLPRGKAA KARREIEHSAGG/TGTAAGPGT PSAATGPGAKSPLAPGQQGWLA ALGINGAGERLFMKVAFSLKTC SLSCSYLRLTLSRGGSVHVLRG NLTVCKPQPALLRVVFHHQRQ ADCGALPVP
14018	44386	C	14100	1	672	

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14019	44387	A	14101	3	1759	RPLRGWRRTRDARAPRRCRG SHGARRCLRKTAATSRCCGGAP GPURSRPPSTGQAAEAGDW/PAG CNP*GGLRAADPGPSRPPRGSI GLLCGQGGQGGSSPWWVHGTTG RCGAGGGAPWGGSRTGAHG VGGRLRHGLLQVPSAPQEGS* GSARNRAQPRWAGTAGGPSTP SAATGPGDRDGEGG/ETGAHVSA LKGTPTGEWPAHGLVPSIDQ TCLIFKVTFKAVVLCGPQTTS STSISCPGSAN/SPPSAG*/GSSG CGSSSLCSAHSVQEDSQPQ*KR TGLQSTTYGRSGSSSNEPRYHSD LPTSRSLRNEDTFFGRRKKL EVQRTGQDPA*SHHTSSYTLPG L*TAEGKDRVENAA*KGSPNQF RSGTFNPKGARKTRQAWHPR APNCOAQGTPPREGSSGPRTLS AAFRIPQEVVNFISGPITRAQR HGEPESPRGQTGSPLGLKTGSE GTDKRKSTGADKKSTGDRQEV EPTESPQGLDRKPTGMDRRSTG NRQKVRRQIGSPLGLNRKPN DKKSTRNRRQEVRRRQSAGARQ ERAGSSTFLRLSALCGLLVDVN REQVAKQKWDLYSSRFTSGNR
14020	44388	A	14102	1879	2607	GKPSLSLHPGHIKCGISRCNGNV SSRLRSPAGFTQWIPHGRCRWS CLPARCALALLSPWVVDGTG RHGAGGGARRGGSGRTGAHG VGGRLRHGLLQVPSAPREGS* GPARNRAQRWAGTAGGLSTP SAATGPGAKSPLARQQGWPA APSIGGPPSPSPPGTPAGPQAPH AAPVPARVPLPPHI.PAS*GSGLQ PWPAQKGAPTVQGGG*RAPQM PKWEPQRGR/VAFTIEVGVL
14021	44389	A	14103	2	272	GHWGMVNSPCRASATVSRGP LPGVLPSTSPPSATSTCRMRCHPR RCPLPFRRLLSPPSLTPP/PGKPL LPRPHSMPPGLGLPLGGLPVFHP

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14022	44390	A	14104	101	1815	QSARQLRPCPGAPSAGVENRKKTTNLTSLAAPDTQSTCGQSCGCLHSMGSSCMQHSYTYGFLRSLWPCRCHRSASFSGQRREEKD SKSVRERSGRSQNVPARPALTSPLTOSPGPLAPGAGSWRSQLG TGTGVLWWQRESATGDFRTES ARSSDPSRRDWPAGRKREEG AATVLWACATASTAAIICQDNAISPLKSGNSPNSHLWRPQQGLPP VLGLAQPKRWRPNRLTTSPSPS RMMARPVDPQRSPDPTFRSSTR HSGKLEPMEATAHLLRKQCPSR LNSPAWEASGLHWSSLSPVG\ PCRP*GLRPSTHGA\RTFFSGARP GLGGYSPPEEAMPF\EFDQPAQ RGCSQLLQV\PD\APGGP\GAA GVPGAPPEEPQALRPAKAGSRG GYSPPEETMPFELDGE\GFGD\ SPPG\LSRVIAQV\DGSSQFAAV AASSHQCLSI\H\IPMS\PSVGRNG LLTKP\PS\TSRRGKLT\RK\DDMYY FV\PRSLNDMM\HML\PIE\DSR WTHNL\DI\N\REQ\KTN\PLAGPKG RPI\SR\TQAA\ASTNS\KTES\QIE KTEEA\PP\SLRY\IN\NNR\SM\PLN
14023	44391	A	14105	39	877	AGPGPPR\PLPPRSSEGPGASIL CSEVPGPSCQGRFRGRRDAMS MPW\REEERSLLAGE*PS*GG*S GRGVSRKCS*PG\RGV\PRP\PL RSRPRAASSE:DQNSPLDQSLHR TRKTI\PS\SGGST\AI\MP\RGSS\SE TFFSAPSKT\WV\LG\IPGETFISGP AAF\PA\GGPRAAPR\PS\PLNSL *SGGNGGP\GPPRLHF\SSCGKGP PRPSNSRN\GGQ\SAC\QGG\SH\LV C*SHRG\SLGE\GH\AY\QGD\PC\SPG HPA\KPSRAHA\QARRSA\HAAS LTSGPCD\AS\Q\AW
14024	44392	A	14106	358	546	CFPSRIR\AL\SL\RA\PKWPA\KRSPS EPE\MS\PPV\WSP\PH\PD\NN\T\APPK EQP\SSP\G\RV\GR\HG\N\W\SV
14025	44393	A	14107	22	549	DHCLCSV\VRN\KRDSV\YPL\PIPP CCKT\TS\IP\PP\LV\DA\VR\PP\DIS\VS KRV\T\SC\LE\PQ\PH\CL\PT\IN\AG R\T\LA\RP\Q\GA\PT\N\KE\GQ\AP\G RAT\AS\GQ\AA\PA\TT\VL\G\DT\T\G PQ\GR\H\RG\TS\A\A\G\PA\PP\FA\VA DQL\PP\DE\RA\A\EG\RK\**AA\FP F\CH\RL\V\Q\DG\G\PP\PA\GG\VP\GA GES

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14026	44394	A	14108	146	2616	LAAVGMAHCFRQRQQSPAV GLRGAGSAYSPA/EGARSSHGQ/ PPWGRGRGGPDPVRGAACR RPRAAAQPARPAARPPARPRPA P* AACCE/VPSAANSVAPSAAAM *SSAGRDGASSQRSSRPHAAAPP RSSALPANGK/PPSPVTRAARTC GARSSNTGA*SAARPKHSAASS RHPPAA/MPLPARHA/PGGTSG RPLPTPQGSAPTSSASPRGPATP PPAGPRAPPPSPRRAAAPRPPGR QLSPAPGTPAAGGGGPPPPALR *SGSVFGRQLVGDGERGRACG ARGSAAVPALRTFVSPVSTVVA GAACPLAVALPAPDPLPCSE*A PLRSG*VPQPASLFCSQFRPOA WQHP*LLRACPRLGAAVPCV WCHSRALDSATPRWM*G*RLP AVWLPAPFSPPPFNQAFVPPCQQ NCSLQNRQTLSASAKIGTEEW IAIKIPENVEVTLELGNENQRLEE FGGLRRRQEDEGKFGPTDWL NGCDQNAQDSNMDSSEGOGEDG GCSFGGAGLRGSGWGWDQTRET FLALKANLRWPFRSSAQSQTSQ EGAAGARSGLKGGKKNPLKLP KKQAKKMKAFAKQKQEKERK KHKELKAKASWKGLRPQVEFK NLAERRGEAAVPGCPVVAAGHS WRLLSLARGCAKRAQRQLLFPSE KLLAALREGSTRGGGAASQPQ RKLRVCMRVLDSSEFDHMDG
14027	44395	A	14109	I	885	MIISIDTEKALDKILHPFILKTLN KLGDIDGTYLKJIRALYDKPTANI IMNEQKLEAFPLKSNTKQGCPF LPLLFNIVLLEVLRRAIKQEKEIK SIQIGREEVKLSLFADDMIVYLE NPISIAPNLLKLISNFSKVKSYKI NVQKSQAFALYTSNRQTEIQMM SELPFTIATKGKIKYLGIIHPLTRD VKDLFKENSKPIL/KELEKTTLN FIWNQKRAHIAKTMLSKKNKA GGVMLPDFKLYYKAAVTKTA WLGDDQFLIPRGRHISDYHMG KNLGQYPAFQDRGPGCGFPQCIV PLVYRD

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, * =Stop codon, - =possible nucleotide deletion, + =possible nucleotide insertion)
14028	44396	A	14110	453	891	LIHLSTDALRWSGVGTVRSFSS HEAIFQTIAWGETLDNTLSSRA EVPAAFHGALCPWFETREWQ* LLQSILLVNIWLRHVLSHSPRSLL KP*FYTT*VFVCSKLGQSGWGK VAGAKLQMNNISAKQLFKVQV LFKIESLMSSLST
14029	44397	A	14111	452	2922	KMGLAREWILRFLVLILQEIRS MRQKENKDQDLSNLSLHQADL IDLYRTLHPKSTEYTFSSAPHC/ RTYSKIDHTLGSKALLSKCKITE IITDSQTTVLSERIKKLQTQ/NRS ATWKLNS/YLNDYWWHNEMK AEIKMFFETENKDFTYQNLW DTFKAVCRGKFIALNAHKRKQ ERSKIDTLMQLSKELEKQEOTH SKVSRPITG/SEIEAIINSFTNPK RVPGPDGFDDEPNFYQRYKQEL VPFLLKLQFQIEKDGLP+N*FYE ASIIILPKPGRGTTKK/EENFRPIS LMNIADAKILKNILANRQHQHKK LLHHHDQVGFGIPGMQGWFNICKS INVIQHINRTSDKNHTISIDAEK AFNQKIQQLFMLKTLNKLGTNG MYLKIVRAIYDKPTANILNGQ KLEAPPLKTGTRQGCPPLSLPF NIVLEVALARAIRQEKEIQGIQLG KEEVVKLSLFADDMIVYLENPIV SAQNLKLISNFSKVSGYKINLQ KSQAFLYTNRQTESQIMSELP FTTAKRIKYLGQIQLTRDVVKDLF KENYKPLLNEIKEDTNKWRNIP CSWVGRINIVKMAILPKVTYRF NAIPIKLPMTFFTELEKTIKLFR WNQKRAHIAKTIISQKNKAGGI RLPDFKLFYKATVTKTARYWY ENRDIDQWNRTEPLEIMPHIYN HLIFDKPDKNQWKGKDSLNFN WCWENWLAICRKLKLDPFLTS
14030	44398	A	14112	3	3349	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met ind	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14031	44399	A	14113	294	1107	RRHRLENYIPRITAQSHPHRKALARSESKRDGGFKNNWSFHDHEEESEGDTDKEPGPLDAPP/ESGPRAPGKGL*RRSRSPGPSERGSAARLTAEPEARNPAASTLLRRGPSSRRARRRCGPWIKKEAWEEDGGRQERRRLGQDLRTTLLNKSKGGIDSRJISLGQHSHPTHAKLWLDQSLREMEVLKIIAGALIMKKKVKEIQIKSARARSTPLHDQIGTTSPRERTIASKRHPYYITPKGIRYEQDTLSRTPIITRSRQRPLGLPTASPPPSFPTLAPPTQAQKPSLHLREGKPPTPTGERSTRPHPEPPRKYEALSSLYPPTYLLAPSTDLGNAHPTQEPMQFNVDATHPRQRNFIPVAGNSPKRSSQFIVFAPKKNTTPPYLDFAAILGLHRRRPPRSFRTSYPPKEFRSSPPERTAPRN
14032	44400	A	14114	2	297	VQKSVLCSFQAGTMEGVEEKKVPAPVETLKKKRRNFADAIQFLQTVFLAF*YTLKGQRQ/VYWLVE*HQFYKISYRKKMVQRIRQHPQSCTVQKSWWP
14033	44401	A	14115	3	754	GTMEGVEEKKKEVPAVPETLKKRRNFAELKIKRRLKKFAQKMLRKARRKLIYEKAHKHYKEYRQMYRTEIRMARMARKAGNFYVPAEPKLAFLVIRIGINGVSPKVRKVLLQLRLRQIFN\GTFVKLNKASINMLRIVEPYIA^EYNPLKSVNELIYKHGYGKINKK*VALTDNTLIAARPLGKYGITCMEDL/IHEIYTVGKCFKEANNFLWPFKLSALSGMK/KKTTHFVEGGDGNRVDQINTLNRRMN
14034	44402	A	14116	1	388	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14035	44403	A	14117	1	1145	MTRNYEWLLEAESSPQPIAQK MEPOQPYNSKELNSANNQCLLE KPKLRLQRKDKYDQGHAVQ CQSWVYVLTQDSCFCQQLILLPS TENFHESRSDTAGHLRTGHVA SNWLSEHSPQTMAPAAMQWDK KMQNTSSWFPQKAKEPKVKPMS KLWQTPSQNDTLYKAVKALT SSPERNINTNKKDVHTETSSK GHQHQRPKVDKSMKMRKNQH KKAENSQNQNASSPPRNHNSSP ARERNWSENEFDELTEVVFRR WWTINSELKEHVLTQCKEAKN LEKRLEELLTRITGLEINQAERI SETEDQQLNEIKHEDKIREKRMK RNEQILQEIWAYVKURPKLRLIG VPENDRENGNKLNTLQDTIQE NFPALAR*ANIQIQ
14036	44404	C	14118	291	551	
14037	44405	B	14119	1	1308	
14038	44406	A	14120	82	367	ITLSSPPHSFIGHKTPASGPPQKI PPQPSQ/CKQWGDPPTVEAC/CV SCPTQGFISPTRGPPCKHESLV VPLVGTPRRNQPGGHHIQHSQR WAPVLT
14039	44407	A	14121	999	2661	VHLTGCGGPGQPVPEAPPRL RSMRC/GP*/GFSPGAEA*TEP/C HYGGRGFPCGPFPSLGCLATNSP WLPGPRPPCSPWAGP/CGLCPLP AAAERQPALSVPGASPSCRLL PLVVLCHGSHLNGRVLRLPG GSPCGHCHNCAGARRGLGHVL QGGAQARQREQLQR
14040	44408	B	14122	164	1042	
14041	44409	B	14123	320	566	
14042	44410	B	14124	1539	1674	
14043	44411	A	14125	185	780	QKAKKGKLRSKQNSFPGLKK TVPSQLVQYCPSF*ISWKPMVY QKVPA*PRPPRTPDHHPDPGPA PHPRQHHPPPRSPDAEP/SPTTPT RRRPTQPPDPHPKRPPPHSKPH PPQOPPTPPPTATPTEQRQHAPP TPRPPTTHPPSTPKHPA/PHTAPP PTKNTKPTPQRITQDKGRQKK PRRQPHISEPINKKSPKAHI
14044	44412	C	14126	1	1128	
14045	44413	A	14127	319	536	
14046	44414	C	14128	231	425	
14047	44415	B	14129	1	1431	
14048	44416	A	14130	75	393	
14049	44417	C	14131	174	371	

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14050	44418	A	14132	79	164	
14051	44419	A	14133	343	775	
14052	44420	A	14134	554	724	SEGPSPKEPTHRMKFSHHDDLI FLDLSN*QPPNSPEPHPPQSP*KP WPQNPNSSRQM
14053	44421	A	14135	20	242	VSFLSMGSGHC1RSTRGSKMVS WSVIAKIQEI*CEEDERKMARES LAESMSTYVMMNHTYDS*GK THILIMKK
14054	44422	A	14136	229	366	
14055	44423	A	14137	131	505	
14056	44424	A	14138	1	1317	AGCSCGSRAMAEEQGRERDSV PKPSVFLHPDLGVGGAERLVL DAALALQARGCSVKIWTAHYD PGHCPAESRELPVRCAGGDWLPR GLGWGGRGAAV\CAYVRMVFL ALYVFLFLADEEFDVVVVCDQVS ACIPVFRLARRKKILF\YCHFA DLLLTKRDSFLKRLYRAPIDWI EEYTTGMADCILVNSQFTAASF KETFKSLSH\KDPDVLYP\SLNV TSFDSCS*KAGMT*SPRGKNS WLLSINRY\EREGKIWTLGTGK ALVQLRGRLLTSQDWERVHLIV AGGYDERVLENVEHYQELKK MVQQLDLGQYVTFLRSFSDKQ KISLL\RQLARVCFYTPRQ*GTL GIVPLGRPCYMAVPQFICCLIRV GPFGSSI*PQCSQGFVCVPDPVH FSEAIKFIREPSLKATMGLGWE EPE*REKFSPGSILQEQLYRYVV
14057	44425	A	14139	1	648	MESKEEEQGGVADHQKATRGP TPQPREVVSERATQRGNRAFST KLCNPKTNRKQQQQYQQQQK GRTKTPKGQHPQRSKLDKLTE MRKHQQQKNTKNPKGQSPCSPP NDCNVSPARVHNWTGDEMEEL TEVGFKKWVRKNCALKEHVL TQCKEAKNLDKRLEELLTRKTS LERNINDLMEALKT/RA*ELCKA YTSINS*IDQAEERISEFEDHLAE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, *=possible nucleotide deletion, V=possible nucleotide insertion)
14058	44426	A	14140	1	1365	MPVKGGTKC1KYLFGFNFWVSERDCRALLSGPTCSRAPDTG RGRECRQLALPAPGRHRAGRES ALRLPAGSKAGSRAGRGRDG RIRVGVSGLFGSTTGLFNQSL AETGFTPYTQKSNDFLVKSLKI WHTYFKNFHQEARLYIRTSPGS NWNWFTLGIIESPEQPGVYEG QRPRVVTKSFA5LTLKRVGTVL LLAA5RINAD5VLVQLAGIAVL AIGLWLRFD5SQT5KSIFEQETNN NNSSFYTG5VYI5LIGAGALMMLV GFLGCCGA5QESQCM5LGLFFG FLLVIF5A5IEIAAAIWGYSHKDEV IKEVQE5FYKD5T5NKL5TKD5PQ RETLKAI5H5YAVCR5LGD5TLLRF LRIVSAHRLNC5GGLAG5GVEQ5FI SDICPKKD5VLE5FTV5K5CP5DAIK EVFDNKFHII5GAVG5GIAV5MPS FRSNH5PD5H5PV5SYLLI5FGM5F5 MILCCA5R5RNRE5MV
14059	44427	B	14141	98	1064	
14060	44428	A	14142	560	964	KRLPRILGIR5GK5C5P5TSRAGR RVRGR5AA5P5CREA5AR5RG5QRR FLPPTWRC5ETGA5T5MP5P5ALT PTPFSVKD5I5N5T5V5P5RS/LGQAA LTKRL5AS5I5S5P5Q5C5A5C5R5R5WS CVILSAV5R5GN*YAG5RA5H5D5CT Q
14061	44429	C	14143	189	452	
14062	44430	A	14144	1	647	

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14063	44431	A	14145	890	2905	LRLSLKFPMSQWTPPEVNEYLYTKVDMKSEIPSDAPKTQVQSLKGILHPEPIGAAKSFFAGVEMINSKVGNEFSHLCDQSQKQEKEMINGNQQEQEKSLLVVRKRRKSQQAGPSVYQNCVKENQGILGLRQHGLTPSDEDNDSSFSCLSSPSSLHFGDSDTVTSDEDKEVSVRHSSQTLNAKSRSHSARSHKWPRTETESVSGLLMKRPLCHGSSLRRLPCKRKFVKNNSQSRQTQKQKERILMQRKREVLRARRKYALLPSSSSSENDSSESSSSSTEGEEDLFVSASENHQNNPAVPSVTVGQPWSKNIKEKTLEINSSQALTAYECLHSAHVINVLSIPFYHHFPSSQE RSVLSTLSTLSNKKTGSVWFTRSPKVQTQFPFGGAITGTLSQRPEREILRPLALPGKGNTPPYFCPSMGCTHCPTSPNEMNQGISEDAAAPVRDIYIKPPSPWDRAPGGRGCGGHSFSRLKSPYLRALKSAADFPAQHSSSDKGQAAASSSSGLTPVYPVVWTPPSRGRQTPHRCGELWLASDGCPSPGRKLPEEGTGSNLCCSAASAGDTQANRDHNSSPAREQWTENKFDLTEAGLRRWVINSELKEPVLTQCKEAKNLEKRLDESPTRITSSEKKNINDLMEKNTAQLHEEHTSINSQ/DQAE*
14064	44432	A	14146	1	737	LNRGEQRAVRYSHMILKLNMAEEDYMSGFLH*CPRRYQTRIANAKANPRSPSKR\EKQQEANLKNRQSLKEEEQERRDIGLKNALGCENKGFAALLQKMGYKSGQALGKSGKSGIGHEASLRKKAEEKL ESYRKKIHMKNQAEKAAEAEQFRMRLKKNQDEMKEGLDLRRSQ RACQQLDVQKNIQVPREAWY WLRLEEETEEDEEEKEQDEDEYKSEDLISKKTYLQIVQDQLLQIMTKIIPNKVET
14065	44433	A	14147	1	1860	
14066	44434	A	14148	1	1203	
14067	44435	B	14149	1	1119	
14068	44436	A	14150	1	1407	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14069	44437	A	14151	1	1731	ERSSSPATEQSWMENDFDELRE EGFRRSNFSELKEKVRTHHKD KNLEKRSWFFEKINKIDRPLAR LIKKKREKSQINA1KNDKGDTA DPTEIQTITEYYKHLVANKLE NLEAMDKFLDTYTLPRINQEEV ESLNRL/LNNRL*N*GNN**LTNQ K/NVQDQMD*QLNSTRGTTRRS WY/RFLKLQFQSIEKERILPNSFY EGIILLIPKPGRDNTKDKNFKPIS LMNMDAKILNKILANR1QQHIK KLIHHDQVGFIPGMQGWFNICK SINVIQHINRTKDKNHMIISTDA GKAFDKIQQPFPMLKTLNKLGI GMNLKJIRAIYDKPTANIIHLNRQ KLEAPPLKTKTRQGCPPLSPLLF NIVLEVLRALARQKEKEIKGIGLQ KEEVKLSLFADDMMIVYLENPIV SAQNLKKLJSNFSKVSGYKISVQ KSQAFPLYTNRQTESQIMSEIPF PIASKRKYLGQLTRDVKDLFK ENCKPLLKEIKENTNWKWNIPC SWIERINI/VKMAILPKVIYSFNAI PIKHPMTFTELEKTTLKF1WQ KRARITKSILRQKKNKAGG1TLP FKLYYKTTVTKJAWYG
14070	44438	B	14152	1	906	
14071	44439	A	14153	3	553	EHSSSPATEQSWMENDFDELRE EGFRRSNYSELKEEVTHRHKEV KNLEKKLDEWLTRITNAEKS DLMEKKTTAREICDECTS CDQLPRPDQFTAEFYERYKEEM VPFLKKLFQSIEKE/VNPP*LT GQHHPTDKAWQRHNNKREF*T NIPDEH*CKNPQ*NTGKPN HQKAYPP
14072	44440	A	14154	1	909	MKAEIKMFFETNENKDDTYQN LWDTFKAVCRGKFIAVNVH KQERSKIDTSQLKELEKQEQ THSKASRRQEITKIRAEK JETQNTLQKINASRSWFERT NKIDRPLARLKKREKNQIDA KNDKGDTIPT DPTEIQTITREYYKHLV ANKLENLEEMDKFLDTYTL PRLNQEEVESLNRPITGA EIEAIINS PTKKS PGPDGFTAEFYQRY KEELECSSSPAMEQS WTENDF DLR EEGFRSNFSELKEEV QTHRKE AKNLEK RLEKWL TRITV NEKS LNYL RLEKT MARELC
14073	44441	A	14155	1	969	

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14074	44442	A	14156	377	687	LI.EGKLTNRKDIHTKTPSVPSSKTKEHSSSPAMEQSWMENDFHELREEGFRRSNFSKLKEEVRTHRKEVENLEKRLDEWLTRITKVEKALNDLMEALKTMARE
14075	44443	A	14157	1	711	
14076	44444	A	14158	1	831	
14077	44445	A	14159	1	744	
14078	44446	B	14160	1	1479	
14079	44447	A	14161	1	810	
14080	44448	A	14162	3	651	
14081	44449	A	14163	2	1067	
14082	44450	A	14164	2	2063	
14083	44451	A	14165	1328	1639	PTNAHETSGRYIAGSSSEKRTSATCGGTSAAARPAGTSMQTRCRQPPSS*HAVPRAVQSSDSGLKATHPQAYQPCGHTPTRLPQESNCIEHERGLGKKKKKK
14084	44452	A	14166	1	620	MTLVGQORGANKDLRTGFDPPDLCTMDNFAEGDFTVADYALLEDCPHVDDCVFAAEFMSNDYVRLTQLYCDGVNDSFLIGGLLRIGCKIERNSSSPAMEQSWTENDFDELREEGFRRSNYSSELKEEVR\TNGKEVRNFEEKKLDEWITRITNAEKSLKDLMELKTTARELCDKCTNLSNRCDQLEERVSAMEDEMNEMKIHEDKFREKE
14085	44453	A	14167	1	514	MGKKQNRKTENSKNQRTSSSPKERSSPAAEQSWMENDFDELREEGFRRSNFSELKEEVRTHGKEVKNLEKRLDKWLTRITNTQKS\LKDLMELKTTARELHDECTSNTNQFDQLEERINN\MEDH*QD**RKERRIK*MQ*KMIKGISPLIPQKYKLPSENTINTSMQIN
14086	44454	A	14168	1	366	MDTFLQAERKDYMЕAYELIEQEEQGEREPVAVNNILSTEALMANAKSTLMFYAVGFLWQPGGGRGHKAASNPVGTRDVVGSSLSTFLRGERSSSPAMEQSWTDNDFDELREEGFR*SNFS
14087	44455	A	14169	1	1026	
14088	44456	A	14170	1	3906	

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14089	44457	A	14171	1643	2721	IKPTKMGKKQSRKTGNNSEKQST SPPPKERSSSPAMEQSWMENDF DELTGAGFRRLVTDFSELKED VQTHIKEAKNLEKRLDKCRTN G*LEWMNG/ITR/ITNAEKSLLKD MELKTKARELHDECTSLRSRFD QLEERVSVMEDQKXNMEMK EGKFREKRVKRNFO\$LOQFIVD YVKRPNLRLIGVPESDGENGTK LENTLQDIIQENFPNLARQANV QIQEIQRTQPQRYSSRRATPRHIIIV RFTKVEMLKEKMLRAAREKGQ VTLKGKHIRLTVDSLQAR REWGPINILKEKNFQPRISYPG KLSFISEGEIKYFTDKQMLRDFV TTRPAIKELLKEVLNMERNRR YQPLQNHAKM
14090	44458	A	14172	351	898	SGVTAPWRPNGLLITAATASH PVAIAPAHLCSPRCPSFLTTVTC SGPOHHAARGRVPFH/SEC GK SFRYRSDSLRRHF/ARHTALKPH ACPRCG/KGFKHSFNLANHRLS HTG/EPYRCASCPKGFRDST/G LLHHHQVKTITT*PD/CGGCLVSN IVGSYSRPPWPCTRGPRRPLGS SPAGGSVCLC
14091	44459	A	14173	1	551	
14092	44460	A	14174	3031	3207	TIHGCWWDPPLSIF*PFWGRGF SHKICQAQISFRVISGTVLSLDK LLIMFHKAIIFASP
14093	44461	A	14175	3555	3957	ENGQKTTWIGTSQRRTGDRM AQIONPDTKCW*ECKATGTRIH CWWECKMVQPLWK\$WQFLT KLSILLPYNLAIILGNYPNALK MYAHTKGFTCMFIAASIIAKT WKQPRRPSVGEW/INNL*LVQT MEYYSA
14094	44462	A	14176	3	883	CQPYPRPRPRTGTHGSCQPPSQ GSAEP*G*CLPTLRLMALKAQP TKVNPRTLDDSDPDVC/S*AAHS RVLITSPSRAPWRLPSP*RRCPA GTCMPSTATSAR*CSQRPGSSW *T*TGSSLGSQACGPSSSTAPPSS SWSACTCGAAAARCSAASS TRSGPTCGSSPPASSCASSTPAP GTTPSSTLTWSWASSPWTCPGS AGPSSWSSSSATPSAASRTIL SPGSPAAP*PWPTALSRLTEQEA VVGAWGISHGNSDWIKETKLV RLPHPCSKSPCFRPSLQPYRAHR AP

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met id	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, -=possible nucleotide deletion, ^=possible nucleotide insertion)
14095	44463	A	14177	3	395	SAEVGAAETTLTELRRRTVQSLIEDLDSMRNLKASLENSLIGILLHLESELAQTRAEGQRQAQYEALLNIVKVKLEAEIATYRRLLEDGEDFNLGDALDSSNSMQTIQKTTTRRIVDGKVVSETNDTKVLRH
14096	44464	A	14178	2	1044	AKTSSQMPSPQEGMCGKACTPALSQADSLCPLLRLASEVEGYSLPACAEPYVQSECLSHLSVWSLQHALSSSLASMSFTTCSAFTNYWSPGSVQVPSYGTQPVSHAASVYAGLGGSGRISVSHFTNGIGGLAGMGGIQNEKETMQSLRDRLASYLDRVRGLETEWKLESKIQEHLNVTRL*LETEIEALKKELLFMKKNNEEEAKGLQAQIASSGLTVEVDAPKS/QDLAKNMADSRAQYDKLARKNREELDKYWSQQIEESTRVVTTQSAKVGAAEMTLTELHRHRVQSLEIDLDSTRNLKASENSLREVEARYALQMEPSLLFSKIIIFGRVWEISYLVHFEKGKQV

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14097	44465	A	14179	1	2040	MPVPQLPPPVSRILAATAASAVT EPGPNPEAVRSASAEPVEKGFSQNHSGVHSNLIPSGVSPSS GRSHYGYASEDGTCSKLRVRPR LAAAPAAPFAFVADLASCCQG LSFFEGILLVGRPYRRLRATVV RDLVAVRMAEEQFTQLCKLP AQPSHPHCVNNTYRSAQHSQA LLRGLLALRDGILFDVVLVVE GRHIEAHRIILLAASCDFYSMSFT TRSTFSTNYWSLGSVLATTYGA RLVSSSTARVYAGAGGSGSRISV SRSTSFGGGLESGGLAAGMAG GLAGMGMGQNEKETMQSLNDR LASYLDLDRVRSLETENRLESKIR EHLEKKGQVQRDWSHYFKIIED LRAQIFANTVDNARIVLQIDNA RLAADDFRVKYETELAMRQSV ENDIHGLRKVIDDNTITRLQLET EIEALK*ELLFMKKTPEEVKG LQAQIASSGLTVEVIDAPKSQD LAKIMADIRVAQYDELARKINRE ELDKYWSQQIEESTTVTTQSA EVGAAETVTLTELRTVQVFGD STWTSMRNLKAINLNESLIGEV EARYALIQMELQLINGILLHLESQ LGQTPRTTEAQRAQAEYEALLN IKVKLAEAEIICHLTRPSWKIGE DFNLIGDSILDERNSMOTIQKTT TRRISWIGQSGVLRPIDTKVLEA LSQQEASGTLLGKQEANKKFQS
14098	44466	A	14180	275	550	
14099	44467	B	14181	729	909	

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14100	44468	A	14182	1	1415	MGTQCDLIAKSLEDCPVDEVEDAFQQLGKEDEEIEQFSDKTFSGQAIDDDWREAHECLAELEVQPVAVIEQTGNGERDEM DLLD DHEENLAERLSKVMVIENELEDPAIMRAVQTRPVLPQPGNSL NSSWDGS/VSSEANPRTTACSGNAY SVCIRICFASEA/SPRVQKMIGTFLNEHYQGGQLHLSLA VLLLELS P*APHLNRWLYPASNPRFCVRS LSMFGP/QMPPRYPAPYGERMSPNQLCSVPNSSLGHFPFPSPVPP VLSPLQRAQLLGGAQLQPGRMSPSQFARVPGFVGSPLAAMNPK SQAPMFRPDTTILHPQHRRLLHQRRQQNRSQHRNLNGAGDRGS HRSSSHQDHLRKDPYANLMLQREKDWWVSKIQMMLQLQSTD PYLDDFYQONYFEKLEKLSAEEIQGDGPKKERTKLITPQVAKLEHA YKPETIIQCALCRALHINYLTKAFQQAFEVSASIITIYR
14101	44469	A	14183	204	560	QGYWRGCTSSGGDGCGRCGWSPGKRR*GLSRTASGPAAVAS PGRPRSPPSARTG*S*PGA*ARP CSRTW/PPPRCPLRPPSAARASA SRV/APL/GEPAPANTNIYCAAL THRATKSSTREF

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14102	44470	A	14184	59	1695	DMPWPVPLWIKDSSPSSLEM NPNTSGLRQKSVEAEPCLSW MVHRYTPQSTGEACTMAAA GPSSPGSCPRPPLGADPWPMSR LSH*EC*KTGTTASGYRRHQET APESSGSPVGLSAGLWLWSA WPVSPACLHPGPPLC/GPPALG LGPSPAAAS/C/PPLEAPPACSP FCP*GEISSGGPLEPVQV*LPGD LSEPPPLGTSPLGRAPGLCSLLRA P/RPGAACPPASPSPRAMPILLS*E APRRPGPSGETSPSPSLAPSEASP G/PPR/HNGRDSEGAGTRTPGA SGSSKG/LGGQPAPHGPGR*G GGRYRGSAAGSVHSAPPGCSP HAPGCA/CDVRG/AKPSHFHSG CQSG*GHQTSGGCPHLGLSPCS TCLCAGQLQQQK/PGSSSGNL* GQGHSSGDLGSAPPHLVPG/PG PLTAGHG/SLVGDSEWGPAP GAVLQNSSGPPDPQRAGRWL SRAEKSGCYTAPPLG*LSAQFQ EEKASWVPPGSGQLEDSPHDPPY TALPLAAPPWGTGTGCPPAWP RL/EPDDCGPRHLSPTCSTLPS WGGCAGS
14103	44471	A	14185	264	643	RCLRPGEGRSRQRRSRTGRK AEEGGARTRQQRRALLPERS ASQPGPRDSPRWRQQRTTRGR ARPASSGGT*GSSWLTLAWP EP*RLRSASAQG/CRQLRLQQR RRGLYQPHRPATCGPRAAD
14104	44472	A	14186	114	1039	QSQRRLRPLADTPRRSNRPCSAA GLLFQPSFWSQEQLSQGAFLLPPS SPCLHCLPGTAAASRIQSRPRT RPSVQERRETHGLCAHRCCEWR AGSPAHP*AHRFVSRAGSPA GP*AHRCISRAGTPARGPYSR* VSEAGSPA/AVVSAPCSLSS*AC VTGICSPAHS*AHRCASRAASP EHTSREDAEQAP*MQGLCPVH QEQQPSRKSVVTSIPHPPETDCR LLPKNPANCANKHOPTATGGRAV PPEVQHVPPIRSGMTLGSQHQPLA LQFQMQATDAARLGLSPQGQQ SPPGPRSTLLLGLSLFQLSLRR

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14105	44473	A	14187	1	1629	MIIYVENPKQSTSCKVRAYTFS KVAGHKAIEKRLEKLAVDPHR DRAQMLKVENVQQAWQQWIN KLPPARREDEDVKEIRWMIEEL RVSYFAQQLDHTGVDRGQPGA STWSASLMSCSVTQPKLKLTRKP GFLLGLGERNCFSVYAGRSW GRGLGSCGFWLPPRTIRAAADV CLARWGWRRAHVRVLAGKNS RAESMLWSFHKAIAEAAARTNII QAQTRVEAAQATERRIAAIDD SELKAPRDRGVQYRVAKPGEV LAAGGRVLMVNDLSDVYMTFF LPTEQAGTLKLGGEARLILDAA PDLRIPATISFVASVAQFTPCKTV ETSDERLKLMLFRVKARIPELL QQHLEYVKTGPGVAWSFLYSI NQTCIQLRLDSIEAKLQALEATC KSLEEKLDLVTKQHSPIQVPM VAGSPLRTTQMCNKVRCVNP* ATVVPPVPQPPTTQQYQGLDA GATTRVPRSLRSEGSQQTQKSP SCGSHSQDNSSGRKAVGARRD RWWLGAGKGPDRCGAKCGLP LSGQKCPTELDPYQVVGCTSKTG
14106	44474	A	14188	3	1010	GLQTQLVPLSSPVASLDNFSNL FGADLHVEKGQVPSDQHLSQ RCHEFPKAPPPWSVCKALLPRSNP ATSLSGTSKPNSSGGDFNSVTKS QPHCELNFSVLTGHSPVLWMM SEHDLADVVQIAVEDLSPDHPI VQSCGTVVVLLENHVVTDEDEP ALKRQRLEINCQDPSIKSFLYSI NQTCIQLRLDSIEAKLQALEATC KSLEEKLDLVTKQHSPIQVPM VAGSPLGATQTCNKVRCVVPQ TTVILNNDRQN/DHCSQDGRPL EQQGTGFPGKMSLASQ*HGTNP TFPCCHCAESHENKSTLSQGTV QHTLHLCGHRVEPGRHRPSSLR SGRAGWAMLNA
14107	44475	A	14189	1	1710	
14108	44476	A	14190	52	457	
14109	44477	C	14191	1	838	
14110	44478	A	14192	92	514	
14111	44479	B	14193	1	531	
14112	44480	A	14194	1628	2008	

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14113	44481	A	14195	2	1616	CPPPRPRPRAPPHRRPPAAGA RTAAAGDRSRHGPASRVTGTP GQQMRKTYCRNSEPSLDQGG GSRGPPRQSKCVRNWWVVLGL TDFKNEAADPHDSGAQLASP FRTRAAGGAACQSRAMRSYSS AIGWMSMGLGAVEQGVVLVGE AQAAQEPMEWVGSGMVGR SRAPPAGRQLRPDKKLSTAPVG RHRWRPSTPSAATGLGAKSLIA RGQQGRLAAPNKTDFKARAVK DKKEGHYIMIKGLVQKESITIINI YAPNTGAPKFTKQLPLDLRNKT DSNTIIVGYFSTPLTALNRSSQ KVNKETMDLNLYTLEQMDLTDI YRTFYPITTAEYIFYSSHEHGTFSK TDRMIGHKTSLNKFKKIEIPISTL PDHSIGKLEINSKKNLQNQNTNT WKLNNNLLSDHWVNNEIKMEI LKKFKPNNDNSDTTYQNLWDTA KAVLTGKFIALNAYIKKSERAQ VDNLRSHLKELEK*EQTKPKPS RRKEIMKIRAEELNEIKT/QKIQK NKSQSWFCEKINKIGRPLARLS KKGREKIQISSLRKK
14114	44482	A	14196	1097	1686	APRPLALRFGPLPSNSQAGLASP SGSTCGLQVELPANSCTVRWQ VSALGWSMGP/GPAGGGSAD QGGSGGTGAHGGVGRFRHGG AAGPEPCPMGEVAKAPARNRA QRQWAGTAGGPGCASS/NSC*PG C*APYCPGWGQPAAPSAGPP SPRPPRTRAGPQAPWAAPVPAH ASPPHLPAS*GSPLRPGIQGSKT YQKSH
14115	44483	A	14197	647	1496	FLNLLSWQNLMCLGKKKKRKQ FKDYEKKVKELNEERDKYRKG SVIYTFGKEPTLNKVLDAACDG KFQAIIDFITPGTQYFMGCRWSC LPVLHCALAGLSPWVVDGTRR PGAVGSAGRGGSGGTGAHGGV GRFRHGGLQVRSPAHEVLRPS EKSSAAQWAGTAGGPGCASSTA ADLGAKPLTARGGGPAGIPPSA GPPSPRPPRTRAGP/PSTVGSPG/ SPPTPLPPHLPS*GSP/SGLGQP RKGLPQCSGGLKGWLLKHRQS GCPGRGGAQSERGLRGLPARC

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14116	44484	A	14198	1	560	MAALLLVGASWL/LLLGVAS WLLARVLAW/TYAFYDNCHRL QCFQQ/PPKRNCF*GHLSCGA/ TEEDMRLMEDL/VPLFRDVQL WWLGSFYPV/LVHPTFTAPV LQASGG*PGFTTTMGI.SFKRAK WQRLA/SEGSVRLEMFEHISLM TLDLQKICFSFDHQCQMVSPG SCTTSRGPRIPGALPTGGARAPE NGDPKEIE
14117	44485	A	14199	175	2225	RWSSVSFASGMPSPCCWGH QCPSAAQPTGSPWAGCRGLTM PNGQASPAS*VPPGAFFLCIKQ PLWENLMTVGKFSREAATLE GPTLPTRGVGPQCRQIADLPLE RTEGWRGDIGNPVRGVQRK QLVAGETAASLLPCQASGESCS VP*QARGPPVFLPQ/WGRRA KGCA SRSCF*PDFRPSIAVPGA REGAGLAAAPKRVARLSPAVPP ACC/GLQGGSSSSAAQAL*PQLS GPRLPREK*GA/PCWRRGGPRCC PQNSA PETLEYVEPRGTGAPGT THTGLPSPSQGCRGAEGW/WGL PGLPGRAGSSPQPRGRAWRPR ARTPPPASWAAKGRGRPLAAG GLARPRDPGPGSGVAPAGSLRP HSSGRGWGRRLRARP TGGNR GSEWPR/RPPGYPGARGPAGP RPQP/PAA*TRPLPVCGGARPFH PVPATVVPHAGPP/SGMGRRRG RYPRPASARPAGRCGAGSAEPG RGTDKGGDGEGKTKRGGG/L GGGAGAPKAAPGAAEPMGGR GAGAGGGGAIR*GGGGGGSG TTGSGSSSRPRPRTRAPPETDP APRPRPGLVRAAGGGAAAGSG TGRGAEGCGVRAARGVPAASLR AALARGAQARVLVSGPAPGWA EPRPAGGARGVGWVGWPVLAGP GRGP RGGAGRGPRALSRGCAA *AWTPGRGAGQRGPGSGRGS

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14118	44486	A	14200	1	2850	MHPQERTAAATNAIIITDGAATQMGVTSTPAPGHPRDGYYQGKDVSLLAHTHSFKISAAJEAKTTWVGMCRWGCKVALDVTFDVHQGKPEGAGRNCQIPFIQDFPFALRSEKRPSLPAATISGKTLPLNTKTCPQLLQCKREGHSLQCLWLQMVPGQLGRLAVGGCHSNAWFSPSKKAVIWEKFHKHNLSGLVSDFKGDKRTGKGLGECLMMMRKMSPALEALTTFDSSLQHHFPRTFPVALEALNPGKPKRQLVTPA
14119	44487	A	14201	1	1570	MQSATS DAGSAPKKKKVMTLQEKGSIAYWFFTAAQEWPNTPPKLRTCTESMGCCLLDCCTGQGDWTRVTLVCRYPFILFGTNAWVANFERPRMNANSLLASPTGLSPYLRFGCLSCRLFYFKLTDLYKKTTLGSLPDAAMAFVNCHGAGGTVAVRTSRGHSRCHFGFVGSGTRYYHLLTPQVWVERQQKQVDSLLGTQQMILEAQGREF/GPPICILPVPTNAPAAKTTTQOPPSPD L*PPNYLFLCVGDHRPIC*EPKQNKSDSFTSQ*SQDG*YCGCS/CRAPRPHGT SATIPMSSCKRFQPSSPF/CKGPYHFRFLEERPLASRP SIHPSCGSYWLRLGCVAVGRTG/SRLNLQLHSASGLQALSKQR*RYCQSA GAGSPEPPRGTR*CCR EAAPGCRAGTCPSAANLPSLRRK/PGTC*PQNPPGRCGSCGASA AVLAETPARIRRSFPRARQSCPRTWMAAGPGSSRRQGTKHVT* *SSTLEKQLDNPTATYFSVPTRKPVH*NQQKDL*VTG*LQJFHL
14120	44488	A	14202	11	356	VSGPPR*APWCPCLAAPGSTS HGSTARSDSTACKVSGATCV/SGCGPGLGVLGRGLSSTRSCCM PAG*CPSSKDTC EKSGGRTQPV PPFEWAAQDASLVRRCRILAHRPCRGTS
14121	44489	C	14204	333	473	

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14122	44490	A	14205	344	1035	QSAAQWFWWPGRSASLGGAK GMQPPLASLAWPHPRSRICLRAP AP!=QFTNATDPRFRSAPRRSQG QQPRGSSGPAAALASPSPRQPNR AGALRTGGAGWATALDTWSC PRTRRRAPMGSCL*AAQQCV TGATWPPPSAIA*QSAAQWFW WPGRSASLGGAKGMQPPLAS WPHPRSRICLRAPACSGPSASS AAVQVACCCSLLACCGPSRQPASQ GHLDGTPITSPECTTSLWSPQR RRAAGPPKVVDIDP*D'RGSRRELPS GRGAPNTTICPGGGSPGAKWIE GCPAQ/RPSPPGHLHAPMASAL LLMPFLQRRRHRSATRLLLRLPGS DCTGKK/GKGFLAGPETKRQRK LCPSPKTLGRALGQQEALPANV RC
14123	44491	A	14206	41	292	
14124	44492	C	14207	480	1637	
14125	44493	A	14208	3	410	SPPCGAPPPPVFCAPAPRAPAPP RAPPLAEAALPGFASAAGSAPA RSGPAGAG*GSRSRPRAASAS LAPASAGDHLGYPSSATAAAAP ASRPWLWRPSLNAAIRLDGPAC GWQASQWAAGSA*RAGSQWA AGEARA
14126	44494	A	14209	1	1274	FFFFHPLRSLLGDLGLHSQERSA PEIKPGALESTWSQARGAALRL AEAR*RAAPAAGTACSGAGAA SSPR*GSRATRRRRGPTAPSRA ATAPGRGAAASAAPAAPART ALMASARGPPVTAASPAQALTR SAPGHLPPMSSELGAVTALCESC PVT/AAPRGSGGEAGGTLASEW GRTCRNYG/PAPGIWPRPPLSAA RPAAASPPARRIWSPPAPVHSA ASPIGLRVAAPCSSGAVPLRSR RASPPCGAPPPPVFCAPAAPRAP APPRAPPLAEAALPGFASAAC RGKLRLALQGGGLGRSGRSRQE GPAAGS*LRTGKSWPSPPPGSA PLPLAQLVQALVEAGSRSRPRA RASASLAPASAGDHLYGYPSSATA AAAPASRPWLWRPSLNAARLG DPACGWQASQWAAGSA*RAGSQWA AGEARG
14127	44495	A	14210	2	335	

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14128	44496	A	14211	344	1062	TRAEVQQKLSRFASPPVRL RSYVSPPAAPTADPWRWPSWST SLRWVVKPNVSAYRPRASNR GYRASDWKLDYA*WTGRLRIT SKGKTA YIKLEDKVSGELFAQA PVEQYPGIAVETVTDSSRYFV \  RISDGTRGSAFIGIGFTDRGDAF DFNVSLQDHFKWVKQSE EISKE SQEMDARPKL DLGK EEQTIKL CIGLC SKPGTTAIQLG PVLNGIG RTLRTDLRNKN DLEGTNL
14129	44497	A	14212	573	1017	TDQGVGSPHICPRFQQGPPRSPR FQQRSPHSPDSSRG/PPHSPRFQ QGSPHPTDSSSG/PPVSPDYSSG HPTP/HTSQQGIPC*DGHGWLP GPVFLWSEAPHLNPGLGVWGQ PRAPALPGNSAESKLWPHDRPA RPETPGAGTAWAHQALRV
14130	44498	A	14213	707	836	
14131	44499	A	14214	724	927	SFMDFRFVLLFFHLVPNPK*RP VS/SPPGSKLLVPPWGKTPVPP HPSPPPAAHGEPLGLPPPPPLPH
14132	44500	A	14215	29	157	
14133	44501	A	14216	1	363	
14134	44502	A	14217	770	952	
14135	44503	A	14218	1053	1995	KSSEPDLSHSFIFCSPNFPSSSL KRPHFOSSILACVFCITADSSRA PCVLRVCDGFAGLTRSSAPSSK EKPCGFSLPEFTPLAVSFPQAL CSLGTVSLRPRPQLTPSWC VLLAGAVCPGLPCAAGCPWA GEEGCPGATSQLDQGVFWFAP APEVLWPCLDSWGVFWAP IPLMASPRFGFMGRSQQPV ILIKEPKAKFSNKNHSIRCCQ QRKWRRGNAAGMCCQPIP GEVKTEFQPVSNSRVNYGCTM HFQETLWTPLRLGLGDGDSNNN NNNNNNNRRITANPGKEAKPE HPHLVKM
14136	44504	A	14219	482	833	THQGARGCTHARVSREMRTR RGRWATGMVRVPACSSVHTTA VQRQQVADQLQTTAELSMELIL N/KWDQDPEAFVRKVATSYET WIS*YYPEDKAQSKQWLPRSGS GATLYSATNQYP
14137	44505	A	14220	195	367	

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14138	44506	A	14221	989	2210	LLVSCAIIILSVSFLHSSSFVRSRS NRDSPACVDAHYRGCGCQCGEG VCGEACSCFPDLNQPOGVHAG EGVLPSCGWEDTFGKNTCLVS YQQIPNKRKPCCTCEECGKAFGQ RSHLVQHTESEKLYACQCECGCTF SNNSSI.VKHWHVHTGEKPYMC GHCGKCFRESSSLAKHQRVH GEKPYVC/GESTHLVQHW^FHT GEKPFAC/HR/CSKAFADFSALL ACHGTYTGERPYECRVCKKA PSLSLAEHRCHTGEKLYACQE CGKAFSHSSSLSKHQVHTECG KAFSQGSYLTQHLKIHSGEKPYI RGEHPPYACGKCGKTFSHSKFLT QHEQVRMGEKPFMCDGCGRAF MQTSSALHQRTHNGEKPYKW NECGKSCIQMSHLTEYYQNLP KGSKDPHDTATVHSPVMD
14139	44507	A	14222	1	245	PPFRKQQAQHRNKTVLVSRSP VPVTVP/PSA^RSTPEGPRAG CDPRP^PCPAGPELPAQMKVLA IEQLLSLHFKKALLF
14140	44508	A	14223	477	947	LCSLSSLPPPPPPPPFPFPFPFP PFPPPSPVPLPPSPRSPPPVSPPPPH SFQGRSPPPSELGSSAEPWLRPGT WV^/PPPLTFSQQEAASSAQK^N CPGESVPQPVPVTVPERQPDAA NHSLLI.PGQQQCFWCQGPHPPY WMGPVDASSSGFLSQSFY
14141	44509	B	14224	438	1437	

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14142	44510	A	14225	584	2866	WHAFAKLSRNTQDHTRPTLGA QAVPATGQPAAPGPAGAGPEW VPFLAVYKEQLVRNDS/LKVFF FPPIFYREGWVCCSVVESHLQE GFVWLFLSQL*PPKLRSLFLSY CLSPSDIEISRGQTPKAVDVLA KEIGLLADEIEIYGK1VSSAGF A*VVAEIL*NSLSPEELR1TPTPL GEGKSTVTLIGLVQAVSGLCP WQLYLVTPALQPGQQSSETFLK INK*KDILFL*FNLHLTGDIHVV SCELSKFMDN*LLCGLIFVLCFF RGIIIVTLCFLFLKLLTFFLNNH *KLGINKTDP1RTMPDTHQVAG PYLSTD*D*SVLFQ*SPAPCGNG HPTGTVAHYLCLGW/YQAQF DIAVASEIMAVLALTDSLGREV PRG*PLPG*YFVRNLMFFSHLPQ IDLGFHASVCLLG*FAFSLL*G TPVFVHAGPFAADRDLCPLCYQL LCQTHIYKIHVIMAEGYFQRYKL MMYAKQTSPLCDL.EQAISLSGC VPCRHSHLKNEFKSCTGC*QYL PKLSPNPDPLTPFSADYGKF ESNHANHSGDCQNLPLFEDNS TYSTCFPTVTEAGFGADIGMEK FFNIKCRDVVLFSRSVV*AFLL AV*LGRFGRQYTGVWVWLFS FLQNIQLVADGV*MVSLSLKT* LNGYRCKTTNIFTRTDTRAEI LVCELAKRAGAFDAVPCYHWS VGGKGSVDLARAVREAASKRS
14143	44511	A	14226	3	587	YPASAGLMLQNFGVIGLRYHF AIHSPAAGGLLDGLHAVAIIQG ITKIEPPNHRQRAPAHWTLLTQ QAHLQPSPLHFNLPLTLCLMHC PTAIPHCFADARTWVNLPTSSL GHKKENLKEFISGSLIVHEILEE VLQAEGDFQPFPTRTVVHWGKG NDQTRGILLDTGSELTLPGPDP KHHYGPVVKVGAYGAQLL

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14144	44512	A	14227	2	1256	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVI <sup>FPV</sup> PECIIGIDMLSSRQNPTGSLTG RVNTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFN <sup>S</sup> PIWPVQK TDGSWRMTVGYCKLNQVTP <sup>I</sup> AAAVPDVVSLL <sup>E</sup> QINTT <sup>PPG</sup> FTWY AAIDL <sup>A</sup> NDFFP <sup>I</sup> PVKAHQKQF AFRWQGRQYTF <sup>T</sup> TVLP <sup>Q</sup> GRWEI NMTKIQGPSTS <sup>V</sup> KFLGVQWCG ACQDIPSKVKD <sup>L</sup> LLHLV <sup>P</sup> PTTK K/EAQCLSGFRR <sup>E</sup> IIP <sup>H</sup> IL <sup>P</sup> IYRV SRKAANFEWSPEQE <sup>K</sup> ALQVQ AAVQAAWPLGPYDPADPMVLE VSVADR <sup>D</sup> ADW <sup>S</sup> CWQASI/GHK VGH <sup>A</sup> QQJHSI <sup>K</sup> WKWY <sup>I</sup> R <sup>D</sup> W <sup>A</sup> R ADPEGTTKGQQGQRRWWQ <sup>L</sup> A <sup>E</sup> RQDSRDR <sup>E</sup> A <sup>I</sup> GERQETAVGK <sup>T</sup> ARDGEAVCD
14145	44513	A	14228	155	531	GNLWSVDL <sup>R</sup> PGTPLRQNFRG <sup>T</sup> RQQHRSRTKNC <sup>H</sup> CSQT <sup>P</sup> LIPRQ TGSGV <sup>D</sup> LSKLQQTCS <sup>G</sup> SLC <sup>V</sup> TIDLANAFFS <sup>I</sup> PVHKA/HQKQFA FSWQY <sup>T</sup> FTVLP <sup>R</sup> LTWLQCP <sup>V</sup> PNLPAAE <sup>T</sup> NTEPSNGT
14146	44514	A	14229	1	518	MTVDYCKLNQVPIAAAVSD VVS <sup>S</sup> LEQINTSPGTWYAAIDLA NAFFS <sup>I</sup> PVHKAQQKQFAFSWQG QQY <sup>T</sup> FTVLP <sup>Q</sup> WYINS <sup>P</sup> ALCHNL IRRDLDCFS <sup>L</sup> PLDITLVHY <sup>I</sup> DDI MLIGSTIKWV <sup>V</sup> HSS/DSIIKWKW YVHDWARAGPEGTT <sup>N</sup> LAG <sup>*S</sup> GTCKKHEWKTGDKGIRGRG
14147	44515	A	14230	281	1140	VRVLSPVEKELKLWKNTHKLL SYPTVGAAVTQLQNL <sup>T</sup> AMGV <sup>I</sup> GSHGARGQVVALNRQRG <sup>D</sup> L QP <sup>F</sup> TRTV <sup>H</sup> WGK <sup>G</sup> /NMQ <sup>I</sup> F <sup>G</sup> LL LDTG <sup>S</sup> EL <sup>T</sup> L <sup>I</sup> P <sup>G</sup> D <sup>P</sup> K <sup>H</sup> C <sup>G</sup> PPV KVGAYGGQVINGVL <sup>A</sup> QVQ <sup>I</sup> TV GPQTHP <sup>V</sup> VIS <sup>P</sup> V <sup>P</sup> ECI <sup>H</sup> IG <sup>I</sup> D <sup>L</sup> SS WQNPHIGSLT <sup>G</sup> IMVGKAKWKQ L <sup>E</sup> LPL <sup>P</sup> R <sup>K</sup> I <sup>V</sup> NQ <sup>K</sup> P <sup>C</sup> I <sup>P</sup> GG <sup>T</sup> VE ISATIKDLKDAGVVI <sup>T</sup> TSLFNS PIW <sup>P</sup> VQ <sup>K</sup> TDGSWRMTVGY <sup>R</sup> RL NQVVTPIAAAVPDVVSLL <sup>E</sup> QIN TSPGTWY <sup>A</sup> AI <sup>D</sup> MANAFFS <sup>I</sup> PVH
14148	44516	B	14231	1	1521	
14149	44517	A	14232	3	202	
14150	44518	A	14233	2	367	

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14151	44519	A	14234	1	553	MTVDYCKLNQVQPIAAAVSD VVSLEQINTSPGTWYAAIDL NAFFSIPVHKAQQKQFAFWQG QQYTFVLPQWYINSPALCHNL IRRDLDCFSPLPDLITLVHYIDDI MLIG PQLLACY/WALVETEHL TISHQVTMRPELPIMNWVLFDP SSHKGVGCAQOHSIIKWKWVYH DWARAGPEGT
14152	44520	A	14235	3	728	
14153	44521	A	14236	1	635	
14154	44522	A	14237	3	266	
14155	44523	A	14238	1	1245	
14156	44524	A	14239	2	837	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTTHPVVIFPV PECIIGIDMLSSRQNPHGTSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSP WPVOK TDGSWRMTVGYCKLNQVVTPI AAAVPDVVSLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSVKDKLLLHVLPPTTK K/EAQCLSGFRREH PHL
14157	44525	A	14240	1	533	
14158	44526	A	14241	1	1043	MTVDYHKLNQVVTPIAAAVPD VVSFIEQINTSPGIWYAAIDL VFFSIPVHKAHQKQSVFCWQG QEYTFVLPQVHINCALCHNP LRDFDHFSLPQDITLVHYIDDIM LIG PV*NMLLHLVPPTKKETQ HLEVLFGFWRQH PHLATPSSP NGPMNKVTMMA/ANVGYAWD QKHGLPLTKANLVMAIGECVS/ SPAAETNTEPSIWHHSQGDSQ VQESKGNGNGSTTHHP**STS KIFASCSDITFCWPRGLSSRGR NAATRRHNNNNFIKPEVKIAFWT LWDPPTFKSTG*ERS*SVGWW D*HELP*NQSTTPQGSVSIIPH GQPPHQQLFGVAKARTFGIT
14159	44527	A	14242	1	336	
14160	44528	A	14243	3	1885	
14161	44529	B	14244	1	1423	

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14162	44530	A	14245	I	1361	MIISIDAEKAFDKIQQPFLKTL SKLEETASPSPVVATYTPQPM PSAFPPLSEEINPVLPEITVPMAS PEAVTRQDNVDSQPKPPPTPMF ASRPITRLKPRAPEEIQRLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAALNHQ RQVPECKIVDILNIRPHIGSL TGRVREIMVGKAKWKPLEQPP PRKIVIQKQYHPIGAITEISATIE DLKETGVVILTTSPFKSSIWPLQ KTDGSGWRMTVNYHKLNLQVET PIAAAVPDVVSLLQEINTSPGT WYAAIDL.VNVFFSIPVYKAHQK QFAFSWQGQQYTTFLPFGYIN SPDITLVHYIDDIMLIGSSEQEV ANTLDDLPARVASWGVPPYDQL T/GGRE*D*GLLHRWSCRICRH PQGSWIQES
14163	44531	A	14246	I	1795	MRKCGKPQFKLGQTNKANSRI QEELIHSKSLIEQEKEPKVQFSA FHRMWQPADSCQCDIISADIWA DPLVRHREITGSGGINRRTRG GRGRGGEAAGGAENCGSREER ERAVGVTAVTQLQNLNTIGIIGS RGGRGQVAAINHQRQGGHSYC KGQQKQNSNQNSVTHVELWII WLNHSVPRSEIDRKPTTFLLNL YKQKTSRDLWPFTRVTLHRGK RNDQTQGQLLDTGSELMILPED TKHHCGPPVKVEAYGGQVING VLAQIQLTVGPVGSGTHPVVIY PVPECIIIGIGILSSWQNPWHIGSLT SRKTDGSGWRMTVHYHKLNLQ VTPIAAAIPDVVSLLQEVTNPG SWYAAIDLANAFFIPVHKAHQ KQFAPSWQGQQYTFTVLPQGE TLVNFSLPQDITLHFHYIDDIMQI GSSDOEVANTLDDLPRKSTTPS G/LYGFWRQHIS/HGLLLTPY* VTQKAA/SFEWGPLEQEKAHQ VQATVQASLPLGVYDADPMV IEM/SLSDPSSHKGVCAQHQHII KWKRYVCDQA*ASPEGTsLY CTSFIMEKEEVC/LSLEQTTLTD MGLPILHAMLLWIHLWIHGLPY PSSWYSTQQCL

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14164	44532	A	14247	55	1241	NRFVRAAPASLKRSAIGIGLLCM PDLTVGIVVTQLKLNAMGITG SELTLPGDPK*HFGPVVKVGA GGEIVNKVYLAQLGLTDDPVGPR THPVAIFPVPECIIGIDILSSLQNP HIGSLTGRVRAIMKGKAIMKG YEGKGKAKWKILELPLPRKIJN OKQYRIPGGIVEMSAIIEELKY AGVVPIPTTFPLNSPIWPRKT DGCWRMTVDYCELNQVVTPT AATVPDVVSLLQEINTSPGTWY ADIDLANAVFSPVHKAHQKQF AFSWWQQQYFTVLPQGWTV NSPALGHNLIGRDLDRFSFPRDI TLLVHYVDDIMLIGSSEQEVAN ALDLLVFSDHAIKVWMHSSIA SSSGSGICVIRLKKVLAQPA MASWGVLYDQLTEEEKIR
14165	44533	B	14248	1	346	
14166	44534	A	14249	485	717	
14167	44535	A	14250	1	345	
14168	44536	A	14251	300	689	TKRAPCSPAAGSRGRARSALL TLYHGHHYPALPPGPTAQQPGR GLAEAAEPRGSEGGNGNSNPCG RA*DGRSRREGRGRLLGGWRPC CEPQPWRQAHDPAGPDRVDGG ERRGAGVLRGQDGQDEKKKPK

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14169	44537	A	14252	1	2430	MAVLQPSRHLRLPQLGLEPDN WHSQQDEVSSVATARAVVPSG RGAAWMGPSPGNIGGSGLVSH CGEGTGAAGSTQLQEGMHFCR QSRWAFLTALCEVYTQLQD VQWLQLCQWSAQGQDDHTLIE WLMGATWTVWNDAREIPETG TGQDAWLGSWGVDDQRPHV ELAIHCSPNVQRVLALVDTGA DCSLVFGNPVRKPDGTWQMTV DDWELNKVTPPLHAAVPSIMD LTDHLTMELGQYHFVYHVHSP TICRGLVAMELAAWKCPKGVL LFHYIDDIMLTSDSLADLKVA PLLWOHLAACGWAINKSKVQ WPGLSAKFLGVIVLWSKTKA AIEEKIQAYPRPTTMKQQLQTFVG LLEYWRPFVPHLAQMICKPLYGL SKKGATWDWDNEAGTDLAA KWAIQQTQALQVIDDQGCPFELD VHVTTDGFVWLVWQRMECFR TPVGFWSQLWKGAELQYSLIQ KELAAAYAALQAYETVTDWA TVIVQMSYPIVGVWTGTAAQTTL AKRGAYLEQQSMLTTPLAAE LQEALGPIVLVMEDKAMGPPEAPL DPEPSLLKKGYPLVPDGA DGSSQGAAAATVAIQP/ITD TI*FDTGCQGSTQWAELRVVE MDILEACOKCPACAAQAYLRQR QLPNVTQQVTVGQMLPTRWQI DYEPLPKLQGYTYALMAADI
14170	44538	A	14253	2	239	
14171	44539	A	14254	3	211	VVYSPNEVKVVAEGFDSANG INISPDDKYGPL*NIFIFQLLWC WPNSLLCFLCQCENSFLDIYGIL
14172	44540	B	14255	13	87	
14173	44541	A	14256	42	854	VLVFVLTAAFLFILPTFSNSMMILQ VSGGPWT/VILRRGVLLGVAPP PSLPAL/PENSYYQERQECYAFN GTQRVVDGLIYNREEYVHFDS AVGEFLAVMELGRPIGEYFNSQ KDFMERKRADQLPDCRDLMP D*GVWISPLGGQQVNPNLTAQKTL QHLPSSKEPQQHHDLVYHV DFYFDSIQVRCFLNGQEETAGV VSTNLLRNGDWTFQILEMLEMT PQQDRT*AGVQLLEVTNLNSLF FLEAQSDSVQSKMLTGARGLFI NYLQLNLCTP

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14174	44542	A	14257	3	571	QGRATPENYLFGQRQECYAFN GTQRFLERYIYNREEFARFDSD VGEFRAVTELGRPAAEWNSQ KDILEEKRAVPDRMCRHNYEL GGPMTLQRRVQPRVNPSKK GPLQHHNLLVCHVTDFYPSIQ VRWFNLNGQEETAGVVVSTNLIL NGDWTFQIVVMLEMPTPQ/GQE DVYTQVETHTSLDSPVTEW
14175	44543	A	14258	1	1677	
14176	44544	A	14259	2	430	
14177	44545	A	14260	821	1428	QVTDVQDFPLKCKIQRWRTVR GDLQ/PFTRVTVHVGKGNQDT FQGLLDTGSELTLLPGDPKRC GPPVKIGAYGGQIINGVLAQVQ LTVDAVGPWTHPVV/ISPVPEC IGIDILSSWQ/NSHIGSLTGRVRA TMVGKAKWKPLELPLPRKIVN QKQYHIPGGIAEIGATIKDLKDT GIVIPTSPFNSPI*PMQKTDGSW RMTVDYL
14178	44546	A	14261	507	910	
14179	44547	A	14262	1	2898	
14180	44548	A	14263	1	2580	
14181	44549	B	14264	159	2657	
14182	44550	A	14265	142	377	NHLLRRQQWQTPFPPPSWS/SPR SSSDCCGSSENFKPVDSLLLGSV GVGPTEPDHLDPWLQPPFQGS RFCLAGVPGATG
14183	44551	A	14266	363	638	EVWKESSGWHLAGAPLGQS RKEQAVIFAVLQPLLVIPKQTGS GVDLQQTPAHLQQRGQLSGCLQ SLCSLTSS*PQRHPQNSSLVNSC VVS
14184	44552	B	14267	1	2424	
14185	44553	B	14268	446	623	
14186	44554	A	14269	245	690	APSRSTWGSSSTAARRNLKTR KLRTPTTPHOKPDRNPHHGPPR TPSG*TPRNPDRHRRPPGAPQVGQ PGCWAPSQGPRGWQOLGC*RE EVPGGGHAGRHSTPVGG/DFL QAGWPWPDASLPTNPFLRGAS TPPHPLSENNKDKFLLQK
14187	44555	A	14270	223	365	

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14188	44556	A	14271	1	687	MSEYIRVTEDEDENDEPIEIPSEDD GTVLLSTVTAQFPGACGLRCRN PVSQCMRGVRLVEGILHAPDA GWRNPVYVVNVPKDNKRKVM LGLPWKTTEQDLKEYCSTFGD VLMVRQSQDEPLRSRKVFVGR RTEDMTEDELWEFFSQQYGDVM DVFVPKPRAFAFPFADDQIA RSLCGEDSMKGIVHSNAEPK RNSNQR/LRSGRFGGNPGFFGN QGGFESYQRCKERKAV
14189	44557	A	14272	1	833	
14190	44558	A	14273	3	447	RGTAGGQPGNGPALARQSP*WC RLGSGGT*GKSPGTSQGRALPW CSC/SVSTWATAAPGSQQRASP CSWAQPGPLASLRLMPRRLR* GHLGHLAWLQLFAACPVCIVH AVMWSLLGIALRKVHGDWAPL AISLTVVCASNLKNLKKKK
14191	44559	A	14274	988	1803	RAARVPRAPLEAVAHRWASAS EDDGTVLLSTVTAQFPGACGLR CRNPVSQCMRGVRLVEGILHAP DAGWRNPVYVVNVFGDVLMLVR QSQDEPLRSRKVFVGRRTEDM TEDELWEFFSQQYGDVMDFVFP KPFRAAFVFPFADDQIARSLCG EDSMKGIVHSNAEPKRSNSR Q/LRSGRFGGNPGGRLQGTRY PAPAPGSPGRAQGLGAG*SRPS GSWLSGHLQRPEQSVGRAPAA PRHAVRRSLRRAALCCRTRAR CRRQLHVSPQRRH
14192	44560	A	14275	3	184	
14193	44561	A	14276	1	352	KAAMVRFKHRYLLCELVSDDP RCRLSLDDRVLSSLVRDTIARV IIGTFGAAACISIGFAGTIRTCQK FLIQYNRRQLLILLQNCTDEGER EAIQKSVTRSCLL*EEEEESEEAA AKAME
14194	44562	A	14277	1	456	PTRAVEAAMVRFMHRYLLCEQ VCDDLRCRLSLLDRVLSSLVRD TIARVHGTFCIAACSIALALARA LNEEGNPEGWRDVAGASAGR KKGHECPSPCTVFCTL/RYPNA YTIVIGLLRCKKELYQVVWSVL YLMTYLENKGHRYPCCFFNTH
14195	44563	B	14278	34	267	

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14196	44564	A	14279	3	395	SAEVGAETTLTELRRRTVQSLEIDLD DSMRNLKASLENSL/GILLHL ESELAQTRAEGQRQAQYEAL LNIKVKLEAEIATYRRLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14197	44565	A	14280	2	1044	SSQMPSPQEGMCGKACTPALS QADSLCPPLLRLASEVEGYWQM ACAEPYYVQSEMNDHLSVWSLQ HGSTTILASMSFTTCSAFTNYWS PGSVQVPSYGTQPVSHAASVY AGLGGSGRISVSHFTSF/GLA GMGGIQNEKETMQSLRDRLAS YLDVRVGLETENWKLIESKIQEH LEKNRL*LETEIEALKKELLFM KKNNEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRAQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMTLT ELRHIRVQSLIEDLDSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLVHFEGKQV
14198	44566	B	14281	247	857	

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14199	44567	A	14282	1	2104	LRGSELAGGVAAPDPSSRARAPGRGQGSEPPRRS*GRGRAPPRAHTPLDDFPGRALSPGRGLSSRRPDPGSAGRPLLCLRPPLHSPPPRGCGAPAFQSLPSIHLARLRRSGEFLWGPGRPAAP*SQRRKPDPARPGLAAAVPLRPV*ASD*GAAQVPPPSPLRDGGQPGGREGVGRRTPHRAAAWLLGE*AA DAAAFHWDGGRPAAPARLLP GAPHHREDRVHHQPRGHPLQHQSPGDPPTPAGEQIHASRH*LCRN PETQKLRH*TSERRDGHREEEH TGTAGVPRSRPATQRPRAVPHAG GLQPHRMLPALSSGAASGGEAEHGLSLGRGREEDGPVWPQLPAGLQGHFRGESPRWPPLCQDGSEN*PGPVQAEFSGG*DPAVSESEDNQPSRSRQFLRLQREEKAKP\DQRFTYLPANVPIIKTEPTDDYEPAPTCG/RGEPGVKSSPKTILQPAARDATRPQLLPRGRLPALSAEKHPDASSPWRPQAPRPFSRCLHQGRCPGPPLSPRTPAAGRRGPRRPGVPRPVATHPGSPQOPPPALLPQQ*MK*YEMTSPARAPTPSC HIGALSSAGVC*LQQTKTFE*IN*THTWYHSEPPTD*MPGAEH*YVQRLALQQEGKQGGRETTVSPGGEVIS*QQKGGRRAEHGRPTVQGP/SHNGNPHAV*PHAQFWH PWGSILEVPYLTRPSGHRIEH
14200	44568	B	14283	41	4224	
14201	44569	B	14284	1	1332	
14202	44570	B	14285	140	215	
14203	44571	A	14286	234	657	VQQPGRGLDLSTDGPQGRSQVGLIWSCCCLH*AASGEPGGRCPGS/GAPGPAGSALEFRARDGVP\GVGGPSWESHSPAAATPPPAECRGPGPPTSPAPGEAAAPEDREDGAAAPGRAEPASIVAPADGSQQQVLATQAGALGA

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14204	44572	A	14287	134	789	PDSSQAPS RNSTR PAASTRKSSS PPAAR SVAGNELGSSSRGIDADPPP QNPTGPAPQSAEVP RCD/SSA WASNGSSISPSFFSLRPWPSS/T/S KVPAGAHHTPPEGAGGASARIS SSLAPSAGAPVPS/A*RSQQLGTW LSVLRP RSL*QSRVRSPSSH VSS PGSMQAPNPSFQPGMNGAWI WWL*THIPLARWP GPPGILVITC PTVTWIKWSFICSFHPT
14205	44573	A	14288	465	1541	GPPKRK L ISNFSK VSGYKINVQ KS* AFLY SKK/QTESQIMSEL PF TIA SKR KIY LGIQL TRD MKD LF KEN YK P L N E I KED T NIW K N I P CSWIGR INI V KIA IL PKV IYRFNA IPIKLPMTSFT ELEKTT LKFI W QKRAHIAK S ILSQKNKAGGI TL P DLNLYYKATVTKTAWYWYQ N RDIDQWN R TEPSEIIPHIYNNH L I F DKPDKNK QWGN DLSF NKWCW ENWLSICRRLKLD PFTPYKKIN SRWIKDLNVRPKT K TLEENLG NTIEDIGM GKD FMT KTPKAMK TKA KIEKWD L I LKSF CTA KET TIRSF GSEQ K SHTL VRA TRL VSD HSQSF EA WLQFLG DTRFGT QKL RDSD
14206	44574	A	14289	1921	3199	GYLAAGQV TSRI HTGR RH FSGP ARCPVSC CRRPGC*PQPA VRP SG*HCRK TAP SHG P SIW QTR**P GSWP NLRPG*GWRWLRAQPRG RGIPVGCRSNQLHPTK NPGSH *GSGSPWQCPGVLL*ASGRQPG SPSGGT*SSG KAGLEPQVH P A IPGHCRN KPAAPAS WERAPR PR AHALACGWW RYSSC*SWRS*S SPETPGPAQV*CHR CPA AWW RCHS**TAQFL*D*FS*FLQTIGE PCICPKPISVPH*PMKQSH/RGIG GCLQYSSH PGIESSLGMSRGF/D RRDL*TLQIGS*RH PRAG PEGA AL*CLAG ESS RTPS ACPGSPH TPGSSA SGNTSPV**ETGCGSRQ GSARL VLES LLSR**CLSGPSRP SCLLRG I S WQCGTAG R LSSGGP AASGAGADAAPGGFP RLPC LEF GTV
14207	44575	A	14290	3	626	

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14208	44576	A	14291	1	1065	MRGSCERSGEDEEQKEEAMVA CGRLSGVPPEAEQGPNEANWDS LETEGTGDLGELVRDTYLRLSC RAHSVVPISCFLRQGSAQELNL RHRGLGPQGARALASSLSSNPY VKRLDLDLDRNGLCGAGAELAG AL/QKQKQHP*CGPVGEPAGSG RSPGPR/VPPS/CNQAMRKMQ LSGNGLEEQAAQHLAELLLAH TDLKSLDLDSYNQLNQDAGPAPS LRAFPQANIFLKVLDISYNGFG DPGASAVGEALKANNVLEELN MSNNRISAMGALSLGLGLRVN QTLRILVLCVRVSQSVRNPMS EGCFGLLKSVDQDNPASALELLD FSDIQVNAEFDGLASSVRGILPG LGIKDWRLQSGV
14209	44577	A	14292	1	416	
14210	44578	A	14293	2	384	ELWVVTSFMAYGSAKDLICHT FMDGMNELAIAYILQGVLKAL DIYHHIMGYVHIR/DLQGYDAKS DIYSGVITACELANGHVPFKDM PATOMLLEFKLNGTPCCLLDST IPAEELTMSPSRVANSGLMTA
14211	44579	C	14294	142	474	
14212	44580	A	14295	1	1470	
14213	44581	C	14296	91	471	
14214	44582	C	14297	195	480	
14215	44583	A	14298	121	1130	SRSTQYELMSFLTNDASSESIAS FSKQEVMSSFLPEGGWYELLTV IGKGFEDLMTVNLARYVKPTGE YVTVRINLEACSNEMVITFLQQ ELHVYKLFNHPNIVPYRATFIA DNLWVVTSTFMAYGSAKDLIC THFMDGMNELAIAYILQGVLK ALDYHHIMGYVHRSVKASHILI SVDGKVYLSGLRSNLMSISHGQ RQRVWHDFFPKYSVKVLPWLSP EVLQQNLQGYDAKSDDIYSGVIT ACELANGHVPFKDMPTAQPM VVLVLSPPDAARETERHSALPVG YQHHPR*GADHEPFALSGQLW PE*QPDHQHPPALQR*LALPPL PNLLPPLPPLC
14216	44584	A	14299	304	412	
14217	44585	A	14300	2	350	
14218	44586	A	14301	191	299	HRPATAVLHVPTRSPSPGSRPS *PPAAALLWTPA

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14219	44587	A	14302	537	5523	LARYYKFMHQDRQGVARNLL CQKEKRR*YTTKCEDNTCHWT GRTSS*PRSV/SNLNSQCGPRLW PPVTIIRQANIKTGEKAH*TSKL LPPVQLKFPARDDTLPWPGYIP* QLRRPSPR*SILSMLPRKVVVPCL *QKP*TCVCKF*EPLSYIIHISLV LKMMIPMPMTLLA*CLTQAL K*SRMERKKGRAAQRSSTLGC QSPRGSPGGGPGGPPGPPAGKQ QSNSVQTTSRLLARTL*SFSSST VKDKELARNTAP
14220	44588	A	14303	2868	3095	PGWAGGLFGPSAGMRRAWATK PSLTPAPAGORCPQGHRC*SG PGIYAVQPPSVPAAAHATTQ ARLCHPRSPPLR
14221	44589	A	14304	693	821	SDRQT*RQEKRRLTRRQSCCLPC N*SFQPETTLFHGPDTFHDN
14222	44590	A	14305	338	645	
14223	44591	B	14306	181	480	
14224	44592	A	14307	155	543	
14225	44593	B	14308	1	1260	

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14226	44594	A	14309	1	2025	VINII <sup>N</sup> AAQESSPPMPVTEALDRV LEILRTTIELYSPQFGAKDDDPH ANDLVGGLMSDTGLEI <sup>I</sup> KDGEE EGESRTAQQY <sup>Y</sup> PGLSESTROPWR RSRTPR <sup>I</sup> TWGWKA <sup>I</sup> TEQQCPDF PPPGP <sup>I</sup> PHLELLIFHCEGQGTGQ KHSTSYPCTLMSEK <sup>R</sup> GLMN <sup>V</sup> F AKYTG <sup>P</sup> AMRK <sup>S</sup> SSL <sup>I</sup> TPSL <sup>I</sup> HLY CADPLHSKPLFNC <sup>P</sup> PTTSKTEI LGSCNC <sup>S</sup> SES <sup>V</sup> RGA <sup>E</sup> KGDQEL LANIKQAEKHEKNHPE <sup>V</sup> TVAM ALTDIDLQLQFSMSQPEALLL AAGPADHLLQLYSGHLSAT GIYGEGRASSATLE <sup>D</sup> LESQYQE LAVALDSSSTIISQLTENINSLVH TLKEEKH <sup>I</sup> HQVQKLGRNLFKL KNQTAEPLA <sup>P</sup> PEPP <sup>P</sup> PARPSK <sup>V</sup> EQ <sup>L</sup> QDET <sup>N</sup> HLRKELES <sup>V</sup> GRQLQAE VENNQMLSLLNRRQ <sup>E</sup> ERL <sup>L</sup> EQ <sup>Q</sup> EGWQ <sup>E</sup> ERL <sup>L</sup> DKNNENKSAL QLEQQV <sup>K</sup> ELK <sup>L</sup> ENLEAT <sup>S</sup> QS <sup>K</sup> QQL/TAQLSLMALP <sup>G</sup> EGDGGG HLD <sup>S</sup> EQ <sup>E</sup> APRPM <sup>P</sup> NP <sup>I</sup> PGDLES <sup>R</sup> EAMVAFFNSAGANAQ <sup>E</sup> EQ <sup>R</sup> VC CQPLAH <sup>P</sup> VASSQKKPEVA <sup>A</sup> PAP ETGGESVCGETH <sup>Q</sup> ALQGAM <sup>E</sup> K LQESTSARGQCQR <sup>S</sup> TRG <sup>G</sup> GH <sup>R</sup> QAGP <sup>G</sup> PGG <sup>D</sup> EEM <sup>L</sup> CTCTQVSS AGRGMGMLTVVLLV <sup>S</sup> LLM <sup>M</sup> LS ASFTWC <sup>M</sup> RSIS <sup>S</sup> CH <sup>C</sup> A <sup>A</sup> Y <sup>A</sup> SAHS SISVFWF <sup>P</sup> REY <sup>I</sup> LA <sup>G</sup> SEMMNS
14227	44595	A	14310	3	564	SLRV <sup>S</sup> LLKAVVDRAG <sup>S</sup> RILSYIA GLGV <sup>D</sup> LGFGGGSRVAGGIADL GRSGGGKA <sup>T</sup> RSRRG <sup>S</sup> RGAGR <sup>G</sup> LRSRH <sup>I</sup> HEEALQL <sup>R</sup> ETPGPG <sup>A</sup> PE <sup>V</sup> PMDQEYAGPGYDIRD <sup>L</sup> WELRK <sup>I</sup> HRAAIKGDAAG/VWSAAMTRR FRDLD <sup>D</sup> ARDK <sup>R</sup> DRTV <sup>L</sup> H <sup>L</sup> TC <sup>A</sup> H GRVEVV <sup>T</sup> LLLS <sup>R</sup> RCQ <sup>I</sup> NDICD <sup>I</sup> N* NRTPLMKAVHCQEEA
14228	44596	A	14311	515	778	GQAQGTGDREGAVL <sup>F</sup> TARAPD QC <sup>R</sup> P*SCSSRRPTASSC <sup>S</sup> PLGH <sup>S</sup> C SPGPLCTH <sup>L</sup> PLQG <sup>G</sup> PPQ <sup>A</sup> PTV <sup>P</sup> ATATC <sup>W</sup> FSW <sup>N</sup> QC <sup>R</sup> CRAV <sup>S</sup> YP
14229	44597	A	14312	411	608	EAEI <sup>P</sup> TGLPGH <sup>S</sup> R <sup>P</sup> PG <sup>P</sup> CL <sup>T</sup> HL PLQG <sup>G</sup> PLGAAAWV <sup>P</sup> EA <sup>G</sup> LGQ <sup>V</sup> P TEAAGA <sup>A</sup> RAGC <sup>S</sup> A <sup>H</sup> K <sup>P</sup> W <sup>K</sup> RRK
14230	44598	A	14313	2	338	
14231	44599	A	14314	1	390	

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14232	44600	A	14315	237	488	PWKTLDSSEAFILRGVSESSAV TLHCMEGQAVGPRQVKRIVHC *ASSA*NPHAMLLLQNR*LALC TSVPQGAAVLCGGWDPGN
14233	44601	A	14316	358	616	
14234	44602	A	14317	13	1155	IKLPPPGCRRRGGRHRRHRYRG RAEPLAPRRRRLPAPEQPQRP PASRFLKNTMSNGYEDHMAED CRGDIGRTNLIVNYLPQNMQTQD ELRSLSFSSIGEVEASAKLIRDKV GHSLGYGFVNVTAKADAERAI NTLNGRLRQSKTIVKVSYARPSS EVIKDANLYISGLPRTMTQDV EDMFSSRFGVRINSRVLVDQTTG LSRGVAFIRFDKRSEAAEAITSF NGHKPPGSSEPTVKFAANPNQ NKNVALLSQLYHSPARRFGGP VHHQAQRFRFSPMGVDHMSG SGVNVPGNASSGWCIFIYNLGQ DADEGILWQMFGPFGAVTNVK VIRDFNTNKCKGFGFVTMTNY EEAAMAIASLNGYRIGDKILQV SFKTNKSHK

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14235	44603	A	14318	1	2340	MFVWRNVÉGHSAAVFSWYSIP FLTPPCSHTRPSNLPVTQWPPTR ENNLPSWQPLLMMSVHQ/AQSQLS ALRKEQDSSSEKDGRSPNKSDFK DHIRWPMSGAGHDLQQAAAPGPG GAHQGHPNQDNRTVSQMLSER WYTLGPNEQMKYQNLAFQNV ARIRYVIVRGNEQQGFFRMHHHLR GVSSLQLGRRRPGPGTYRLEV DMITIDARYRCGSLRSPPDPH LKSVDLHRNEHFFLQKARWEIH LVLQATPSQIQLLHVAFVLAQ PLRCRKQTLFLISVVGTKKEKV ASEGRNPVRPLRGHWRLPASPP AAEHFAAGGADRKSRLSAPRSA ATATPANEQRADVQGQWAR ARGGRVRAAGRSGSCALRRSR CRRRRRRHRRHRYRGRAEPLA PRAAASGQPQGKLARRGGINCNA SSIPMLQVVRISIHKCQMAR VAGEGSLPLSHAQLTHCVFGN KQVQRTIAYLPQQQQVGQVQGFL KNTMSNGYEDHMAEDCRGDIG RTNLIVNYLPQNMTCDELRLSLF SSIGEVESAKLIRDKVAVGLSL CVPIRNEIVASTWWSLPLAP YVPRGIIRRSQPSTLMDLDCRS HQAAAPFTASVLLYISGRVKAH TAAQGFNHIPEEGVSEAGSG WSQAWKDGWLTVNFMFSCCTG HSLGYGFVNYYVAKDAERAIN TLNGLR/PPVKNH*GRPLQLGFL
14236	44604	A	14319	701	1050	LIVHFCLQVGCGVGNTVFPILQ TN/NTNSEYDPSRCFAFVHDLC DEEKSYPVPVKSSLIDIII.IFVLSAI VPDKMQKAINRLSRLLKPGGM MLLRDYGRYDMAQLRFKKGKIL KVLNPNH
14237	44605	A	14320	701	1519	LIVHFCLQVGCGVGNTVFPILQ TNNDPGLFVYCCDFSSSTAIELV QTNSEYDPSRCFAFVHDLC DEEKSYPVPVKSSLIDIII.IFVLSAI VPDKMQKAINRLSRLLKPGGM LRDYGRYDMAQLRFKKGKQL GNFYVRGDGTRVYLCHTRCNW TRFSPTAGLEKPQKPVDRRLQ VNRGKTTDNVPGLDSVQIQLQAP SVQHQLRGYLLPTRCKPVVVS GLFLKKKIVALGVV/RCL*SQPL RRLRRGGSIE/HQQSNLGKIVRD PVSESNNDKIKRI

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14238	44606	A	14321	756	1334	PGKPVILMSFLDPQPPTRILEVGC GVGNNTVFPPIFTNRTMTQDSLVY CCDFSSTAKELVQTNSEYDPSS VFAFVQGPV*RESVTQCPRAV LDIHLIFVLSAIVPDKMQKAINR LSRLLKPGGMMMLLRDYGRYD MAQLRFKKEELDTLFTTAGLEK VQNLVDRLRQVNRGKQLTMY RVWIQCKYCKPLLSSTS
14239	44607	A	14322	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRKIKYLGIGL\TRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
14240	44608	A	14323	1	5796	
14241	44609	A	14324	1	2721	
14242	44610	A	14325	1	3438	
14243	44611	A	14326	1	3306	
14244	44612	A	14327	1	2364	
14245	44613	A	14328	1	2091	
14246	44614	A	14329	1	2334	
14247	44615	A	14330	1	1986	
14248	44616	B	14331	1	2559	
14249	44617	A	14332	1	1671	
14250	44618	A	14333	1	1845	
14251	44619	B	14334	1	2055	
14252	44620	B	14335	1	1554	
14253	44621	A	14336	1	2559	
14254	44622	A	14337	1	1714	
14255	44623	A	14338	1537	2204	

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14256	44624	A	14339	2004	3751	YQSLAETQQQKKKNFRPISLMN IDAKILNKILANRIQQHQKLH HDQEGFIPGMMQGWFNIHKHSINV IQHINRTKDKNHMIIHSVDAEKA FDKVQQHFMKTLNLKLDIDGL EVLARAIRQEKEIKGIQSGKEEV KLSLFADDMMIAYLENPIVSAQN LLKLISNFNKVSGYKINVQKSQ AFLYTNRQTESQIMSELPIFTI ASKRICKYLGILKLTRGVKDLDFRE NYKL^PLIKEIREDTNKWKNPIC SWIGRMNIMKMAILPKVN^YRF NAIPIKLPMTFIIGLKILLSSY GTKKRAHIAKTLRQKNKAGGI TLPDFKLYYKATVAKTAWYW YQNRRIDQWNRTEPEIMPHFY NYLIFDKPEKKNQWGKDSLNFN KWCWENWLAICRKLLKLDPLFT PYRKDINSRWIKDLDNVRPKTIKT EENLGITI^D^IGV^GKDFMSKIPK AMATKAKIDKWDLILKLFSCFT AKETTIRVNROPTKWE^NIFATY SSDKG^LISRIYNE^LKCQYKKKTN NPIKKWVKDMNRHF^SKEDIYA AKKYMKKCSSSLAIRE^MOKITM MRYH^LTPV^RMAIIKKSGNNRC WRGC^GE^ITL
14257	44625	A	14340	519	1286	LNLEERA^FRHKSS^EHLPHLKVN FRHSSCGIKTKSLLHVSPP^T^LIF PYPP^LWG^N^PSN^*ARP^PCSVHSG PYPOGLASIAAHGSPGNVRGVH V^*INDSEGGS^R^P^ST^A^SH^K^E^T^P^R^ P^P^TP^A^R^H^A^D^L^A^A^T^P^R^S^L^T^T^P^S^ \^G^A^G^P^R^P^A^/P^S^R^A^G^P^S^V^G^G^L^R^P^ S^G^R^A^P^E^V^A^L^P^A^G^L^S^P^A^L^G^A^ P^P^P^G^R^S^T^G^A^L^P^P^A^A^P^T^T^S^G^P^/P^ A^S^T^P^P^N^A^P^A^P^G^H^T^L^S^S^R^S^P^H^R^A^ A^R^P^P^P^H^C^G^A^E^W^T^G^F^T^M^R^P^S^W^ R^I^S^Q^S^F^I^V^K^D^S^
14258	44626	A	14341	482	700	

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14259	44627	A	14342	1368	2416	SSMTQSSCPMTSYLKSKFGEPLMPSVTNPTELGVSKLNVKNTQVF TYAHKGPVSIYFDACQAAHLSK LNNIWTTSVKI^DKKESASRATK AITEESKKECPDCDNQWTTHEF NQHLYTGRAALFASQEEKIGYT TGTCYPLNLTILKPNMTFWTKG HKGLLTTFDQAGALLGLGIPLV1 TKKTQRTQVQLSP1QQFRFYKS FNEHFNSEVSVKIQ1PP1STENLFV QLAKSIANNLGVTSVYCGGA NMRDQWPWEARELMQLQDNFT LPEFVTKFNANPSVWLLRNPIIG KYCIACWGKSFQNQIGETTCLG QQYFEESENRTQWRSFIDDSIG HFNPFLQFPTLNQSWSYQLE
14260	44628	B	14343	I	1071	
14261	44629	C	14344	89	283	
14262	44630	A	14345	244	315	NPKGQKDREAPLSRSVFLKIKI KRAFALLHGRF*PSTAASASP ASKSPRGSGKALASALFYIVQL TK
14263	44631	A	14346	1228	1656	QVYRPSQTPHLALSPEVAPGR RAAGR LAPEARAPRGSP/LPPHR VSEK TIRVVVFHGPARGAGTP PRAPRGDTGGAPGA/PTYSTPL MSLH RARLESSPTGSSFPADSA KPVLAVVSLDSR*GQWESRSS IHAWTN*MTRH
14264	44632	A	14347	2	705	GSPWGLDDGSATRILACPWPGL GDGPAAPKANPLPVRWKPCQCF RGEGL*GSSCFSATLLTGDLW ACCSSRSTASARLSTYPSAFTSG WCSSLGPTEEAPGSWINCPLAG ILGAATSPKPSAIPQASPEVSLD AEDTGMKP*DSA/GPPGPARGL CGRGCGLSPACMGLRP/PSPPA QSPSTALTSLTPSPFHPPRKKW SPPSAPAPSAPSPAPASLTPSPAP PAPSPATPAPAP

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14265	44633	A	14348	367	1174	WVRGQPSQSQLDLLACSTPT* WPPGRAPPPLP/PPPLP/P/PTP ASPLLHIPPRAAPPPPV/SFTP ASPPDPVPRPTKALTGLP/LCP LPCMGR/PFVPLGGLLPCLG DFSSL**SPGGWDRPVRPL/GISQ IPEAPPLTMGL*MQ*IPP*PRFQG HYAPLPLPQLTLCISVKTPGRNRP GLPMHKILQPQNPSQPPCELPQ AHCPTTPPKQCP/FAFSILPVT FADKDPGAAPEGTVKAPMPTQ *EL*PLRPREHRLSGPTAGQT
14266	44634	A	14349	332	988	RAGTPASWGIHNGARAKTPSR ACACLGLYPIHQPTARRAPAIR SHGPGLPPALPRKGAAHGRSRS HHPLRPCSRSCLAWPCLHHPQ PLHCHPHRHWPKWHPHPLAPH PLLGLHPRSRPQTTPWTSCGPSR RLPTPSGSWPAPFDRDWPN*AR PSALCCPFCQEPQLTPCLHLCPH PHPHRHLPGLSCPCHRPRWRSP QSPCPWWLLWWWTGQWWQPGE
14267	44635	A	14350	190	718	FVLQLPPAKSGLGRWGSPPPG QFSSSQRTGTVGRGRCAEPRG SLPHPT*GNNK*HGNWMLGS QGLIGRQPGEDKHCYQR/IVG GAHLLRPPHQRIIRSLLTGSTGSCS HPWSRELGCSWDGQRASAPLA LRQAWGEGLAGRNHTIVPFHG DISIAPRLLCPCRETLFSALCGGES
14268	44636	A	14351	1	486	MKGEVSKQHQDALQQLWA MLQDADKQVRRAPGPVENENH CDFVKLREMLICTNMEDLREQT HTRHYELYRRCKLEEMGFTDV GPENKPVVRVLLFKSLSDSKRVK YDEEWIRLPVE/MKY/MLERKV TQKQP*VPLVFVSWRSR*ESLR REEEEENQQCHVLEL

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14269	44637	A	14352	1	2380	MMWSVII.QPVVLAVERQGE ALEFLIGVPESDGENTGKLENT LQDIQEDFPNLARQAHVQIQEI QRTPQRYSLRRAATPRHIIIVRFTK VEMKEKMLRAAREKGRVTLK GKPIRLTADLSAETLQARRDRG PIFNILKEKNFQPRISYPAKLSFT SEGEIKYFTDKQMLRDFVTTRP ALKELLKEALNMERNNRNFFG VTFAFFVGQQLSGKALQETSIPF LREEDLEKTSILETGNDWEAT RGLPEECAGMRERDCQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTISIYMFYQ KVGDNNSIDSWSKNAAGRVKDSD KFDANDPILKDQTQEWSGSAATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFGDGKTYQNQQFIDEQ NYTSQDNHTLDRPHYVEDKGH KYLGLIPTYDISSNLYLISKSLW QANFRLNSALAQSAPAITNFQFR GHSLKTLDDLMKNLDSKVNII PVIKADTVSKTELHKFKKIKFM SELVSNQVQIYQFPTDDDTIAK VNAAMNGQLPFAVVGSMDEIK VGNKMKVKARQYWPWGVVQVEN ENHCDFVKLREMPICTNMEDL REQTHTRHYELVRRLQLEEMG FTDVAPKNPKPASVQETYEAKR HEFHGERQRKEEEMKQMFVQR
14270	44638	A	14353	105	328	
14271	44639	A	14354	107	676	IRPDLSPSASPAQDFYAASSNTF PA/DRWSALTAKIYEDQTSNIP SQ/TLIQSKAKTLCNSVKAKE EAAEEKFEVTRVVHIRGLIDGV VADIVEALQEFGLISYVMVMS KKRQALVEFEDVLEACNAVNY TADNQIHIAGIHPAFVNYSTSQK SRPGNSDDPPEREQCASLYHPEP HLFDHHGCSLHYR
14272	44640	A	14355	221	648	LDWLRRVVGIPSLRWTATLV GTRRAARHRCVNWECCGLKE ITY*SVEGLCRA/EKPKPLALLE ETCKLPERQVYNAKEKFLEEIK SATPVNT*MIRKRNCIITDMEK V*AVWIEDQTSNHLPLSQLSIES RALTLFNYVMA
14273	44641	A	14356	122	317	

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14274	44642	A	14357	338	489	WLGQN RHGKQPGPGVGVHGTVW*PHSACWAPAPQGAPTEEEGCHF
14275	44643	A	14358	1	459	RPVWRNSQPPTAAYWRSAGSRMWSTSFSRWNKTPSGKACSSSDKGPPMAQVPIPQRNVPPTK/QPLVLCHGEAPDFSRPQQHRRPSLQKHPSSTG/PSHSPLPTSAPASSRAGLPPPLMTDLTSGWRLWTPIQFRLPPIGSCREGTILLCSVMD
14276	44644	A	14359	609	2077	GLKAQPSSSRGHRSRGPGACAAAPASRVHLPVIFCEPEPNSSPCPHCTGGWGRGQ/PACAGNPTASSPCQIECPALRSCLHALMDLGSPQ/LRGAPRTGVPPDPRHLLLPQPALSSPPVLLRGPLL-RGTCPCLAARQGQSPPAPGLLGHPGSHRGRRLPPAQGGHRLPQPPGPGRRRHRAQPQDPRRPGLRAAAASGPGLAAWGAVRAAERPGSGLPGAGPHHARAQPGPRAAPPAAAAPGVAPAGGGAVPGGHPHRGGEAALPAHGLPAPAAERTAPR1QPCPACGLIARSDVHHPPVLP/LSGPAPAPGRLVGQLGVRGAPSSPVPHPALHFPRAQPPGKGITTTSQTPAGSPSPCMPPAATPGARHPPGSA/GHRAGV*GHTGCPDPHGPGHHGHAQLL*/DQAAVGVRGPGPWALSGMSQPPTLPTAGHPAPACGVRAFDQDTRPPRAKPAL/LSDKGPPMAQVPIPQRNVPPPTKHPCPGPQSSTWMRQ

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14277	44645	A	14363	47	1250	EPRPSRSSGGPQLGQGLPRPMK KIPGSSAKTAGPLATRPEVPRAP *SAGRQPWFQRPWGRKRGKRT *NHGSPGVK/P/TPGPLNNDKGE KEERPRQDPQRKALLHMFSG KPPEKPLPNKGKSTESSDYLRA SVTPGPWSFSPQVASGPMPVH TTKKPA*APPQVL/EPKERQTGA AADMPQPAVRHQQGREPLLVK PTHRSRPEGGCREVPOAA/SQNP PAPGLQTPGTRQTS/VTQPQCP PAATHSLGLGSNLSGPGAKRP AQAPIQACLNFPKKPRLGPQFQIP ESAIQQGELGAPENLQQPPAAT ELGPSTSPQMRGRTPAQVPSVD RQPPHSRPCLPTAQACTMSHHS AAGHDG/DPASQSLPETGKRT LELQPPGGPLISLS*EAGSLSRSE PSCVREV
14278	44646	A	14364	23	714	EAPEIPRQNRRMTMKERPVWL PHK*IIIPNVAKWSRVPVQVQK NPQFQE/PTPEFIPVPGTSPEAAG FWH*GAHDSPGTRDRSEVEPGR GHPHLGPRDSAAADPGEHSPCD CP*ACPEVRRWPA/APVQJQVIIIP SVDDFSLEFHQAQDGDISDMRRE NVPFSAEEGKAAPLYQQPLMI PQANHIMAGISPS/SPTAAEFQHR DVHHHRGPGRDRHTETGRVC PHPVPTDSPAL

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14279	44647	A	14365	3	1869	ITTVAPSRPASSEDCESDGS*EQD AGPGSRMGPEK*AGRPRTRVRG RWSQTHSQTDDTSGAVVPEYP SDR*YAGGRGPG/PGGPTVHP* KRRS*NPQETKMMARRDPKSW AKRLSPV*PRLAALLTSASPSCP LEPVLPLFRVPPSHGI.CEGTSYP NSPGTT*RPPCRSSAKTAGPLATR PEVPGAP^SAGRQPWFQRPWG KRKGIGKPETMEAPG^SQGPAL EQG*GREGRETKA TRPAAEGSP PHVFRETSREAAA EWRKRIHGVF *SSEGHPG*FPFSFSPSAGGNRGT PLSCLLGVRDSTILPGCKRANA GPHNQ*EAARGPCPR^SISAAE MSGGRGSV/LASLSPLRKASLSSSS SLGPKERQTGAAA/AHPSACSQ APGPRASPRGEAD^TQPPRG*LP RSSPGCLQNPRPAPGRQTPGTR QTSCGDL/SSPARQPHITAWA* APISASGQEPERDLPSSDSDLPEL PQETETGSLPDPRKRHPGR*AG GPGKSPPTSASRNRTWTKYVAP DQQEDTGPGAQRRPAASAQQT LPAYCPGLHHVPSLSGQ*WGP ASQS/GSSGDWKTDAAGAPASW RPPHFTLLRSREPSSLRLALMCQR SLRLPVFVSHRASSMRTFRFPPP QRTAILTWS
14280	44648	B	14366	1	1519	
14281	44649	A	14367	312	1326	TTKTGQDKDRLEEFSMQMQLSGS KRKMSTQPRTELUPPNRHTTTTS TTPA TNTCTATVPPQHQSYH DINVYSLAGLAPHITLNPTAH QLKQCVRQAIERAVQELVHPV VDRSIKIAMTTCEQIVRKDFAL DSEESRMRIAHHMMRNL.TAG MAMITCREPLLLMSISTNLKNSF ASALR/PDGSSAIQL* SND*SCS WRPKLYDADFWDLSSLRV**PSR PEGEGRVSSSEGMEGLPFSSSW PRQYQSLCICWTDAPARNTED R*SHNKVVLSSVY*NVC*NQLPC SG*AAAQSCCQSHHDPSQVLSQ PGCLCSTHCTARETLRGHHQHC HKD*SAEQGL

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14282	44650	A	14368	2	1120	PEPEPGARGGEQLNEDFEG*VA VPTCLHCPALSRTQSRAIQALT VRGEATIRPPPCDDTKGHHRF LNELIKVVS PKVGAPS PSSDLC RMWGEERGWTVGLPPEEVKIAE AYQMLKKQGEAHRGWGATRA CLPLPHHERPKNVIFEDEEKS VRLOGGTYGDSEPRWGSVGSI KEMVQE/DSGRAQSTGRRDG GIELGHNVKLLTMEVMMSHSQG GAAAGSSEDLMKVHLPPCLPHS LPTPQPTRTLRLMRPTLFLRASDT EDNDEALGEPRAGAEVRSPLPL PPAPAVRGEEVNGDATAGSIPG EEVAGELGGHPSGWRGTESYP AMPTRPGEQASPEQPSASVSSL DDELMSLGEEGARPGGGRAQQ
14283	44651	A	14369	1	432	GTRQEVTAGVEPAREWQRRLM EVQWGLERAPYCIQHAPR*RRS PARPGTQSCLGACWIQ*GALS SPHCTSISRRCHSLAGSTPAVTS CLV
14284	44652	A	14370	16	471	
14285	44653	B	14371	66	206	
14286	44654	B	14372	234	390	
14287	44655	B	14373	207	427	
14288	44656	A	14374	2	572	FLLERAPYGVGFSLLPGWLGS RAGVGRHHDKRVGLGRAPTW LEGAVSSM/TPRQLQCVP/WPC WGPSSPGG*QQLGQLSCSYSLV DR*VALLWFMLVGSPLVKGH CPTPWSRFVDFSVP LATPPGIVY WGLFAVFLFSHLLPARPGEQMS ACCRHLHAPSPLLTLDLSLIKVY SCNSQGKLVRVFPFGD
14289	44657	A	14375	175	499	KQNKSMGRKSQGFVASFGNHL YCTASCGMPASSTSTQTWPRVL PLHSQ/ESSHGGCSWRGRR*GP RPRPHKTPVPMVMDSTARNRA RRELVLAWCKSPLATALLVSW DK
14290	44658	A	14376	408	625	VFGEQEVFGYMNKFSSGDF*DF GAPTTLSSEHCTQCVVFYPSAP SFPFPVPKVHCVIPHSLVPTYE WEHTM

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14291	44659	A	14377	1263	1812	AGDAAPEDPAGRQGEDLYDEELPGWGLCIPHPACLQPCHA*VTKAG/ARVKVILPS*DTQRTKDILKAGGG/PSSIHFIINSAHKGKPAVIVRPRGIWVLNTIPLSGQWGPYIGVYTAATVDMKSLGSGSGLQI ALPLAASWLGVLTEARVFGEQVVFVGYMNSFFSGDFWDWFGAPITRAVYTVPNV
14292	44660	A	14378	1	693	
14293	44661	A	14379	2	1299	WDYV/KRPNLRLIGVTESDGENGTKLENTLQDIIHENFPNLRQANIQIQEIQRTPQRYSSRRATPRHIVTFAKVEVEMNEKMLRAAREKGRTVHKGPIRLTADLSAETLQA RREWPPIFNILKEKNFQPRISYPAKLSFISEGEIKSFTDKQKMLRDFVTTRPALKELLKEALNMRERKNRQINETENQQGYPGIELGSAPSPPNPLFCRHLQMSVDGRHLQNSPPQINRITYIFLAPIHHTYSKIDHILGSKTLLKKCRTEIIITNLYLSDHSAIKLERIKKLTQNCSTTWKLNHLLLNDYWVHNEMKAEMKMFFETNENKDITYQNLWDTFKAVYRGKFLALNAHKRKQERSKMDLTSQLIKELEQEQTHSKASRRQEITKIKEELKEIETQKTLQEINESKSWFFERINKIDRPLARLTKKKREKNQIDAQN
14294	44662	A	14380	2	383	
14295	44663	A	14381	1	1536	
14296	44664	A	14382	2	1118	REHLAEGMAVGTASADLNISACWLREQQQISQHSARALLRDRLPPQENSSWHPAGAPLGRNFQRKEQAAIFAVLQPPLVIPRKTGSGVDLEQTPADLQKRGILTTRKTNKQKAIASSTERTPTQKPPFKSHQHQRPNVDKSAKMRKNQSKKAENSKNQNTSSPPKDHNSSPAREQNWTENEFDTELTEVGFRRVWITNSSLKEHVLTOCKETKLDKRLELLTIIITSLEKNINDLMELKNTAGEELRDAYTSINS*IDQAEERISEIGDQLNEIKCEDKMREKURMKRNEQLQEIWVDYVKRPNLRIGVPESDGENGTKLENTLQDIIQENFPNLRARQANIQIQEIQRTPQRYSSRATPRHIVRFTKV

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14297	44665	A	14383	1	1154	MLPILGSRHPSSLGQARKLDYR PSKSQCLEPGTPRACLVLYTTLV AKLIYNDYFHYFAPRGLPPME KNVVFVIDISGFMFGTKMKQD HNFSLAREQNWTENEFDKLME VDFRRWVITNSELHEHVLTC KEANNLEKRLDELLTRITSVEK NINDLMELKNTAGELREAYTSF NSCNDQAEKISEIEDQNLNEIKP NLRLIGVPESDGENTGKLENTL QDIQENFSNLAKQANVQIQEIV QRTQRYSSRRAATPRTH/IVRF TKVGNGREKMFKGQPGKGRV VTLKGPITLTADLSAETLQAR REWGPINFILKEKNFQPRISYPA KLSFISEGEIKYFTDKQMLRDPV VTRPALQELLKEALNMRNN RYQPLQNHAKM
14298	44666	B	14384	1	1554	
14299	44667	A	14385	1	909	
14300	44668	A	14386	2	207	DIMSCILQNYNRPPVIMALIPIA VKFLHGRNKELCRNMNSNYLSL AAITKADULLADHTEVIVKSILQ
14301	44669	A	14387	496	1207	PLITGTHDGSVESQLKLITM HQLFRVLGQKDLRSAGDLFS *NNSEIEDSLTEALEQIKIHSSSD YQTNNNDQAVVEICITRITTAIR ETESIEKHAKALVGLWDSCLEH NLRPFGKDEDTPHAKIASDIMS CILPELQOPTQSMALAPIAVKFL LHRGMKECRNMNSNYLSAAIT KADLLADHTEVIVKSILQGMVR KLSLGTFCGRYLKVFSSSIYGL WEARPRVLEAN
14302	44670	A	14388	219	448	VSLELCLTTGPDGCQTSQTP PAAAAYHHL/PGAGLPCGPRLP LCCSCPMPGARPL*HHKR/DPSRF QEKTHTYLPLSSH
14303	44671	A	14389	542	1365	GTEGVMANRSQEGNNGGGSWR AKQVVVTVPF*EQSLVIMLWR RGGNT*QRPSEGTTSRSHICSFH MSRHICQ*CKCLLKEP/VSAEAR DALDTKTHPPLAMIPSYLLNG NIGELPEGPAGGCACQNPGLWAS /RGPAR**RSQASSSPERVRWPPG QCGLRGRPCCKKEPRPHPWSRP CASPYRGAGGQQLRRACSAAG RKTPDRRPLPEPTRGPVSQLRAV LGKLRAAAGHRIPIGDLDGDSL LGAPPAGRHLHTVPLRREFSP CEDALGIGEQQGKKRVT

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14304	44672	A	14390	3	723	PVLRGGIQEFAYIKALYERKFL VPKPIDYNRHA <sup>VD</sup> MELINGPL C*IH <sup>HE</sup> DPASVYDEAMELIVE LANHGLI <sup>H</sup> GDFNEFLNL <sup>L</sup> IDESD HITMIDFPQM <sup>D</sup> STSHPN <sup>A</sup> EWF DRDV <sup>K</sup> CIIDFFMKRFSYESEL <sup>FF</sup> TFKDIRREDTLDVE <sup>V</sup> SASGYTK EMQADD <sup>EL</sup> LHPLGPDDKNIETK EGSEFSFSDGEVAEKA <sup>E</sup> VYGSE NESERNCL <sup>E</sup> SE <sup>G</sup> CY <sup>A</sup> SDHLET <sup>L</sup> NK*RK <sup>T</sup> VYQKRVL <sup>M</sup> HGV <sup>L</sup> K
14305	44673	A	14391	I	1889	MGSKVKEVEDDSQMSDLVRG MNAFSKTGSGGVEQGRTQGG TN <sup>G</sup> H <sup>I</sup> KKAKARDRDRFKKTP QRKVGNNDNLQLPLRWT <sup>E</sup> QHAE THIMNFC <sup>S</sup> KNYNRNP <sup>G</sup> PKPRESI DTLNEAACRGRRLSKTARKLWS EAQDQR <sup>S</sup> FQATEM <sup>Q</sup> ALFLSAK RIAEEKKTII <sup>R</sup> RRDLC <sup>S</sup> IWG <sup>K</sup> LL PRPGSQSVPAQ <sup>I</sup> PENLQE <sup>E</sup> ERA KWLLN <sup>G</sup> RSKFP <sup>T</sup> STLGKV <sup>T</sup> SNKTGVKEPELESRQP <sup>N</sup> LLKVE MG <sup>M</sup> MKNHEI <sup>V</sup> PGSLIASIASLKH GGCNKVLRELVKHKLIAWERT KTVQ <sup>G</sup> YRLTNAGYDYLALKTL SSRQV <sup>V</sup> ESVG <sup>N</sup> QMGV <sup>G</sup> K <sup>ESY</sup> YIVANEEGQQFALKLHRLGR <sup>T</sup> S FRNL <sup>N</sup> KNKRDY <sup>H</sup> KHRH <sup>R</sup> INV <sup>W</sup> SL YLSRLSAMKEFAYMKFR <sup>T</sup> LEIR DYFYWVKINVLTGPCSPKR <sup>G</sup> SS GEFVPCLLQLLGFGDCWHS <sup>G</sup> LW <sup>H</sup> ITPV <sup>S</sup> V <sup>S</sup> ML <sup>T</sup> LLPS <sup>L</sup> LV <sup>K</sup> QKKPTLDSRMGQFD <sup>V</sup> VELQL YLCV <sup>L</sup> REVIREYPPDGQ <sup>I</sup> FG <sup>R</sup> Y FDRDV <sup>K</sup> C <sup>I</sup> KDFFM <sup>K</sup> RFSYESEL FPTFKD <sup>I</sup> RREDTLDVE <sup>V</sup> SASGY TKEMQADD <sup>EL</sup> LHPLGPDDKNIET <sup>E</sup> TKEGSEFSFSDGEV <sup>P</sup> KEA <sup>E</sup> VYG SENESENCL <sup>E</sup> SE <sup>G</sup> CY <sup>A</sup> SDH <sup>L</sup> LE TLNK*RK <sup>T</sup> VYQKRVL <sup>M</sup> HGV <sup>L</sup> K

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14306	44674	A	14392	150	1910	STPPGGPSVLM*STEEPAGRS QPLCDDLSTRPLSCLGAGCCW PAKRISAKEEPWYSSRSDKKE KNYSSPETTTSGGCHSPGDSQY QELAVALESSVTINQLNENIES LKQQKKQVEH!OLEEAKTNN EIHKAQMEQLETINILTEKADL KTTLYHTKRAARH!FEEESKDLA GRLQYSLQR!QELERALCAVST QQQEEDRGHCLSSPDQNFSLFT! QSSSCREA VLHRRLQQTIKERA LLNAHVTQVTESLKQVQLERD EYAKHIKGERARWQERMWKM SVEARTLKEEKKRDIH!RQELER SLSELKNQMAEPPSLAPPAVTS VVEQLQDEAKHLRQEVEGLEG KLSQVENNQALSLLSKEQKQ RLQEQQEMLRREQEAQRVREQE RLCEQNERLREQQKMLQEQGE RLRKQEQRRLKQEERLKEEER LTKAGKEAVGPGEAVEEGGE ATKAGGEARALPEPQARQAA RATVQLRGSEQRKERTAVGA ASKGAAAGEARRGEGDAVHGHL SAADL*EGGAAQAVTAADPVR GPAAAAGSLGQSGAPRSCQPPE PTARDPAKPRGSPWRRRWRTT
14307	44675	B	14393	463	3755	
14308	44676	B	14394	175	1835	
14309	44677	A	14395	102	465	RAYCWAYIIRLSCLTVILIAWCS QESALSEEEDTTRPLETVTFKD VAVDL!QEEWEQMKPQAQRNL YRDVMLENYSNLVTVGCVVTQ PDV!SSWSKKRSPG*WRKKCL GGTVQNPSEEERTAV
14310	44678	A	14396	I	330	
14311	44679	A	14397	I	531	MLLNIPQI!TRQSPRAKNYLAQ NVNSVKAWCQESALSEEED TTRPLVRLKHLFVSCII!LQCSYV LLPLTPEYQLNKFLYVVITMPN FDDFKLISIMFLQETVTFKDV AVDLTQEEWEQMKPQAQRNLYR DVMLENYSNLVTVGCVVTKPD V!SSWSKKRSPG*WRKKCLGG

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14312	44680	A	14398	1	539	MPTTTTREM TQNSSETIKNKG KKQRKQRKNSKKNRRQKDE DKTRQNKRRHKKNDINPEEE RTAVRLKDGGAPAPQAVQEH D AGICSASGG/AQETYILVEGKGE ASTSPGQS KGSREGGVGANETC SKKLYRDVMLENYSNLVT/VG CQVTKPDVYSSWSKRSRPG*W RKKFWEALSR
14313	44681	A	14399	322	1227	FDLKMSKCRKTPQLQALASPASF SPDILADIFELFAKNFSYWKPL NNEWQLPDPSEIFTCDFTEFNA FPWI*RTP*NEVKKPTGVIRTW DEWHEHTCFH**SGE/ISFPHGR KSVNAELWTQAWCKFHEILCS FPLIPQEAFQNGKLNLSLHLCEAP GAFIASLNHYLKSHRFPCHW SWVANTLPYHEANDDLMMIMD DRLIANTLHWYWYFGPDNTGDI MTLKFTGLQNFISMMGTVHLV TANGSFDCQ*NPAGDQRMVKG HCYFP SWNLHLSKHTQCNGNE FIFMTKKKQSLTAKSLPDTS
14314	44682	A	14400	3	183	KRKEITNSLDAASRGTVPAAL AGVQYLEPRAGAAGRLGGAG WGRVPRPGSS/SSLSLVGR*GW CPVLRTOGRCCRPPGCGWVGA RPKAWEWLSLVLGV
14315	44683	A	14401	21	399	IWN SAAPTASRRPWSLA PGSPRS TWCVASTPPCAPGKAREPRDRS EVPPATAPAVLQSHWPCPRSSR SG SAGNCVGP PHSWAPGHSQH LTPGP G HGGP RGP CWHLLMQT AWPALT PPGAMPGEAEGQ
14316	44684	A	14402	59	478	RCSQPWHCPAALAGVQYLEPR AGAAGRLGGAGWGRVPRPRL LSLSLVGR*GWRPQE DQLFPH LRRPVGTRSESTWG NRAGAAT W/RAATPSPWRT*NGTKSKQW TASGLWQKG DGDW D*GSGKPL PLSVPAGORL VPVC
14317	44685	A	14403	1150	1319	PRLPLTACT*RS/CSRYWMVP KSPRMTMMMWTKLARMGAQ W*PRKSNACLSRAASS
14318	44686	A	14404	34	304	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPRRAPPPAPRRPVPST TQ/EARRSAASLLSPARPRAH RD GTNNSSRATLRAVTLTARVRG F

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14319	44687	A	14405	I	360	SSSLSYLPAGQGSGPAARHA*ASHPLHGGLI.CGPSPNHEHPLIQLGAQSH*PPKG*GVRAGHVGLAGRSTCSP/ECGIIH*VKPAGLSSLFGPRCFYEL*QSPRRSAAASLLSPARSRAHRE
14320	44688	B	14406	80	1166	
14321	44689	C	14407	I	543	
14322	44690	B	14408	I	930	
14323	44691	B	14409	I	1473	
14324	44692	A	14410	388	606	
14325	44693	A	14411	I	798	
14326	44694	A	14412	687	832	
14327	44695	B	14413	I	1218	
14328	44696	B	14414	I	642	
14329	44697	B	14415	I	807	
14330	44698	A	14416	554	724	
14331	44699	A	14417	216	494	
14332	44700	A	14418	I	3408	
14333	44701	A	14419	330	858	VPSLDGQRGLELDTECRLVYQLQSLST*RFSTSSPEQLDTECRLVHSQTLCTQGADWCYIKP*VGLQVELPASPAPWLAFLSPWVNVGTGRHGAGGGARRGGSGCTGAHGVGGLRLRHGRQLQVSPAPWEGSCSLSPIGPPFKRAHSVLQKGSTSTMVGTCAASSPKVVFHLLS
14334	44702	B	14420	182	1513	
14335	44703	B	14421	I	1608	
14336	44704	C	14422	I	1830	
14337	44705	A	14423	167	433	LPSRGAGLGTCSPPCLSLPPTPAPVRSEPPRRAPP/PGSTVPSPINHPRAEECEMRDWAQAAAPAAPVRDPLGEASWAPEFFGSMPL
14338	44706	B	14424	32	352	
14339	44707	B	14425	103	451	
14340	44708	A	14426	158	921	LPSRWAGLGTCSPPCLSLPPTPWAPVRSEPPRRAPPSPAPRPPVPRPPKG*GVPAGHAGLAGSSTCSPDICRVCRSEGTPEKPLYHPCVCTGSIKFIIQECVYSPDMPSRLPIQDIFAGLVTSIGTAIRYWFHYTLVAFAWLGVVPLTAWHQLLDLGSTLNPGCSHLVILKLTSTKTLFPNKATFILVLSQDKTLMEDPRMEDKWKEDRFSFPNSEALEITLGERHRPQTASVIPWFCCSSRHVLNLGKINFEVD

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14341	44709	A	14427	242	515	IQSVHWCIHKP*ARHRVLIGVFT IPELDIKVLHVPTRLRNPGFTH WILHRDCRCSMPVLRHAPALL SPWVNVNGTGRSRAKGDTHRGG SG
14342	44710	A	14428	759	988	TWPRKPLFPPRPLGL*WEGMLQ RSLTCGDIIFPIILVISIWLVTY ANFGSWL*FLPRKWWVFFPFPVP NKFLIF
14343	44711	A	14429	130	788	VLQLIKAVWTPRTQEPSWLPVV NPARELQVELPASPAPCARTPQ LLGGRWDWAPWSRGWRSFGE ARAAQKPMEGVGGSGMAGCR SRALPHGKAAKARRAIEHSTGG LALLGDPVHSPQPLARVLSPSLP RASRAGWLRLVRGPPSPRPPGT PAGRQAPHAAPVPARASPSTPP/ CRAERVGSSPGQPRKGLPQCRG EAEGLLLKCHQSISPGRGEELW HSR
14344	44712	A	14430	108	1686	ANRCPLPHPGTGAGRCLGASA GRAEEAGV*GPLHEGLGYRPA GLFLRADTGHRTPGWGGGGGG AGGRGGAAPGPVGATRFFAG RRGCARHGAAPVAAVRCCERL VLNVAGLRFETRARTLGRFPDT LLGDPARRGRFYDDARREYFFD RHRPSFDAVLYYYQSGLRRLRP AHVPLDVFLLEEVAFYGLGAAA LARLREDEGCPVPPPERPLPRAF ARQLWLLFEFPPESSQAARVLAV VSVLVILVSVIVFCLETLPDFFRD DRDGTGLAAAAAAAGFPFPAPLN GSSQMPGNPPRLLPFNDDPFFVVE TLCICWFSFELLVRLLVCPSKAI FFKNVMNLIDFVAILPYFVALG TELARQRGVQQQAMSAILRVI RLVRVFRIFKLSRHSKGLQILGQ TLRASMRELGLLIFLFIGVVLF SSAVYFAEVDRVDSHTSIPESF WWAVVTMTTVGYGDMAPVT VGGKIVGSLCAIAGVLTIISLPVP VIVSNFSYFYHRETEGEEAGMF SHVDMQPCGPLEGKANGLVD
14345	44713	A	14431	1	427	
14346	44714	B	14432	8	323	

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14347	44715	A	14433	20	1050	FNLVYMSHVSDEGALSESAT AASWPPHGLQHFVPGPQVPI CLYLLGQKTG\HMAPLLRQVT GSPIPPKTPGRGIRNMKRNEKR RYKTLMAKGWELHQELSLGRT SSLPPYKGPGPWSPGFQKVSKG ANPVEIKRGVMLAVDAVIAEL KKQSKPVTKPEELAQVATISAN GDKEIGNIISDAMKKGCRKGII KISSVQSVITALEIANAYCKPLV IIAGDDIDGEALTTLILNRLKVG QVVAVKAPGFGDNRKNQLKD VIATGGEVGEVTVIKDYAMLL KGKGKNSQIEKCVQEIIDQSDV TTSEYEKEKLS\EKLSGDGVAVL KSHPWFCTKIPYPLT
14348	44716	A	14434	3	764	TTATVLAWSIAKEGFEKISKGA NPVEIRRGVMLAVDAVIAELKK QSKPVTTPEEIAQVATISANGD KEIGNIISDAMKKVGRKGIVITV KDGGKTLNDELEIIEGMKFDRG\ YISHPFINTSKGQKCGISRDAYV LLSEKKVSIQSIVPALEIAHAAH RKPLVIIAEDVGEALSTLVLN RLKVLQVVAVKAPGFGDNR KNQLKDMAIATGGAVFGEEGL TLNLEDVQPHDLGKVGEIVTK DDAMILLKGKGDK
14349	44717	A	14435	1	3288	MKLMETLNQCNAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVQGYTIEQI NHMRDVFGTRLRRAEDVFPVPI GVAIHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWPVDLHIIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCALHRIETELMGKFDEGKL PTDPHMLRLAIETVVAHDYDV VIDSAPNLGIGITINVVC
14350	44718	A	14436	2	422	

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14351	44719	A	14437	529	2484	WGINIIKKNKAAAPRAFGVRL ECQPATENQRWQDLNVISSLLK SFFRKLPPLPFTDEELPLAPSFCP EEENGGRGGGSPRYRLEPMDT IFVKVNKEDGPAHRAGLRTGD RLVKVNNGESVIGKTYSQVIALI QNSDDTLELSIMPKDDEILQLPA ERESGGEASEPPRVVRPEPSTRA LEPPAEDRGDEEVLRQKPPTRGR KVQLTPARQMNLFQGDESPEPE ASGRGERLGRKVAPLATTEDSL ASIPFIDICVRCPACWLHALLDW MAQQRVLDMQGQSIGMGVSW DRELEEKGSEKGYDEPTSPSIDL QAKHVPASAVVSSAMNSAPVL GTSPSSPTFTLGRHYSQDCST SAHLNIFAGIFDIDNDDHLQVSTL ESNFTRIHLTHYTGGNHFPAWLA WDAVPESSDLLNLGVHVLETG AGTPFLGSACSSDGIASQMNIA GLPQIRDLPGHYYETLKFVGHV LKTIAHDHSEKNKMEPRNLALV FGPTLVRTSEDNMTDMVTPHA *PLTRSWETLIQALQTGSSVTKR YKGKENPCGLTRSLRQCPTLST FLPNIWQDSAPWRPGVSGPVGD LKDSTTCCSAKSKGSWAPKKEP YAREMLAISFISAVKPQAQEAA GDAGAGQQHRRRLGAGGAQS LGRGPQRGGHQERS
14352	44720	B	14438	1	1473	
14353	44721	A	14439	5	694	VPDKWGWLMSRYLETAIRT AACAAASPRLNPGRCASAARGPS SQSPRPPWSGHKRRTASPGWG GQSAAPMPPSRSPWASPVGGE FRLSETPSRPFTLSGMK*GWQV HSWAPALFCSVMSFSPDTCCLC K*AHSPCSPSPSTVILLRETSSN WDWQPEDLGAPKASASPPSTT RITRLRSELQLRRLNPSDSDCHR GFCFSFRCLLTPEHVLPKTVLRI QPGCKVA
14354	44722	A	14440	303	757	MAWKVSLRGRKVAGRAPSQR WASPPSSGQSVKSLLLPPARRL CPGPVGPARCHRRI*GLGPGRG WRGEWRRDTNPWEPPQPRSPS/ G/PNCAWSDGCPRGAPRRPRA *AGAARRAAPARI*VPWWRGSAG GCSNRRLQVPAHE*TPTPFIRYL

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14355	44723	A	14441	1	534	RHEDHSEPTFLISPSSLFCFLPPSA PPLPRLTPPAALLVPAVQRME PVLFLPAPGAAACRVWHPALPP PRQAAVSSSRPCYPVCVARSAPA GRVRAAGVPPAPPSSPRLGRV GGRSRSPNVFRVRAAAGP/PG L*ISPWTP/PLNEAS*RQRGCPAS FAVYGGQEWRPPQWPGPGRGP
14356	44724	B	14442	157	2143	
14357	44725	A	14443	258	4089	QLITCLSRPETGGKFEVDTQRP VCPPSRARAARASA^AAA TUTPTMDSFDLALLQEWLDLES LCVYEPDRNRALRRKERERRNQ ETQQDDGTFNSSYSLFSEPYKT NKGDELSNRQNTLGNYDEMKT DELTDRTNQSHLVGVPKPGVPQ TPVNKIDEHFVADSRQANQPSI CSTTSTPAAVPVQQSKRGTMG WQKAIGHPPSDGQQRATQQGSL RTLLGDGVGRQQ/HSGQTSVQC GGGPSPDPGEATCHGGQ
14358	44726	B	14444	1	1326	
14359	44727	A	14445	453	710	SQHFGKPRQVDHLRPGV*DQP GQHGETPSLLKIQKLTGRGGAC LW/OSQLLRRRLQENRRLNCGG GCSEPGSCHCPPAWATERDSVS
14360	44728	B	14446	32	290	
14361	44729	A	14447	244	426	
14362	44730	A	14448	69	221	QWRFCGIERGERWQKD*EIGW LPCLCGKK*IWETFVLFCTKNN SSALGSC
14363	44731	A	14449	27	220	AVILTAKICSFTEPEPSKTTSPGG TNNSRATLRAVTLTVKVCFSFT P*GSAASFLLKSVRPRTHQ
14364	44732	A	14450	115	732	EPETRIDPLSWNSQLPVAALH LPGMSSVGAGQAIICNLCLGLD VSPSSLPALERTGPPPWNRGPK GRGRLPLSL/TVSQPSLVIPPGTG KSEVNADRSRPPAYCSNLGRYS GPGPPSLVIPPPTGKSEVNADRS GPPAYCSNHFPSALP**RSSMRS LSLQTSAWTCRHFHTSILKSR WRFPNLNSCLLCRPNNTWKP CLGACTL
14365	44733	A	14451	528	875	EHGYFQGTLGQKGCKSGKPPG GTLKTLTTLREPGRQLQSP*TSL WVSERLP*YP*GDTGENCPKLS FHLRNLGPS*AG*RERRPPQGGL YLPQQAYRLLMQGSAFWPLFGY APSPQR

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14366	44734	A	14452	2788	3414	ACFSYIAFWRINTTSTANLSKESLTSTTSRSWVINVNIVIFCTDWLFYKWLKKNPFIYFYMMPPFNQITFHMSGSCAARASPTSTTPCSTA PSPIDHPRAEESSTRRVTRGRQLHLQPAKICSFTPEPSKTTSPPGGTNNNISALP*EL*HSPRRSAASLQFRTR*YPYRYQSQQPGSHF*LPLPLPSSIHDF*LFHLQHTFQS HALLP
14367	44735	A	14453	662	1338	VLQLIKAVWTQRPLGGRWDWAPWSRRWCSSGRLRPHRNQWSGWEAQAWGLQVPEPCPAGRQLRPGEKSSTA PVCTSCCRTRSTA GPTGCPSTRRDPTTLSASPS*TSTS TSLATATASASMWAGSCTSISTRGSASLVHQALTWPQSGPASPRKRTGSHPVA*AGVRWRAHRSLQPQTGGLK*SSHFLSPSGWNYRHSNHPISQSFPHLSPLSIPQNH CHHGPFSM
14368	44736	A	14454	3	415	DFLLFSEILPASQASASAILPALPASHRCPCCLDVPLPVEVPGPARLP VAAASVWRPVQHQLSLGLRWA GPT*DRTESRETNAEVEADLPP LYAHGRLEPTAGPSGASAVLSSSEYCPGPHPKMGHRRVTSCLSTCQS
14369	44737	A	14455	659	818	
14370	44738	A	14456	2	710	
14371	44739	A	14457	349	493	SS*VRWVSGR*HPQ*STLSAPLG ETSGCHQGLHDLKIVVL
14372	44740	B	14458	1	1338	
14373	44741	A	14459	83	426	
14374	44742	A	14460	93	345	APALCLQILLDKSVRNRRTSRF RPREVGIQQYKKGGGAAGKGG TGNAPGFLFSKDS*KDPTPLPP PLLL*GQRDH*IQLHQE
14375	44743	A	14461	1	1302	
14376	44744	A	14462	1	1174	
14377	44745	A	14463	274	1428	
14378	44746	A	14464	411	627	HCLSHFQNTGPRGDVDFQQLAFPVLMADIRKEERSHLCRSSRR TWTILDKS*IQGSRLLSSKEQGW GWGTSRK
14379	44747	B	14465	1	1553	
14380	44748	A	14466	226	449	SLQPDI*CSGLRGSSLV*PKSD
14381	44749	B	14467	1	2061	
14382	44750	B	14468	10	1099	

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14383	44751	A	14469	34	406	GGGFISLDTGHSHKSHPGGS*H ALGWVRPHTLNNSP SQQPGNC GNPAWEC*GPHG/APSRWCSCT PCRPSIPKVPAVRVAGPAGGCT PYRT/PTRRTPR*RPGPCAACDR PLHPHCGPRGPAGAYPR
14384	44752	A	14470	623	1671	VLRSVSSWLPSTMATVLAPM LRAMSAGRLLM*PPMSRCPSL GSHSGGR*PDS/GHAGAHVPPQ GAIFVDSHG*GDDICGHVEVRQ P/QGPQSAYPGRPDGCC*RQT Q*TWR*LG*GPTQVPAKSCS WPTPGPAASCGWRCAAPRTTLR *KSQWTCRPPGPRGPPLMLP VLRCASSPWPRPRLAQGQWC P*APSPSGRSRSCAGPRAWRKPS RRAHAAWQGGCAKRGGADSA GAGAPSTSCAYLATPRCAWGP HPLGGAGLAA*GRAQPCSPAS APAGR*APGPPGPQ*GCSR VAGSARSASARRPSGRVRYGV HPPAGPATLTAGTLGCYPVRRP PGVPG
14385	44753	A	14471	32	972	QSGTFSTKNEGRRTTDVYDGR GPRVGRCGTCVYVRYVHDPH APPHERARRNDGNTQRTGNAR PGTAMPTA TTDQPKGRSTRHK ETKRGRTARNGKQQNPRK/RP RKDKRKQGSAGEGERGAGGKE KGQPRDTEAKGDRTDFPPNG P*GQSKRGANIGGWFPPLRLG PNPPLPGPQSAQVSGP*TPQMW MPTGTGCCGSQ SGSPPWC SP*PVAEALFHST/PAPRHPSP SSSPKHSHPSTPPP*ISLGQG RPPKRPAPDOPQVPRCEPSC AYLATPRPTMRRMQSACRGSAR SRASARRPSG
14386	44754	A	14472	1	3128	
14387	44755	B	14473	239	5474	
14388	44756	A	14474	542	781	PASIIIMTGSISHITILTLRVNRLN ASIKRHLTDWQIR/IKSQDLSV CYIQETHFTCKDPHKLKIKGWR KIYQVN*KQKKK

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, =Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14389	44757	A	14475	724	1340	QLTLQGRRVAPR*PSRVALEQE/ CGYNALLRYEGFENDSGLDFW CNICGSDIHPVGWCAASGKPLV PPRTIQHKYTNTWKAFLVKRLTG AKTLPPDFSQKVSESM/QYPFKP CMRVEVVDKRLCRTRVAAVE SVIGGRLRLVYEESEDRTDDFW CHMHSPLIHHIGWSRSIGHRFK RSDITKKQDGHDFTPPHLFAKV RSFYKNPHL
14390	44758	A	14476	1822	2226	KRLFTNRTRITPFVAINSHHHHH HHIIINTIIITTSINSTHHHHHH YHHHHHHHHHHQHTTTNTT TTTTTNNNTTTTTTTTTTT TTTINSTHHHHHHNQCHHHHH HHHH/HHHHHQYHHHHHHHHHHYQ HHHHHHHHYHHHHHHHHHHHHHHQ/ HHHHHHQHHHHNQHHHHHQHH DHHHHYHHHHQHHHHHQHYQH HHHHHHQHCHHHHHHHHHQH HHDPHPPHHQH*HSHQHH
14391	44759	A	14477	232	625	EGCCCA^IMVQKYQSPVRYK YPFELIMALRK^YPRCCVTC* TGGAAQQVGFRFLDPLSLCTP* CLWRRTSSNF^RKAAGCSGRL QSHHFGLIPQPTAPKWPWSSPLHI TKPQTLGQRDPGPRTRKRSK
14392	44760	A	14478	1	808	MPKTTACNVHTVTWASCENAD SDSTGLRHHDSCEDPASPGRSD LCLVPHPTRPAVRGGRPAGGR PAVPAEGPWRHLQQAEGELKR LAGGLERLLENPVRRALPQGA QGHRAEPTEARPHPAPEIIIRRAG AAAERAERLESQVGASAAAA SAASARIPLYLVAVPAAGPPRHR CRRHRRGPGTSSGPRITALRPT ARARAGIVSEPRTAAGATRARP WRQGSHNPVAPSA^LLRGPSIP WQIRPMPCPTSHQTCSEERRPSG RWQMPGSACRRSLETTSSAGAG RAQEAGGRLLGETSGES/GAGL YLKELRAIVLNQQLRVRTQRQS IDELEERRLNELSA^NRSLWEHP QLPQAQPPPGFLTS^PSPLPALL GTAAAAATAGA^QEHLQDHGQRS SARPLPAPELASFQNHEQLLAQ PEPDPPGGRAHTTQSPhQHPGTL GVKANKEKKGPPGCCAACGTP LQQESPAPSARES

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ~possible nucleotide insertion)
14393	44761	A	14479	1	831	MIRYFGDYWTQALLTJPGDPK HPRGPPVKVGVYGGQGYINSL ALCHNFIFIWRELNRFSLLQDVPL VRYIDNIMLIGS1KFLGVQWC ACRDIPSKDPADPMVLEVSVAD RDAVWSIWQALIDESQQRPLGF WSKSLPSSADNYSFPERQLLAY YWALVETERSTMGHQVTMLPE LPVMNWVLSDPSSHK/ANGLA GWSGTGKKHDKW1K1GDEIIRR GMWMDLSEWSK/D/KIFVSHV SAHQRVTSAEEEFNNQVDRMT RSMDTTQPLYPTTPVIAQWAHE
14394	44762	B	14480	56	3476	
14395	44763	A	14481	3	591	DPADPMVLEVSEADRDA1VPIS ESQQRPLGFWSKALPSSANNYS FFKRQOLLACYWVVLVIEHLM GHQVTRMPELP1INCLVSDPCSH KVGHAQHS1KWRWYIHWDWA EGTSKLHEEVAQ1PMVSTPSLP QPAPMASWEVPYDQLTEEKT RAWFTDGSARHAGATQKWT VALQLPLSGTSLQDSSEEKSSQW
14396	44764	A	14482	1	1275	MEKNIDQSRRRKVVEMNENV QLVRYGEQASDLK1TAKFKSPS EVKHIRFIQQAFIGSKLLMRPW TTVTQKQILSLSAKIALSES1LPC RKRAFFVEKQTQAFIMQVSDL QQKVHAQPSQVSTVKVKALIG KEWDPA1TWNGDVWEGPDEAG DTEFVNSDEAFLPEATAFPSPEV GNDQTVWGLLDTGSEML1LPG DPKYYRGPPVKVGAYGGQVIN RGLAQIQLSMDPVGHTRPVVS SPLPECIIGTDLSSRQNPHIGSLT DITLVHYYDDIMLIGSSEQEVIT LDLLVQAVQAALPVGPYDPA DPMELKVSADRDAVWSLWQ APIVTMRPERPIMNWVLSDPSS HKVGCAQHS1KWKWYIRDW ARSGPEGTNHSRVC5/LPQVQ APSAR*ATARRGGQAASGCCF WSCTCFNSFDV
14397	44765	A	14483	604	1760	NSWCRWFNFRY*YPTFYWES* NT*1PLREWFG*NHDASCP*TLD SKSFSE1TRTGSPCSSSLQTAYC GTLWIVQGV
14398	44766	A	14484	2710	3060	
14399	44767	A	14485	3	227	
14400	44768	A	14486	3	266	
14401	44769	A	14487	2	564	

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14402	44770	A	14488	2	503	FFFFLPIGFWRQHIPRLSVLVQHY*VT*NAASFEWGPQEAKAL*QVQAVVQVALPLGPYDPA DPMLLEVSVDKDA GCTRLQAPIGE SQWRSLGFRSKALRSSAENYSSFERQLLACYWALVETECLTLGHQVTI*PELPIMNWVLSDPSSHKVGHEQOHSIIKWK
14403	44771	A	14489	2	469	
14404	44772	A	14490	I	633	MTVDYRKFNQVVTPMAA/AVPDAVSLLEQINTFPGTWYAAIDLANAFFSIPVHEAHQKQFAFLPQGYINFPALCHNLIRRELDFFLLQDITLVHYIDDILLIGSSEQEVVNTLDLLIHKRSKEAHTAASRIRVSCLPFEQKSHEQTL.PWEQVPSSGDIKEYFPNAFVLLTTASLQQQDNTSQLQLTWKAPEDIKMSKT DADADEEIEALRG
14405	44773	A	14491	I	518	MTVDYCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSIPVHKAAQQKQFAFSWQGQQYTFVLPQWYINSPALCHNLIRRDLDCFSLPLDITLVHYIDDIMLIGSTIKWVVHSS/DSIIKWKWYVHDWARGPEGTTNLAG*SGTCKKHEWKTGDKGIRGRG
14406	44774	C	14492	33	932	
14407	44775	B	14493	27	2457	

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14408	44776	A	14494	332	2158	RGYVFCSWKKT DGS/WRMTVD YCKLNQV VVIPAAAVSDVV SLL EQINTSPGTWYAAIDL ANA PFSI PVHKAQQKQF AFSWQGQQYTF TVLPQWYINSPALCHNLIRRL DCFSLPLDITLVH YIDDIMLIGP RQLLACY/WALVETEHL TISHQ VTM RPEL PIMN WVL FDPSSHKV GCAQQHSI IKWKWYVHDWAR AGPEGTTTPVISQWPEQCGH GRDGGYAWAQQCRLPLTKAD LNTATAKRPICQQQRPTLSPQY GTIPQGDQPATWWVWDYMG S LPSWKGQRFVLTGIDTYSGYGF AYPACNASAKTAICGLTECLIH HHIDIPHSI ASDQGTHFMAKEVR QWAHDHGIIHWSYHVSHHPEA AGLIEWWNGLLKSQLQCQLGD NTWQGWGKV LQKVYYALNHO PIYGT VSPIAK I HRSRNQGLEVA PLTITPRDPLAKFLLPFPATLQS AGLEV LVPEEGTLPPGDTMIP L NWKLRLPPRHFG LLLPLNQQA KKGVTVL A GVTDLDYKDEITL LLHNGGKEEYAWNTDPLG LLL LIPCPMIKVNGKLQQQLKPEAL VPKGVVFPPGDTTMSLSWKL RLPSGHVGLL MPLSQQVQKG V
14409	44777	A	14495	1	3187	MAEGKEEQVLSYTDGSQRQEN EEDAKAETPDKTIRSHETYSLPR EWYEGNRPHDSITSQWVPPTR GNYGSTIODEIWVGDHSGYVRP VPVPRSLNSDISYFGVGGKQAV FFVGQSA R MISKPADSQDVHEL VLSKEDFEKKEKNKEATYSGYI RNRKDDYDNHTGIDL VGTIIATI KGSNEEDTDTPLFIGKV R VTLEFP FVNGSAEIMLMP SNSQQHKTDE KGRANLGVFSVFA PRGEHTLQ VKAIYNKSI EGP
14410	44778	A	14496	266	467	
14411	44779	B	14497	152	1245	

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14412	44780	A	14498	1	1445	MLRAAAGGQGLAAAGMGLCARPAGGSQLPRERMKGNAACLP LPPAVALTKGREKPDAGHQGR STQMMRESERGPCTHWTEERP GRQLKILLQKQMRQNTLMAFQ VSWDGRNKEIERTFPHATPAHT QQLIFAMKIKRTGVTVEPWGLF ETGORIRPIQAAGL*LSSSTTC VALAPLLTMHVKSALLSAP/Q MGALSTITSITTRRQTPAESHF PAARFHLLAPHSPTLPPCCGP SESAVTVLCFAKGKTAQDAAV PTTSLTAAGHLAGPRS*SSWSRM PVKVRAPDSSLPESTAHLPLT H*SWLPSASWGPASRALPGSEW VLKPVWQ/AITGPVQSITSSPGIP KPIGPLQA*GSAHPQALGFSVL QIPLSNSPSTMPTPLPRKISNS SLPSQ/PPQALFPNRWTNSSSPV HVITSAAQPRPTPREWFAVSFYR TTATTASLIPHLWAPPQEN*QTS PAQNGSTLPCMSQATFHFPS
14413	44781	A	14499	44	455	HLRNTR/PSQITPHIYNHLIFDK /PLFNIWWWWENWLAIRCKLKL PFLTPYTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/TGKDFM TKTPKAMATKAKIDIWDLIKLK SCTAKETIIRVNRLPT*WEKIF AIYP
14414	44782	A	14500	1	346	
14415	44783	A	14501	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKCKCSP SLAIREMQIKTTMRYHILTPVRM AIKKSGNNRCCRRCGCEIGTLH CWWDCKLVQPLCKSMWRFLR DLIDPAIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTNQ

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14416	44784	A	14502	1	2142	MHILDAEKAFDKIQQPFMLKTL NKLGIDGTYLKIRTAIYDKPTA NIILNGQKLEAPPKLTGTRQGCP LSPPLFNIVLEVLAQAIRQEKEI KGQLGKEEVKLSLFADDMLY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGRGGIALVDIPVNVDKL MVLLEVLRALARQKEIKGIGLQG KEEVKLSLFADDMLVYLENSIV SAQNLKLISNFNSKVSGYKINVQ KSQAFELYTNNRQTESQIMSEFP FTIATKRIKYLGQLTRDVKQDLF KENYKPLLKEIREDTNKWKNP CSRIGRINIMKMAILPKVIVYRFN DIPIKLPMTFTELEKTTLKF NQKRCIAKTISSKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSIYHN LIFYKPDKNKKWGNDSLNFNW CWENWLACRKLKLDPFLTPYI KIHRSWIKDLNVRPKTIKTL LGNTIQQDINGKDFMTKTPKA MATKAKVDKWDVILKSFCTA KETTIRVSRQPTEWKEIFAIYPS DKGLISRIYKELKQIYRKKTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKITM
14417	44785	A	14503	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT**SDSPKLK**KKC*GQ PERKVKLPTKGSPSD*KRISRO/ KTLQARRQSFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQTIREYYKHYANK LENLEEMDKFLDTYTLPRLNQ EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKGNFRPISLMNI DAKIL

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14418	44786	A	14504	1	2877	MENDFDELREEGFRQSNYSSEL EDIQTGKEVENFEKNLLECITR ITNTECKLKEMLKTKAQLER EEWRSLSRSCDQEERVSAME DEMNEMKGEGKFREKRIKRNE QSLOQEIWWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTIISEYYKHLYT KLENLEEMDKFLDTYTLPTLQNQ EEVESLNRPITGAE
14419	44787	A	14505	1	2347	MELKTKARELHDECTSLSRRFD QLEERVSVMEDEMNEMLNPLTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNPSYEPSII LIAKPGDRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIKKLIIH HDQVGFIPGMQGWNRKHSINV IQHINRTKDKNHHMIIISDAEKAF DKIQQHFMLKTLNKLKLEVLA RAIRQEKEIKGIGLQGKEEVKVSL FADDMIVYLENPTVSAQNLKL IGNFSKVSGYKINVQKSQAFY TNNRQTERQIMSELPTIASKRI KYLGIQLTRDVKDLFKENNPL LKEVKEDTNEWKNIPCS梧VGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRC IAKSISFSQKNKAGGITL.PDFKLY YKATVTKTAWYWWYQNRDIAQ WRNTERPSEIMLHIYNNYLIFDKPE KNKQWGKDSSLFNKWCWENWL AICRKVKLDPLPTYPTKCMNSR WIKDLNVRPKTIKTLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLKSFCATAKETTIR NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKQ/GGIWCD RIL.*R*TTCRVAKEIQL*RRU/W KRLQRLTLSIPVLDVA*PPMF*AS
14420	44788	B	14506	1	2265	
14421	44789	A	14507	1	2832	
14422	44790	A	14508	1	2109	
14423	44791	A	14509	1	2757	
14424	44792	A	14510	1	2304	

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14425	44793	A	14511	1	2685	MGDFNPLSTLDRSTRQVNK DTQELNSAPHQADLIDIVRTLH PKSTETYTFSPAPHHTYSKTDHIL GSKALLSECKRTEHTNYLSDDS AIKLELRKLNLTQNRSTTWKLN NLLLDYYWVHNEMKAEIKMFF ETNEKDFTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQKLEKEQEQTHSKASRRQ EITKIRAELEKEIETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAICNDKGDITTDPTIEQ TTIREYYKHLHYANKLENLEEM DKFLDTYTLPLRNQEEVESLNR PITGSEIVAIINSLLTKKSPGPDG FTAEEFYQRAIRQEKEIKGIGQLGK EEVKLSSLFADDMMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDETNKWNIPCSW VGRINIVKMAILPKVYRFNAIPI KLPMTFTELKTTLNFIWNQK RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWWWYQN RDTDQWNRTEPSEIMPRIYNL IFDKPEKNKQWGKDSDLFNWK WKNWLAICRKLKLDPFLPTYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIJKLKSFCATAKE TTNRVNRQPTKWEKIFATYSSD
14426	44794	B	14512	1	2337	

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14427	44795	A	14513	1	1544	HINRAKDKNHMIISIDAEKAFD KIQQHFMLKTLNLKGIDGTYFR KSNINVQHINRAKDKNHMISID AEKAFDKIQQHFMLKTLNLKGIDGTYFRKSI KPVLIISIDAEKAFDKIQQQFMLK TLNKLKDNIIVYVLENPIVSAPNLL KLISNFSKVSGYKINVKQSQAF LYTMSNTESQIMSELPTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDETKKWKNPICSWVG RINIVKMAILRKVIVYRFNAIPIKL PMTFFFTELEKTTLKIWNQKRA PVAKAIALSQKNKAGGIFTPLDFK LYYKATVTKTAWYWWYQRDI GQWNRTEPEITPHVYNYLFD KPEKTKQWGKDSLFNWKWCWE NWLAICRKLKLDPLFTPYTK SRWIKDLNVRPKTIKTLEENLGI TIQDIGHMGKDFMSKTPKAMAT KDKIDKWDLILKKSFCATAKETT IRVNRCQTEWEKTFATYSSDKG LISRIYNEKLIVYKKKTNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSSSLAIREMQIKTTVRYH LTPVRMIAIIKKSGNN
14428	44796	B	14514	110	2153	
14429	44797	A	14515	1	3210	MVKGSIQQEELTILNIIYAPNTG ALRFIQKQVLRDLQRDLDSHTIJM GDFHTPLSTLDRSTRQKVNDI QELNSALHQEDLIDYRTLHPKS TEYTFSAAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCNLSDHSAIK LELRKNLTQRNSTTWWLNLL LNDYWWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVERGK FIALNAHKRKQERSKIDTLSQL KELEKQEQTHSKASRQEITKIR AELKEIETQ
14430	44798	A	14516	3	2820	ENKDTTYQNLWDAFKAVCRG KFIALNAHKRKQERSKIDTLS QLKELEKQEQTHSKASRQEIT KIRAELEKIEETQKSLQKINESRS WFFERINNIDRPLARLJIKKK NQIDTIKNDKGDIITDPTIEQTII REYYKHLYANKLKNLEEMDKF LDTYTLPRLNQEEVESLNRPTG SEIVTIINSLPTKKSPGPDGFTAE FYQRYKEELVPFLKLFSQIEKE GILPNSFYEASIIILPKPGRDTTK KENFR

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14431	44799	A	14517	687	2274	I.RDCKRINQHPVKTDQS AFCK M/API/MQDV VLEV LARAIRQEK EIKG IQLGKEEV KLSLISNFSKV VYLENPIVSAQNLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSEL PFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWK NIPCSWVGRINIVKMAIL PKV IYRFNAIPIKLPMTFFTELE KTTLKF IWNQK RARMAKSILSQ KNKAGG ITPDFKL YYKATVT KTA WY WY QNRDV DQWNRTEP SEITPHI YNYLIFDKPDKNQW GKDSL FNK WGWENWLAICRK L KLD PFLTPYTRIN SRWIKD LNV RPKTIK TLEENLDITI QD IGMGK DFMSKTPKAMATKA KIDK WDL IKLKSCF CIAKETTIRVNRQPTKW EKIFAT YSPD KGLISRYN ELEKQI YKKK TNP IPKK WAKDMNRHFS KEDIY AAKKHMKRCS S LAIRE I QIKTTMRYH LTPV RMAII KNGSG NN/R/CF*WQKPGP GSG*ALRSWK EDIAGTSYVGMNQCQMRKNTK TLI
14432	44800	B	14518	1	3192	
14433	44801	A	14519	1	2814	
14434	44802	A	14520	1	3144	MGDFN TPLSTLDRSSRQKV NK DTQELNSTLHHADLIDYRTLHP KSTEYTFSSAPHTYSKIDHVV GSKALLSKCKRTEII TNCLSDHS AIKPELRIKKLTQNRSTTWKLN NLLLNDYWVHNKMKA EIKMFF ETNEKD TTYQNLWDTFKA VS RGKFIA LNAHKRKQKRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAE LKEIETQKTLQKINES RSWFLERINKIDRPLARLIK KKR EKNQIDVIKNDK

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14435	44803	A	14521	1	2616	TTYQNLWDAFKAVCRGKFI NVHKKRQERSKIDTSQLKEL EKQEOTHSKASRRQEITKRAEL KEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDAI KNDKGDIITNPTEIQTTLIREYYK HLYANKLENLEEMHKFLDTYT LPRLNQEEVESLNRPITGAEIVA IINSPLTKSPGPDGFTGEFYQR YKEELVPF/LKLFQSIEKEGI^M NIDAKILNKILANRIQQHKKLI HHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDAEKA FDKIQQQLFMLKTLNKLGIDGTY FKIIRAYDCKPTANIIINGKKLEA FPLKTGTRQGCPPLPNIVLE VLARAIRQEKEIKGIGQLGKEEV KLSLFADDMMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPTIA SKRIKYLGQLTRDVKDLFKEN YKPLLKEIKEADANKWNKIPCSW VGRINVVKMAILPKVIRFNAIPI KLPMTFFTELEKTTLKF1WNQK RAHITKAISLQSKNKARGITLPDF KLYYKATVTKTAWYYWYQNRD IDQWNRRTQPEITPHYQNYLFD KPDKNKQWGKGSLFNKWCWE NWLAICRKLLKLDPLFTPYTKIN SRWIKDLNVRPKTTKTLLEENLG ITIQDIGMGMDFMSKTPKAMAT KDKIDKWDLIKLKSFTAKETT

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14436	44804	A	14522	782	3024	SKTVPTGNSLEPTQNCWLQQWLPQDIEIEKQEQT/HSKASRKRQETKIGAELEEEIETQKTLQKINESR <sup>W</sup> SWFFEKINKSDRPLARLIKRR <sup>W</sup> EKNQIDA <sup>W</sup> KNKDKGDTTDPTEIQ <sup>W</sup> TTIREYCKHLYANKLENLEEMN <sup>W</sup> KFLD <sup>W</sup> TTLPRLNQEEVESLNRPITGSEIEAI <sup>W</sup> NSLPTKKSPGPDGFTAEFYQRYKEELHINRTKDKNH <sup>W</sup> MIISIDA <sup>W</sup> EKA <sup>W</sup> FDKI <sup>W</sup> QRFMLKTL <sup>W</sup> NKLVL <sup>W</sup> EV <sup>W</sup> LARAIRQEKIGVQ <sup>W</sup> LGKEEV <sup>W</sup> VL <sup>W</sup> SLFADD <sup>W</sup> MIVYLENP <sup>W</sup> IVSAQNL <sup>W</sup> NNLISNFSKV <sup>W</sup> SGYKIN <sup>W</sup> VQK <sup>W</sup> SQAFLYTNNRQTESQIMSE <sup>W</sup> LPFTIASKR <sup>W</sup> KIYLGQL <sup>W</sup> TRDVKD <sup>W</sup> LFKENYK <sup>W</sup> PLLNERKEDTNWK <sup>W</sup> NIPCSVVERINIVK <sup>W</sup> MAILPKVIY <sup>W</sup> RFNAIPIKLPMTTFTELEKTLK <sup>W</sup> FIWNQKR <sup>W</sup> ARIAKSIL <sup>W</sup> SQ <sup>W</sup> KNKAG <sup>W</sup> GITLPDFKLYYKATVTKTAWYS <sup>W</sup> YQNRRIDQWNRTEPE <sup>W</sup> SEILPRIYN <sup>W</sup> YLIFDKPE <sup>W</sup> KNKQWGKDLSF <sup>W</sup> FNK <sup>W</sup> WCWENWLA <sup>W</sup> ICRKL <sup>W</sup> KLDPFLK <sup>W</sup> PTKIKSGWIKD <sup>W</sup> LNVR <sup>W</sup> PKT <sup>W</sup> IKTL <sup>W</sup> EENLGLITQD <sup>W</sup> IGMGKD <sup>W</sup> FMSKTP <sup>W</sup> KAMATKAKIDK <sup>W</sup> WD <sup>W</sup> LIK <sup>W</sup> LKSFC <sup>W</sup> TAKE <sup>W</sup> TTIR <sup>W</sup> VNRQPTER <sup>W</sup> EKIFATY <sup>W</sup> SSDKGLISRIYKELKQIYKKRTN <sup>W</sup> NLIKWWVKDMNRHFSKEDVY <sup>W</sup> AAKKHMKKC <sup>W</sup> SSSLA <sup>W</sup> IREMQIKTT <sup>W</sup> MRYH <sup>W</sup> LT <sup>W</sup> TPVRM <sup>W</sup> AI <sup>W</sup> KKSGNNR <sup>W</sup> IT <sup>W</sup> VLLPGSL <sup>W</sup> IVRSF <sup>W</sup> HVTLN <sup>W</sup> AILLHP <sup>W</sup>
14437	44805	A	14523	I	1701	
14438	44806	A	14524	I	4434	
14439	44807	A	14525	I	2913	MGGPAALCIAVVPGDLVVALC <sup>W</sup> LEEGLGSGIATWACSPW <sup>W</sup> RISQG <sup>W</sup> THLTFRSSLAVAA <sup>W</sup> AIPEGLP <sup>W</sup> IVVM <sup>W</sup> VTLVLGV <sup>W</sup> LRMAKKR <sup>W</sup> VVKLPI <sup>W</sup> VELGCCS <sup>W</sup> VLCSDKTG <sup>W</sup> TANE <sup>W</sup> MTVTQ <sup>W</sup> LVTS <sup>W</sup> DGLRAEV <sup>W</sup> SGVG <sup>W</sup> Y <sup>W</sup> DGQGT <sup>W</sup> VCLLPS <sup>W</sup> KEV <sup>W</sup> IK <sup>W</sup> EFSNV <sup>W</sup> V <sup>W</sup> GKLVEAGCV <sup>W</sup> VANNAV <sup>W</sup> VIRKNA <sup>W</sup> MGQPTEGAL <sup>W</sup> MALAKDQ <sup>W</sup> EDIY <sup>W</sup> FMKG <sup>W</sup> ALEEV <sup>W</sup> IR <sup>W</sup> YCTM <sup>W</sup> NNGG <sup>W</sup> IP <sup>W</sup> LPLTPQQR <sup>W</sup> GAGPGD <sup>W</sup> TALP <sup>W</sup> SAAS <sup>W</sup> AFARMSAAERND <sup>W</sup> AFQG <sup>W</sup>

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14440	44808	A	14526	1	3009	MGDFNTPPLSTLDRSRQKVKK DTQELNSALHQADLIDYRTLH PKSTEYTFSAPIHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDGS AIKLELRKNLNTQRNRTTWKLN NLLNDYWVPNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAEELKEIETQKTLQKINESR SWFFERINKIDRPLARLKKKRE KNQIDTIKNDK
14441	44809	A	14527	1	4800	MGDFNTPPLSTLDRSTRQVKNK DTQELNSALHQADLIDYRTLH PKSTEYTFSAPIHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRKNLNTQRNRTTWKLN NLLNDYWVNNEMKAEIKMFF ETKENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAEELKEIETQKTLQKINESR SWFFERINKIDRPLARLKKKRE KNQIDTIKNDK
14442	44810	B	14528	1	2901	
14443	44811	A	14529	569	3443	RKH*TWKRTSSSTSHHKNMPN* LEKQEQTHSKASRRQEITKIRAE LKEIETQKTVQKINESRSWFFER SNKIYRPLSRLIKKKCREKNQIDT IKNDKGDTTIDPTEIQTTEIYYY KHLYANKLENLEEMDKFLDTY TLPRLNQEEIESLNRPITGTEIVT IINSLPTKSPGPDGFTAEGYQR YKEELVVFLLKLFQSIEKEGILP NSFYEAIIILAKPGRDTTKKEN FRPISLNMIDAKILNKIIAKRIQ
14444	44812	A	14530	3591	8157	TGTSQKKTFMQPKKHMKKCST ITGHQSNAQNQHNEIPSHTKLE WRSLKRSGNNRDVGNVVEAM YGDLPPIMLIGHSMGGAIAVH TASSNLVPSILGLCMIDVVEGT AMDALNSMQNFLRGRPKTFKS LENAIEWRNKDLSWADSKNV AAASLACISGALPASA VTTSPD NKRMARVNVLKYERLIAESPNH VVAEA VIQRPNIPHLQTRDTYE GLCQTLGSQPTLYQIPSLYCSYE TNSNAYLLLQPIRKEVI

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14445	44813	A	14531	172	328	AVKTEPEMKSQATKLSVHVKE KSQEGKPKEHTEPKSLPKQASD TGSNDAHNIAVSR^SHROPSCL LWFMRKNPKKESRKNTQSQKA YPSRHQI^QEVMTLTI
14446	44814	A	14532	3	660	TSPDCWEEGRSVWDWPRPGPALS LHNCKLDSLIEGGTLQQPTPSF* PTGTRAV/PTRRRSRQE^TQLNSE RTVSPGSR**EKRTSRAW/RSPL QGPGPGHAGQVQAGGTGPRTGS TRGD/TLQKCGKIQSVPLNCELI PI^/PSILPKVLPCLCPGIGASSS CPSD*VFFCTS*PWPYLLSYPLS MNFYRYHDHILKLLVQVYTLYL LLQFLQVLLKYLLSHPKQHS
14447	44815	A	14533	1	1086	MVDNDVPWPVLVVAQEKGQPD LCLSSKGYRPLALVQLDFHQVS VTSKIFILSGALRSLTGAAATAD WTCRVLVITYPHDIMADSECNSL LVPSTTRKIMKHMLASEKIKTQ NFNYNVDECVSLLYHHKANKL EAAEARQECELLRVAASVSRH W/RDPAHPHSCWPRC*APHCLG PARAPNARPAKATTWNLRRS APCAAPVPTQSWAGAPSGTAG AEPS*ECRPPENQARTAGSGVH AEACAPATCPACPGPGPCSGLP SSGRALFL/CATLAIPCV*V*LC FLATPPPCR*HVTAAPSAGKCIW* PDA*VTK/PRDLCPVQVARDN GPRQVAQKKESSSYVSWGFTI SRVGDRSPPPRAATL
14448	44816	A	14534	23	506	PDIDNIFSEFGAKSKPYLTVDQ MMDFTNLKQRDPRLNEILYPP KQEQQVQLIEK^YEPNNSLARKG QISVDFGMRYLSGEENGVVSP KLDLNEDMSHPLSHYFINSSH TYLTGMNFLVLCYFSQSHQISP TSTFCCSEAEV/WFSSISCEVPLR TLGFHH

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14449	44817	A	14535	341	1248	KNAFTSFLTSFPPGQISVDFMR YLSGEENGVVSPEKLDLNEDM SQPLCFMGIWGLFCWCFIAQQL AGNSSVEMYRQVLLSGCRCVE LDCWKGRTAEEEPVKILAY*IV MCSHF*EVIEIAECAFKTLSLP TFLLLFLFSLSPKQQAKMAEYC RLIGSSIFKEYAFHFY*LESGVPL PSPMDFLMDYKILVKNNKKSHKS SEGSGKKKLSEQASNTYC*NGD MMICY*NLTGEADTESD\ADAS GNV/CLFYSYFQGTAGSEAMAT EEMSNLVNFLTTPFFFVLLLNSE RNKSFEMSSSVETKGL
14450	44818	A	14536	574	647	C*PGNM/HISQQHLVAGEKEAE SEDEEEEDMKLLGTPEGGSKFT QKKVKLAADEDDD/DDDADEDD DDDDDDDDFDDEETEAKPV
14451	44819	A	14537	3	630	PGATHASAPPGVRLKCGSGPV HIIGQHLVAVEEDAQSQDEEEE DVKLLSISGKRSAPGGGSKVHQ KKVKLAADEDDDDDDEEDDD EDDDDDDFDDEEAEQQAPVKK S\RDTPAKFNAQKSQNQNGKDSK PSSTPRSKGQESFKKQEKTPKTP KGPSVVEDIKAQMQAIS/EKKG GSLPKVEAKFINYYVKNCRSRT DQEAIQDLWRWRRSL
14452	44820	A	14538	1	1971	
14453	44821	A	14539	316	1169	RVGGQSHGTQRISLCRHSVCSP LARQSPSNMK*VRTEIQMAVS CYLKRWQYVSDGIVPLKQGLR LPQTAEEELAANLTVHRESHCAD IVSAV\PCQAEPOQQYEV/QFGRL RNFLIDSDSPHSHEVMPLLYPLF VCLILSLVQNSPKSTVESFYSR FHGMFLQKASIQKGVIEQLQTT QTIQDILSNFKLRAFLDNNYVV HLQEDSYNYLIHYLQSDSYTAL CKMFILLI\LDVQPAKTTD*QL YASGSSSRSENNYLEAPDMPSP LQNDAALEVLQERIKQVKDGC PSLTTVCFYNT*QLLNTAEISPD SKLLAAGFDNSCIKLWLSQSRK LKSESCQVDMRSRIHLACDILEE
14454	44822	A	14540	1	297	

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14455	44823	A	14541	2	1089	APIILGECRSGRGLASSRSRRRT TMTQSVVVQGKLRRAGRDLVA AESSHGVSCLMSSYSLSFLLSSGRS RLALREHAAVNQVPARRREPPR LSARSSSPYSFHQLQSE*L*KKIH* LYFIFLSQLAVLIDMEEGVVNEIL L*IRTNQIKK*MQGIFKIHILFR AVGHKVFGLYQDQILKEFKQIL HNYILNHLC*FLKT*SSGTGSG LGTFLLKVLEDEFPEVYRFVTSI YPSGEDDVITSPFLVEYHLHPLF LIAISLPMFFPQKSLFDIISKIDLM \VNSGKV/GGTTVKPKSL\VTSSS GALKIELHLKCIILKLKIFS*C* LFSSARFEGSLNMDLNEISMNL VPFPSS*EIVSLKVLVLYFN
14456	44824	A	14542	129	461	TCISGWHLFRASVTCPGIQTSPH NWHISDNSSLNPNNIFIVCNLL GMTRNYIIFIEQPLKMNLIWKIA TSKIRGKAFSDGISGNPQCNTR FHVVEKRTGQLLPGRYYSKPF
14457	44825	A	14543	1	522	
14458	44826	A	14544	1	927	MEDLLEARSPTYWGRARAKIQ DSCWSVTSDPNAGSVDILAPLL LPSPSSYLPNFTCTVSVVTSHLH EAFLDLGFRGTGGSNCKTSRQV QLNNQKRKKKKSKSLPFHMSL QIQNYKTQEEPHAKPSSQQHQH SEHESIQTKLVFRSSMTYMHTL KLIREKGSIMLSLTQGECPNSTC RWPAAEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICSIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNWKIA TSKIRGKAFSD GISWEPQCNTRFHVVEKRTGQT T*INPDKISIQQKHDIHAYIEAD KRKRKHNAVIHTG*M/YQI/GTC RWPAAEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICSIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNWKIA TSKIRGKAFSD GISWEPQCNTRFHVVEKRTGQI LNVKTMRMKTFMMIYHLMN

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14459	44827	A	14545	1	882	MAEILTQVPPDDMLKKKTPRVK SVWRSQRGSCTPLIGTTTLD TSHMSIRNMDRSHINVHTVRKP SADLPYFRTHEWAHTGGKPYD CEECGKSFISRSSIRRHIMHSG DGPYKCNFCGKALMCLSLYLIH KRTHTGEKPYECKQCGKAFSH SGSLRIHERHTHTGEKPYECSEG KAFHSSTCLHAAHKITHTGEKPY ECKQCGKAFVSFNSVRYHERT HTGEKPYECKQCGKAFRSASH LRTHGRTHTGEKPYECKQCGK AF*PRFQMTC*RRKLPE*NQCG EVSGVH\HSLNRHHRADTGHKP YEYQEYQKPYKCTYCKKAFA YLPYFRTHEWAHTGGKPYDCE ECGKSFISRSSIRRHIMHSGDG PYKCNFCGKALMCLSLYLIHKR THTGEKPYECKQCGKAFSHSGS LRIHERHTHTGEKPYECSEGKA FHSSSTCLHAAHKITHTGEKPYEC KQCGKAFVSFNSVRYHERHTHT GEKPYECKQCGKAFRSASHLRT HGRTHTGEKPYECKQCGKAFG CASSV рIHERHTHTGEKPCSSNTS
14460	44828	A	14546	3	395	SAEVGAAETTLTELRTTVQSLEI DLDSSMNLNKSLENSL\GILLHL ESELAQTRAEGQRQAQYEAL LNIKVKLEAEIATY\RRLEDGE DFNLGDALDSSNSM\TQKTTT RRIVDGKVVSETNDTKVLRH
14461	44829	A	14547	2	1044	AKTSSQMPSPQEGMC\GKACTP ALSQADSLCP\LLRLASEVEGYS LPACAEPYVQSECLSIHSVWSL QHALSSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRSIVSHFTNG\GGLA GMGGI\NEKETMQLRDRLAS YLD\RV\RGLE\TENWKLES\KIQEH LNVTRL\LETEIEALKELLFM KKNNIEEAKGLQAQIASSGLTV EVDAPKS\QDLAKNMADSRAQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMLT ELRHRVQSLEIDLDSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLVFEGKQV

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14462	44830	A	14548	1	1212	GPGTGIAGGLAGMGGIQNEKET MQSLNDRLASYLDLDRVSLETE NRRLESKIREHLEKKGPCQVRD WSHYFKIIEDLRAQIFANTVND ARIVLQIDNARLAADDFRVKYE TELAMRQSVENDIHGLRKVIDD TNITRLQLETEIEALK*ELLFMK KTPEEEVKGLQAQIASSGVLTVE VIDAPKSQDIAKIMADIR\AQY DELARKN\REELDKYWSQQIEE STTVVTTQSAEVGAET\TTEL RRTVQVFGDSTWTSMRNLKA NLENS\GEVEARYAL\QMEQL NGILLHLESQQLGQTPRTEAQRQ AQEYEALLNNIKVKL\AEICHL TRPPSWKIGEDFNL\GDSLDER NSMQTIQKTTTRRISWIGQSGV LRP\DTKVLEALSQEASGTL GKQEANKKFQSFK
14463	44831	A	14549	1	2382	
14464	44832	A	14550	2	173	
14465	44833	C	14551	1	732	
14466	44834	A	14552	455	682	AWKRAVALGKSRPMGAVAFK RRMQPVAGPRAMQEKPFPSSSS SLSIPP\AF*YRLALSLAEPSSRW RARTGALMQL
14467	44835	A	14553	158	368	
14468	44836	A	14554	87	251	
14469	44837	A	14555	1	1026	
14470	44838	A	14556	201	578	
14471	44839	A	14557	336	767	AFVRAGSRGGTPGARPDPA TRAPNPVGQSRH\LAASSRGR FLRRTRDRKFP\PRRPLSRRLLG A1\GCRWNQPRAAEKSFSA LDFSPGLSCLPAVQGSGPAARH A*ASHPLHGILCCPSIPDEHHPL LHGAQSHRPPKG
14472	44840	A	14558	6	535	ARHRVLI\GVFTIPELDILSTSPPD SGAQLASPNSDPAPGLQV ELPAS PARCARIPQPLGGRWDW\AQ TQEPSWLHLVEPA PGLQV ELPAS TPCACIPQPLGDRWDWAP PSR GWCSLGRGLGPHRSPWS GWAEAWRAAGPEPCPTGRQLRLGEK SSAAPVGWHCWTQYTLRSH WPGC
14473	44841	A	14559	375	638	
14474	44842	A	14560	92	514	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14475	44843	A	14561	54	380	SCHHYCRIHRRCARFLAGP*LPSRGARLTCSPPCVSLPPAPWAPVRPEPPRAPPAPQRVPSTTQGLRSAGARRGTGRQLHLQLRGSAASFLLKSVRPRTHQFRTH
14476	44844	A	14562	531	773	
14477	44845	B	14563	92	1774	
14478	44846	A	14564	1	390	LHDILQLSKPLSDDTALTQDGG/QPLPARWWAQPGRLQRCARFLAQP*LPQR/WGRARDLQPAQMEPPTPSVGSCAAQASPTSAACPSMAPSPIDHPRAWPVLCFCMLLSLFVASISSCSQHQPMQVGTVMVC
14479	44847	A	14565	165	545	SLHSKLCWWLQQLWVTDTCPRCSVQDCRQRWASAGNQS*RLLVDPAPGLQVELPANPVPCARIPQPLGGRWD*APWSRGWCSSGRQLGHRSPPWSGWEAQAWRAAGPEPRPAGRQLGAMSCKVETGT
14480	44848	A	14566	1	309	SACLAGRPIRGEGRPRDLQPMPEPPTPSMGSCAARASPTSATCSTAPSPIHHSRAEECGHHTALG/HGRQLHLQPRNLPQTINWRRTYS
14481	44849	B	14567	1	843	SFPATLNRLDGGG
14482	44850	A	14568	143	535	
14483	44851	A	14569	375	571	
14484	44852	B	14570	289	972	
14485	44853	A	14571	27	363	
14486	44854	A	14572	2	490	
14487	44855	A	14573	574	961	RLTLPDRLGSPPDTHQAAQQITWALI.PQGFADSPHYFSQAQISSSSITYLGIIHLHENTRALPADHV*LISQTPISITKQQLLSFLGMVRFC
14488	44856	B	14574	182	1513	LWIPSFTILTQPLY*FTKANLADPTDKSFPHSSFRSL
14489	44857	A	14575	894	1305	QTQEPSWLHLVDPALGLQVELPASPVPCARIQPLGG*WDWAPWSRGWCSSGRGLPHRSPWSGEAQAWRAAGPEPCPAGRQLRPGQHPL/RHMNKSQALSLIJAQPLGINLLSWWPPKYNRPVPLIGL
14490	44858	A	14576	531	801	SGLLIPATF

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14491	44859	A	14577	441	783	RAPPPAPWRPVPSTTQGLRSAG EQRGTGRQLHLSAAPVRDPRG EAIWAPESGRSAASILKPARPPA HREERRTPDAPP*EL*HSPRRSA ASLREDPWLHS*SQ*DQEPTNS GHTVSQDQSYY*LEVSETKNP PIPDTL
14492	44860	A	14578	344	1632	FLAGPYLPSHGAGLGTCSLPCL SLPPTPWAPVRPEP/PPMSTTPCS TAPSPIDHPRAEECERTAQDWQ AAPPAAPVWDPGEASWAPES GTNISITPGNATFVTRVQGQAW FASCITGHDMSSLKTSSVVVLR RQSEALLPANLTCNWQDSSAL ATLESALSQVRHKRFTFTLMVF TGSAIDIMATVSIAVVTSITESVQ TTAFVDNLAKNICDELLQDM DEAGNQHSQONNTRTENQTPH VLTHKWELNNENIRIQGGEHYI LGPVGRDEKTLRLRTYCLKSQ EGADTKCRNKHKNKETQKQSKS LVYSSTLNPEKLLVCKRLSLEL TRPENTLRCTNIGKLKAVAGG MSAASGIYLETDTQPYPLKQEL KEIKECVGKNSVVVFLVRKK LSVSQYAFARCLDAKHSTENV EIAGKLRIQSFEVGKQL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, ^=possible nucleotide deletion, ^=possible nucleotide insertion)
14493	44861	A	14579	3	2233	NWLPSSVRSCQETHKIAANQLT QRQMPLTSLYCDVVLPLVSGL ESLQSPYRTSPCDPVSQFCLIK ISASSLPVSLWKTLNKAQSYQ RDYRHNDNAHYFQKLVTMQE NLYVLLCDEELDAVSLEAVHQ QKMKNRQAHSSSGCCQKVAN APRNEESSGGQFRVIGNEKFEKG PCGVRQQIFEKVLLPNRTECFV TPRFNRNFEDLKDLSAAETLID FLVYEPKNQRRLVNRPRLPCKL LHNLLGHPLKTDAASQSPRKP SWMPSFGSKPPSHPPLVSPHLNP QVWDTSPPSLATEHASLTISLKP NHPYPAQSQYSIPQHALKGSKP VITRILLEHGLLKPKINSPYNSPILP VQKLDKSYRLVQHLCIYQIVL PIHPMVPNPYTLSSIPFTTHYS VLDLKHAFFTIPLYPSSQPLAF TWTDPTDTHQAQQITLAVLPQCF IDSPHYFSQAQISSSSSVTYLGIIL MKTHIGLGAVEQGVVLLVGEAR AAQEPMEWVGSGSM/CGLQVP SPAPWEGS*GPARNRAQ\PTVIV PVLDFNPAFHIIIPDTTPDHHDCI SLIHLTTFPFPHISFFPVPHLEHT WFIDGSSTRPNCHSPA KAGYAI VSSTSIIEATALPRSTTSQQAKLI AYTDSSKCAFHILHHHHAVIWEER NFTLTMQGASIIINAFLIKTLKDI LLPKEAGVIIHCKGHQKASDPIT QDNAYADKVAKKQLAFQLLSD
14494	44862	A	14580	1	642	SGTPPTFVRTVIAQAGARTV QQSLIGSLYIFRHCVRCQGIESV FVIIWRSRVGYDEKGFCFLFTSVL GVWGHVRTKPCLLITWRTLKS RSGLE*PAGFSSSPGTSPQIIRKQ KRGVPQHPVCDLPGFRPRAGT PLAAQIQVPGLPPCGHQE*NRR WAGSSALCPYLCARAGTGA CRACEPAGV/AGWA WAWWAP HSEHAASPGRQWGT
14495	44863	B	14581	393	549	
14496	44864	B	14582	1	591	
14497	44865	C	14583	226	828	
14498	44866	A	14584	1	1362	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14499	44867	A	14585	1	585	MANVHQTMPMRLRKLPDSFKP PEPKSNSQRVSTEAGTAGALTP QHVRRAHSSPASLQLGAVSPGTL TPTGVVSGPAATPTAQHFQQSS FEIPDDVPLPAAREMAKTSGQ RYFLNHIDQKTTQQDPRKTM SQMNVIANPPVQQNMNSVQPS PQGGVIMGGNSNQQRQMRPQ QLQMEERLQLKQQ*LLQQELA LR
14500	44868	A	14586	345	1053	RWRLQNLSCFCSSCSGSGSEGAT CFARGRQQSNLQSFKIKFPSNTD SRSTGYNSSFDRQPNCFYKRQE TPHTGPPIPVPPEGRPYPMPC*CG A*SPGPFFASRN*SEKN*SYKCSL HTAFNVIFSSV!*RYCTRQW\HI VKCLDSFCDPFLISDELRRASTD AGTAGALTPQHVRRAHSSPASLQ LGAVSPGTLPTGVVSGPAATP TAQHLRQSSFEIPDDVPLTSW GEAKTSSGSKIPF
14501	44869	B	14587	607	1185	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hind	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
14502	44870	A	14588	1	2142	MIILIDAEEKAFDKIQQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNQGKLEAFLPKTGTTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGQLGKEEVKLSLFAADDMLY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLNLKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDPNVNDKL MVLEVLRALARQKKEIKGIGLQ KEEVKLSLFADDMLIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPILLKEIREDTNWKWKNIP CSRIGRINIMKMAILPKVIYRFN DPIKLPMTFFTELEKTTLKFIW NQKRCIAKTIILSKKNIAGGIFT PDFKLYYKATVTKTAWYWWY NRDIDQWNRTEASEEVTSYHINH LIFYKPDKNKKWGNDSLNFNKW CWENWLAICRKLLKLDPLFTPTY KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGHMGKDFMTKTPKA MATKAKVDKWDVIKLKSFC KETTIVRSRQPTWEKIFAIYPS DKGLISRIYKELQVYRKITNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMGIQKTTM
14503	44871	B	14589	1	1647	
14504	44872	B	14590	1	2025	
14505	44873	B	14591	4	2121	
14506	44874	A	14592	2	1879	
14507	44875	A	14593	1	2130	
14508	44876	A	14594	1	3018	
14509	44877	B	14595	1	3171	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14510	44878	A	14596	1	2700	MEKKQSRKTGNSKNQASPPP KECSSLQATEHSMENDFDEL REQQFRRSNYSELKEEVRTHGK EVKNLEKRLDEWLTRITNAEKS LKDLMELKTMARELLDECINLS SQFDQLEERVSVMENQMNEMK PNLRLIGVPESDGENTGKLENT LQDIIQENFPNLRQANIQIEIQ RMSQRYSSRRAIPRHIIIVRFTKV EMKEKMLRAAREKGRVTLKG KPIRLKADLSVETLQARREWGP IFNILKEKNFQPRTSYPGKLSFIS EGEMKSFTDKQKLRYFVTRP ALKELLKEALNMERNNRYQPL EKQIQTIREYYKHLYANELEN LEEMDKFFDTYTLPLRNQEEVE SLNRPITGFEIEAIINSLP/TKKSP EPGGFTAEFYQ\RIEKEGILPNSF YEASILMLKPGRDTTKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHQDQVGFIPGMQGWPNIR KSINIQQHINRNTNDKHNKIIISDA EKAFYKIQQQPMLKTLNKLGIID GSYLKIIIRAIYDKPTANIIQNGQ KLEAPPLKTGTRQGCPPLSPLLF NLVLEVLRALARQEQEIKGIQLG KEEVKLSLFADDMVYLENPIA SAQNLLLKGNFSKVSGYKINV QKSQAFLYTKNRQTESQIMSEL PFTIASKRICKYLGQLTRDMKDL FKENYKPLLNEIKEDETNWKWNI PCSWEGRISILQMAILPEVIYRF
14511	44879	A	14597	1	2310	
14512	44880	A	14598	1	1305	
14513	44881	A	14599	1	2148	
14514	44882	B	14600	1	777	
14515	44883	A	14601	2	2971	
14516	44884	A	14602	1	3810	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
14517	44885	A	14603	1	1773	MNIGAKIINKILANQIQQHIRKILJ HHDQVGFIPGMQGWFNICKSIN VIQHINRTKDKNHNMIISIDAEKA CDKIQQRFLMLKTLNKLIGIDGKY LKIIRAIYDKPTANIIHNGQKLE AFPLKTGTRQGCPSPLLFNIVL EVLARAIRQEKEIKDIQLGKEEV KLSLCADKMINVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNRQTESQIMSELFPFTA SKRIKYLQIHQTRDVKDLFKN YKPLLKEIKEDTNKVNIPCSCSVG RINIVKMAILP/KELEKTTLKFIW NQKRARIKTSILSQKNKAGSIM LPDFNLYYKATVSKTAWYWY QNRDIDQWNRTEPSEITPHIYN YLIFDKPEKKNQWGKDSLGNK WCWENWLAICRKLKDPLLT YTKINSRWIKDLNVSPKTIKTLE ENLDITIDIGMGKDFMSKTA AMAAAKAMSTKAKFGKWDLIK LKSFTCAKETTIRVNRISSYASS STSLQAFSRKILNCSKRFKIAQ MCKLVELRPQDMHTSRGSGNC SEARTLLCDFSAGRTSVNHGRI WRQIREAGAADPEIGLEVCNKN PTSFTLFYFLSYTTG
14518	44886	B	14604	1	2070	
14519	44887	B	14605	1	3190	
14520	44888	A	14606	1	3370	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met box	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
14521	44889	A	14607	569	3030	RKH*TWKRTSSTSHHKNMPN* LEKQEQT/SKPSRREITKIRA ELKEIETPKTAQKINESRSWFSE RINKIDRPLARLRLRKKREKNQI DTIKNDEGDTITHPTIEHTIIREY YKHLYANKLENLEMDMKFLDT YTLPRPNQEEVESLNGPIAGSEI QAIINSPLTKKSPGPDGFYQRYK EELVPRFLKJ.FQSIEKEGIL.PNSF YEASILIPKPGRDTTKKENFRP SLLNINAKILNKLILANR1QQH KLMHHDQVGFIPGMOGWFN KSINVQHINRTDKDNHMIISID AEKAFAKQIQQPFMLKTLNKLGI DGTYHKIIIRANYDKPTANII QKLEAPLKTGTRQGCPPLSP FNIVLEVLRALARQEKETEGIQL GKEEVVKLSLFADDMMIVYLN VSAQNLKLISNFSKVSGYKIN VQKSVQFLYTDNRQTESQIIS PFTIASKRKYLGIQLTRYVK FKER/YNEIKAEDTNKWK NIPCSWVGRINIVK MAILPKVIVYRFNA SIQLPMTFFTELEKTT LKF1W NQ KRAHIAKSILSKKNKAGGIMLP DFKLYYYKATVTKTA WHWYQN RDIDQRNRTEPE SEIMPHVYNH LIFGKPD KQWGN DLSL FN KWC WENW L WLA I CK KKL KLD P L PTY T K T L E EN LG NNI QD IG MGK D FTS K TP KA MAT KDK I DK W D L M K L K S C T A
14522	44890	A	14608	1	2742	
14523	44891	A	14609	1	3828	
14524	44892	A	14610	1	2667	
14525	44893	A	14611	1	2325	
14526	44894	A	14612	1	3057	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mol. wt	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14527	44895	A	14613	603	2973	DNTARGTIRQQHLLFTNIRCSA ASAADTQANRQVWSGPANSNR PAAIRVLTVRKTKQKGHPH QNPICTPSSKIKETQTTIREYY KHLYANRLENLEEMDKFLDTY TLPRINQEEVESLNRRITESDIE AIINSLPTKKSPGPDGFTAEIFYQ RYKELVVPFLLKLFQSIEKEGIL PNSFYEASIIIPKQLGRDTTKKE NFRPLSMNIDAKILKILNANRI QQHIKKHHGQVGFIPGMQGW FNIRKSINVIQHINRFTNDKNHMI VSIDAEKAFAFDKIQQQPMLKTLN KLGIDGPYLUKIRAIYDKLTANII LNGQKLEAPPLKGTGRQGCLLS PLLFNIVLEVLARAIRQEKEIKG QLGKEEVKLCLFADDIMIVYLE NPIVSAQNLKKLISNFSKVSGYK INVQKSQAFLYTNRQTESQIM SELPFTIASKRKLYLGQLTGDV KDFFKENYKPLLNEIKEDTDKW KNIPCSRVRGRINIMKMAILPKVI YRFNAIPKLPMTFTTELEKTTL KFIWNQKRARIAKSILSQKNKA GGITLPDFKLYYKATVTKTACH RVGRAQQHSISKWKWYIHDWS QVGPEGTNDSDARYPDTTQKWT AAALQPLSRTSLKDHSIEGKSSQ WAEELRAVHLVLRFAWKEKWP DVQLYTDSSWAVASGLAGWSG TWKKHDWKIGDKEIWGRATPV IAQWAHEQRGHGGRDGDYAW
14528	44896	B	14614	1	3105	
14529	44897	A	14615	1	3654	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
14530	44898	A	14616	735	2839	RSFPRSRPSPFLLSRYLRIHMVFSQLPGLQNPKYLLSGSLQEKFRTPGINSHKTLDPNRVIKVRRLREKEKALRAYVGKSEVRNMHLRERCKL*KKREKNQIDTIKNDKGDTTDATEIQTITIREYYKHLYANKLENLEEMDKFLDTYILPRLNQEEVESLNPITGSEIAJINSLPTKRSGPDPGFTAEFYQTYKEELVPPFLKLFQSSTEKEGILPNPSFYEASIIIPKPGDRDTTKENFRPISLMNIDAKILNKILANRQHQHKKLIHYDQVGFIPGMQGWFNKRKSINVIQHINRNTNDKHNMIISDAEKAFDKIQQPQFMLKTLNKLGDGTYLKVIRAIYDKPTANIIILNQKLEAFPLKTDTRQGCPLSPLLFNI VLEVALARAVRQEKEIEQIOLGKEEVKLSSLFADDMIVYLENPIVAQNLLKLISNSFSKVSGYKINIQSQAFLYTNNRQTESQIMSELPTFTASKKIKYLGQLTRDVKDLFKENYKPLLNEIKAEDTNKWKNPICSWVGRINIMKMAILPKVICRFNAIPIKLPMPFPTELETTTLKFIFWNQKRARIAKSILSQKNKAGGITLPDFKLYYKATVTKTAWWWYQNRDIDQWRNRTPESEITPHIINYLIFDKPEKMSIIDTGGWYEAPVSSFFKEGLCRTGTENQVRNQPPAASPFKVVVSCTGSLSLHPRHYFLE
14531	44899	A	14617	I	2250	
14532	44900	A	14618	I	2870	MKAEIKVFFFETNENKDTTYQNLWDTFKAVCRGKFIAALNAHKRQERSKIDTLSQLKELEKQEQTHSKASSRQEITKIRAEELKEIQTQKTLQKINESRSWFFERINKIDRSLARLIKKREKNQIDTIKNDKGDTTDPTEIQTITIREYYKHLYANKLENLEEMDKFLDTYTLPRLNQEEVESLNPITGAEIVAINSLPTKKSPGPDPGFTAEFYQSWAETQPKKENFRPISLMNIDAKILNKILA KRIQQHKK

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, -=possible nucleotide deletion, + =possible nucleotide insertion)
14533	44901	A	14619	248	2623	RQWAGVVGRCSHLASWVSSNT SETGAIRSSTEVDPDDSMLLST CDIDLTAARRAWLGCLPTKKSPP GPDGFTAIFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDDEASILIL PKRGRDTTKKENFRPISLMNID AKILNKLILANRNQQHIKKLIIHH DQVGFIPGMQGWFNICKSINV QHINRRTDKNHNMSIDAEGKAF DKIQQQPFMLKTLNKLIDGDTYL KIIRAIYDKPTANIILNQGKLEAF PLKTGTRQGCPPLSPLLNIVLEV LARAIRQEKEIKGIGLQGKEEVKL SLFADDMIVYLENPIVASQANLL KLISNFSKVSAKINVQKSQAF LYTNRNRQTESQIMSVPFTIAS RIKYLGIGQLARNAKDLFKENYK PLLNEIKAEDTCKWKWNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFTTELEKTTLKFIFIWNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITYVTKTAWYWWYQNRDIDQ WRNTERPSEITPHIYNYLIFDKPE KNKQWGKDSLNFNWKWCWENWL AICRKLLKLDPLTPYTKIHPRWI KDLNVRPKTIKTLLEENLGNTIQ DIGMGKDFMSKTPKAMAACKA KIDKWDLIQLKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKEKLQIYKKKTNNPIKKW AKDMNRHFSKEDIYAAANKHM KKCSPSLAIREMQIKTTMRYHL
14534	44902	A	14620	I	3253	MGDFNTPLSTLDRSTRQVKVN DTQEALNSALHQGDLIDIVRTLH PKSTEYTFSPAHHTYSKIDHIV GSKALLSKWKRTEIITNLYLSDH SAIKLELRIKNLTQSRSRTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDPTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQKLEKQEQTHSKASRRQE ITKIRAELEKIEETQKTLQKINESR SWFFERINKIDRPLARLICKKKRE KNQIDTIKNDK
14535	44903	B	14621	I	2758	
14536	44904	A	14622	I	5178	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=-Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14537	44905	A	14623	1	3382	MGDFNTPLSTLDRSTRQVNKDTQEFSALYQADLIDYRTLHPKSTEYTFSPHHTYSKIDHIVGSKALLSKCERTEITNYLSDHSAMKLELRINKNLTQNCSTTWKLNNLLNDYWVHNEMKAEIKMFFETNENKDTTNQNLWDAFKA VCRGKFIALNAHKRKQERSKIDTLSQLKELEKQEQTHSKASRRQEITKIRAELEKIEETQKTLQKINESRSWFFERINKIDRPLARLIKKREKNQIDTIKNDK
14538	44906	A	14624	965	4091	TWKGTTTSRCKIMPKYRSTRQKVNKDTQELNSALHQADLIDYRTLHTKSTEY/TFFSAPHTYSKIDHIVGSKALLSKCKRTEITNYLSDHSAIKLELRINKLNQNSRSTTWKLNNLLNDYWVHNEMKAEIKMFETNENKDTTYQNLWDAFKA VCRGKFIALNAHKRKQERSKIDTLSQLKELEKQEQTHSKASRRQEITKIRAELEKIEETQKTLQKINESRSWFFERINKIDRPLARLIKKKREENQID
14539	44907	A	14625	3	3229	
14540	44908	B	14626	1	2791	
14541	44909	A	14627	1	3158	MVKGSIQQEELTILNIYAPNTGAPRFIKQLLSDLQRDLDSHTLIMGDFNTPLSTLDRSTRQVNKDTQELNSALHQADLIDYRTLHPKSTEYTFSPHHTYSKIDHILGSKALLSKCKRTEITNYLSDHSAIKLELRINKNLTQNSRSTTWKLNNLLNDYWVWRKQERSKTDTLSQLKELEKQEQTHSKASRRQEITKIRAELEKIEETQKTLQKINESRSWFFERINKIDRPLARLIKKEKNQIDTIKNDKG
14542	44910	B	14628	1	7849	
14543	44911	A	14629	1	3985	MENDFDELREEGFRRSNYSELWEDIQTGKEVENFEKLEECITRITNTKECLKELMELKTKARELHEECRSLSRSCDQLEERVSAMEDEMNEMKGEGKFREREKIRNEQSLQEJWDYVKRPNLHLIGVPESDGENGTKLENTLQDIIQENFPNLARQANVQIQQEIQRMMPQRYSSRRATPRHIIVRFTKVMEKEKILKAAREKDRSTRQVVKNDTQELNSALHQADLIDYRTLHPKSTEYTFSPHHTYSKID

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14544	44912	B	14630	64	5735	
14545	44913	B	14631	891	6894	
14546	44914	A	14632	33	476	
14547	44915	A	14633	1	360	GQGEPKQLGRHPGVLRPHVVSAKTGDAC/IWTQVRNLFLPERPKVQWKEGCA\LSQSGNSQESVTEQGSKVSAYSLSSPLTLSKADYEKHKLYACEVTHQGLSSPVTKSFNRGEIEGEVPPCI
14548	44916	A	14634	40	508	LPGECHRAQQQQQLPQLLGLLMLWVPGSSGEIVMTQTPLSSSVTLGQAPASISCRSSQSLVHSDGNTYLTWLQQRPGQPPRPLIYHVFKRFSGVPDPRFSGSGAGTDFTEI/ISGRVEA*DVGVYYCMQG\TQFPCSFQGQTKLETKRTVAAPS
14549	44917	A	14635	3	652	AWWNSETPAQLLFLLLLWLPYTSGEIVLTQAPGTLSSLSPGERATLSCRASQTIGSTYLA\WYQQRPGQAPRFLIYGASSRATGIPDSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSQQYNNWPPGGTFGP\GTKVEIKRTVGCTHILFFIFPAHLMQLKWIELPSACVPVCNNF\VPREVSYSQGKVDN/VPSNRVTPRESVTEQDISKDSTLQPSAATLDA
14550	44918	A	14636	3	440	
14551	44919	A	14637	457	1270	SRRVSFPPSA*QAVSDPSRQQLPSSLRLRWGPEGRSPFAENLGRGVRWVGGRDPLAALP\SSGLPNA GRLFARPOESGAPRIGNVRDVP RAREDVTGQAGRERREREPRFLG PAAVGGERHLSPPFRAAGAGGRAGAAGRSAPPGLGSCRSCRISAGPHGNDVPTLGGRGW/PL*NSGAEKL*EQ*G*/TGTGSWSLAAILGGVPREP\GFRGAGRETLGPRGLWVMLSRAVLLHSVLCLCTHSSWWLLHSIDLACHADNNPDIQSCLFPMMSKY
14552	44920	C	14638	90	465	
14553	44921	A	14639	116	439	
14554	44922	C	14640	278	364	

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14555	44923	A	14641	116	687	EIKDAALQLPLWRAQDRERAM KERREKRREREKERDREKKRK EKMFCKRSCHTMEPTPELSCV LPCLAPIVLAPPPLPL\PVLPV ATR*LPQQRQSTL\TEAHGL\TR GPITLATNRCMPSTTRDRRRLT PPSTLPNTTNTLSWGVRREGPNQD PEPSLSPCVPHDPPDYNAESLFS YWLVSVTPMTAHTP
14556	44924	A	14642	474	1166	HPNRQGLRAPATAPGHPGREQ ALCEAPQGPQGKCGPRAQE Q/GTEPRASRAAGACRHHWP QVAIRPGAGAPAGAARLGGV*E PGRAAA/APRLPLPSQCCHR*GTS PAHLSASRSSSATCPWRRTAGR SGSPCMTLKQROQHPRDGW RAPSCDVTNRGLSSLNLGGSA QQLLLASRPLGGSGGAALEAH GKSAPLPWEPWLHGTHNPVHGK DPAGTSHWPRPPAPRT
14557	44925	A	14643	283	806	PRGSFSSTGRTRNAAGSTSNC RSLSARIEERKVSRVCGVPNHR HRLRLGALTTRPSWNGAIP KLPKRC*RRSGRRSKTWS PGT*LGNAEEMICASARPAGV PGPALPTPLRAPLPGVPWTSSR GRMCARLSCC/HAGRPVPARPG AARARRAAAGERHRPPALRV
14558	44926	A	14644	1	338	
14559	44927	A	14645	1	1091	MSNDGRSRNRDRRYDEVPSDL PYQDRTIRTHPTLHD SERA VSA DPLPPPLPLQPPFGPDYSSDT EEPAIAPDLKPVRRFVPSDWKN FFRGKKDPEWDKPVSDIRYIS DGVECSPPASPARPNHRSPLNS CKDPYGGSEGTFSSRKEA PRDPYGSLDRHTQTVRTYSEKV EEYNLRYSYMKSWAGLLRILG VVELLLGAGVFA EWYNLFGYSQPYGMGGVGGL GSMYGGYYTGPKTPFVLVVA GLAWITTHILVLGMSMYRTIL LDSNWWP AAAISLM*MPTRGGCLCYPLF NTPVNAIGSAG*KEDR*LQ*SSC LSP**FISLVLWFA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ind	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14560	44928	A	14646	398	1107	SPGLVCGLLIFCKTVPIAGPY RCPFGGLRH*SAR*QPPSGLREN GARPPGEWLCP*FPPP*PLNSR WKLPPRLVT*GEPWAAGEKFP RLGACTGPAAGEGLPRARDWE PGRAGPERWAPGRGPAGTPAK TAAVKRSAPLPGS\GDYANGER KPPPSFCQVKSGNL*VLCG*RL SLPAA*KPKKA*RRGRQRQSPGK TGYQVQQTQPKNDPKSS\GPSP KNRQSLCLQPLWFLQI
14561	44929	A	14647	1	540	MGVRDPLEEAVCALAEIQLHCA GRFAALFRASRQERLSSLKLCP QLPLPPRALSQGYKPLIG\LLAF FQRCTAQRGGI*RGSLATVTL\ S CGGLCPV*TSQRCL\ PVRGLP TQASVMANAPPRTQLQHRLRSTS DCCAGSENFKPVDSLSSLGSGVG GSTEALDHLPWLOPAFQGSEW FYLTF
14562	44930	A	14648	169	487	EVCVYPPSETYFCQFVKLILCPV LFPCWQGVVIQPKLSCMRLCLST \LLRGVSQ*GYMGVRDPLEEAV CPLAELHEHAGRSAALFRAGRQ ERLSLLKLRPQLPLSPSA
14563	44931	A	14649	1	210	
14564	44932	B	14650	1	1683	
14565	44933	A	14651	1	529	MDSEVQADDEVSDENGELIGN WGKGGMGVSDPSEEAVCPLAE LERSAGRSAALFRASRQECLSL LKLTLTAAAPSPRGTAFRSPFKS PAQRSSII*Q/LYSCKTFRSTVA PMPRLCLPQASGKVQ*EN*SWA IPA*QGTSPPMCSLCSGAPHQPG APLVPLPLPPVNRLLRRELQCWL
14566	44934	C	14652	295	430	
14567	44935	A	14653	452	637	
14568	44936	A	14654	151	446	MVLSHWHSRCHWGMKKNYLQ LARCLPKWLPSFVFETQGPCDV STQGTLVYGLQRPWEKHSI*A R*HHPSQHGPSQLPLARGSSP TPCASRMQRQHPT
14569	44937	A	14655	2	335	EDRSAFRPRQPHTLHPLHARSL APRSPTPPSPSPDTQLGLSGPTS GPESAPTA/PGNPSWRSSRWGSS SPCAAASST*KSPYP*/CSPT/CAFP SPRLPFCRSAYQPAAGAGRK
14570	44938	B	14656	373	502	

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14571	44939	A	14657	1	400	GSPAPAAAMDEERALYIVRAGE AGAIERVLRDYSDKVKSPGPGR AVSHPRAALRACTSHSPPPPSFR GCALVPPPKTFPAWACVFVPPAF SIHAS/SHPTPTVAPTPLIPGPA A*PPVLLSSVQVTTPESVDVHL
14572	44940	A	14658	659	1177	ARKGSALLRLYLSNAWCVCVK VLRIFSTASAYITRDRSSLGPVW TFLNFSFGSPGEIPTFFFFPVFP LPLVAWFCPASFCLPQCP\LVPS EPSPPPHSGDAHCSPPKTFPAW ACVFVPPAFSIHAS/SHPTPTV APTPLIPGPA*PPVLLSSVQVT PPESVDVHLCVPVHS
14573	44941	B	14659	1	318	
14574	44942	A	14660	2	131	
14575	44943	A	14661	354	762	CPEIRPPS*THGTK/SHFPTTASG THSVLEAL/PDTQRQSPRVRHQ DPSPA/IALLPSPEHGHPQHLL QLPSHRCHPDATAPFNCDAVKAC PGHATAALEHPYLSGRQSPPSP THLPKLPAGRGYTVCAALPKPG ERSAV
14576	44944	A	14662	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRNCWRGC GEIGTLLHWCWLDCKLVQPLW SVW*FLRNLEIIPFDPAIPLL
14577	44945	A	14663	1926	2448	DFIAVITTRQQLTKYNAHHSK QAITKHFSPKISDLILCLKKIM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTTPVRM AIKKSGNNRCCRRCGEIGTLLH CWWDCKLVQPLCKSMWRFRLR DL\DPAPILLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTNQF
14578	44946	A	14664	1	1584	
14579	44947	A	14665	1	4729	
14580	44948	A	14666	1	1566	
14581	44949	A	14667	1	1424	
14582	44950	A	14668	1	576	
14583	44951	A	14669	1	3325	
14584	44952	A	14670	1	2195	
14585	44953	A	14671	1	3162	
14586	44954	B	14672	287	2018	
14587	44955	A	14673	1	1073	

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14588	44956	A	14674	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVQLSDLQRQLDSHTLI MGDFNTPLSLDRSTRQVKVNK DTQEELNSALHQADLIDITYRTLH PKSTEYTFFSAPHHTYSKIDHV GSKALLSKCKRTEIIINTYLSDHIS AIKLELRIKNLTQSRSTTWKLN NLLNDYWVHNEMKAEIKMF ETNENKDPTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEIETQ
14589	44957	A	14675	1	1838	MIIPIDAEKAFDKIQQQPFMLKTL NKLGIHGMYLKIIAYDVKPTA NIILNQQKLFAPFLKTGTRQGCP LPPLLFNIVLEILARAIROQEKEIK GIQLGKEEVKLSLFADDMMIYLE NPIVSAQNLKLISNFSKVSGYK INVQKSQAFLYTNNRQTESQILS ELPFTIASRKIYLGQLTRDVK DLFKENYKPLLNKEIDETNKNW KNIPCLSIGKINIMKMAILPKVIIY RFNAIPKLPMFTFTLEKTTLK FIWNQKRARIATILSQSKNKG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTPESEIIPHV YNHLIFDKPDKNKKWGDKDSL NKWCWENWLAICGKLKDPFL TPYTKINSRWIKDNLVRPKTIKT LEENLGNTIQDIMGKDFMSKI PKAMATKAKIDKWNLIELKSC TAKETTISVNRQPTEWKIFAI LSDKGKLSRIYKELKQRHKKKT NNPIKKWAQDMNRHFSKEDIY AANRHMKKCSSLALIREMPIKT TMRYIILTPVRMAlIJKSGNNRC WRGCCEIGTLSHCWWDNCNLVQ PLWKAVWRFLKDLELEIPFDPA ISLLG/YPKDYKSCCYKDTCTQ STFTCRQHPL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
14590	44958	A	14676	1	2354	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDIVYRTLHP KSTEYTFSSAPHRTYSKIDHLV GSKALLRKCRTEIIINCLSDHS AIKLELRKIKLTQNHSSTTWQLN NLLLNNDYVVIHNEMKAEIKMFF ETNENKDTTYQNLWYVVKDTRI SGMLWVVKAVCRGKFAILNAH KRKQERSKIDLTSQLKELEKQ EQTHSKTSRQRQETKIRAEELKEI ETQKTLQKINECRGKFAILNAH DRPLARLIKKKREKNQIDAIKN DKGDIIDPTEIQTIREYYKHL YGNKLENLEEMDKFLDTYKLP RLNQEEVESLNRPITGSEIEAIIN SLPTKSPGPDPGFTAEFYQRYK EELRIKYLGIQLTRDVKDLFKE NYKPLLNIEKEDTNKWKNPICS WVGRINIMKMAILPKVIVYRFNA IPIKLPMIFFTELEKTTLKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMLHIYNHL IFDKPDKNQWGKDSLFLNKWC WENWLAICRKLKLDPLIPTYK INSRWIKDLNVRPKTISLEEDL GNTIQDIMGKDFMSKTPKAM ATKAKIDKWDLILKLKSFCATAKE TTIRVNQPTEWKEFAIYSSDK GLISRRYNELKQIYKKKTNSPIK KWTKDMNRHFSKEDIYAARKH MKKCSSLALIREMQIKTTMRYH
14591	44959	A	14677	1	3144	
14592	44960	A	14678	1	2745	
14593	44961	A	14679	1	2742	
14594	44962	A	14680	1	3264	
14595	44963	A	14681	1	2982	
14596	44964	A	14682	1	3102	
14597	44965	A	14683	1	1443	
14598	44966	A	14684	1	3723	
14599	44967	A	14685	2	1841	
14600	44968	A	14686	572	744	DLLTTIRMPPTDVKKCSSSLAIRE MQIKTTM*YHILTPVRMPIIKKS GNNRCWRGCGEI
14601	44969	A	14687	1	3588	
14602	44970	A	14688	1	5569	
14603	44971	A	14689	1	3992	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14604	44972	A	14690	755	2415	QELRVSGWSPASAPANT*CPPA QPCPTRRSGGQRAPARTSRPG SRPRTASALPRPAA(QKAARSRA RASRTPYTAGKPLPSVESALQ EAAIGEAHAQQRVSCCTAAAPA APPSPAWPWSAARSAAPPRT* ASAPA*SPL/PVRLKKSPGSSNC EARGEGLWKT/PALPVQLGAHGP PQPAAVPCASPAGPGRWSRS ARRTPRGLPLQRGRTWVSPDGR EATPSGTQWPQKTRGSLPGS*C APETPCSAA*SSGTSPPRGAGGC CPGTVPPALEGHN*PQRWGSHS AGRVEVTRAEGPQCQGAPAGC SLGVGGQRGPPGLPPIPVPGLC* TCRSS*MEAATGSVEKKRMA SLMQASRWSFLRVAPVSGQVK YTPGATARWAEPSSLGSDTTLVP GAS/RAPADGGFGLKFLSHLVS DGVLRCGGPRPGTASAPAGLR AAAAAPSVPSLVPGPWRGGLGAG WLGFLSWAFSPTDLSF*PGPA LLNLMSALNS*KNFFMVAARS CGGGTRGRGGTGPGRGRRRR PATGRK*KKKKKKKKFTSPPEV PPSPGLPRDNRL
14605	44973	B	14691	1	822	
14606	44974	A	14692	1	2789	MAAVRKQLPREGVLGYGGSGAL LSTAADTSLLLGSQERKSAS AGPGYLRSSVAWSGLWLTGA SEAHSSVVLACFSRKDVEASLV GLPVHPDASCARRLDAADGVA GGSPRLPQSTDGWRLTAHSLPQ STDGWRLTAHSLPPTDGWRL TAHSLPQSTDGWRLTAHSLPPP TDGWRLTTHSLPQSTDGWRLT AHSLPQSTDGWRLTAHSLPQST DGWRLTIHSLPQSTDWRLTA HSLPQPMGDWSCRSAQWCV
14607	44975	A	14693	176	440	
14608	44976	A	14694	114	253	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptidc sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
14609	44977	A	14695	124	890	GSRAWRDPRLLEVAATTLFY GYGFVSAELKKASKRMTCHKR YKIQKKAPEHHRKIRGEAKKR GHNKPRKDGPVPNSAP FKEAL  LREALRKQRLEELKQQQKLD RQKELEKKRKLET*SWIFKPSN V DPMEK FPGLCRKTEVNKAIRSG KQNSKKLYCQE KKVIEASDV VLEVL DARDPLGCRCPOV EEA  V QSGQKKLV /YLNKSDLVP KEDLIESWLKLF*RKDLPNSGCF RASTKTQRVKGKITKVFSIS
14610	44978	A	14696	553	997	EVTACWQSSQPSLTLGASSAW APTLAALEEPFSPLHCGSPFLG WPRLEAPSAPPWAPVRPEPPQ QGPPSAPGRPIPSTTQGLRSADA GRRGTQLHRQPAKVCASF/IS* QRDHEPTRRNEQLQTRRLKSCN THREDLQLHSRRKLI
14611	44979	A	14697	1410	2036	
14612	44980	A	14698	3	630	RYKGSPRPHQTQEPWSLHLVDP APGLQVELPASPAPCARIRQPL GGRWDWAPWSRGWCSSGRJLG QHRSRWSGWEAQAWRAAGPK PCPAGRQLRPGEKSSTAPVGRH CWGIQYTLRSHWPGC*VPHSSG PAGLAGCSTGPAQPAHAA VPARA/CSLHTSLQAEVGSSL GQPRKGLPQCRWGLKGSSNAA KVGAAQAGEVQARALRTAS
14613	44981	A	14699	190	383	ASHPLRGLRSGRSLPDERHRLL HSAQSHRPKG*GVRAQGAGL T/WQLH*PQCGIHWWVKPAGLL
14614	44982	A	14700	1	1095	
14615	44983	A	14701	1	777	
14616	44984	A	14702	1	933	
14617	44985	B	14703	1	996	
14618	44986	A	14704	978	1207	ASLPLRGLLCCPSLPEERRPLH GAQSHRPKG*GVRAHGAGLA/ WQLH LPRRCGIHWVKPAGLLS LGPHQQSSKSA
14619	44987	A	14705	111	558	

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14620	44988	A	14706	1	1103	MKPWALKVSVTALKVARLEFPDVRCMSEFLPCGVKLQLTFAVSVTALKAAARLEFVSPGGLVVS LASGVKLQTFFPVSVTAHKSSVD PRSEQQQDQLLQRAKEQTFHTVE GDRSGSPPDSGAQLASPSSGSRTRAAAGAACQSRALRPHSSALG WSMGLGAVEQGAVLIREARAAHEPMERVGSSGMAGCRSLALP REKAAKARRETEGSAAVSGWL SGIAQWPKIDHEGFRAVKMPQAAWLKAVTFIDLTLSGDDTS SNIQRLCYKAKYPIREDLLKALNMHDKVAAGFPAGQTHLKTRL EEIFLAVEDGATEIDVVINRSLVLTGOWEG/LYSPPVYSLPCN*HSRFLPSGNALLLWLWCLHS
14621	44989	A	14707	2	2300	
14622	44990	A	14708	2	1058	ARSNIRMVTAFRSLPAGSSGAA RAIMSAHNRGTELDLWSIKIQVNHPAVLRRAEQIQRRTWK KDWQAAWLLKAVTFIDLTTLS GDDTSFNT*RLCYKAGYPIREDL LKALNMHDKGITTAACV\YP ARVCDAVKGTSRPA/CVNIPV GISRAAGF\PAGI\QTH\LKTRLEE\RLAVEDGSLQKIDV\VINRSLGA*QAQWE\ALYDEIRQF\RKAC GEA\HLKTILAITGELGTLTNVY KASMIAMMAGSDF\IKTSTGKE TVNATFPVIAVMLRAIRDFWK TGNIKGIFPAGGIRSAKDSLAW LSLVKEELGDEWLKPELFRIGA STLLSDIERQIYHHVTGRYAAY HDLPMs
14623	44991	A	14709	576	998	VLQFLKACCPFVPSGVPMCE YLPSGGFVVSLASGVKLQLTFPV SVTALNRLLELFVPPGLMVS LASGVGSCRSSR*VQLIKA VWT QRPLGGRWDWAPWSRGRSFG EARAQQKPMEGVGSSGMAGCRSRSPAPREGS
14624	44992	A	14710	2	589	RHHPRHAVQARPFPAGPLAGA QRGSGA*RGPOQSPVPGAGLS GGESLP\GETDRGADKEERGRQ RWQRALGRLSAGADPLPAELR GRRQRRGR*AGQRAAQEAA CAPIQGSGARNGRRG*GRRL*GC YQ*V*FPGLTRGWWGRSRPSAV HCGWEPP*AGKPSGQTPRHSG* PAGIVVDGLPPKVTGPPGTPQPR

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14625	44993	A	14711	1	1596	MRLTRCQAALAAAITNLNLVLF YVSWLHQPRNSRARGPRRAS AAGPRVSLPPHPLTCVWRCSPR AMDRPPAASRPETTVATEFVAL VLDGARAEAHALLERMVEALR AVSARLVAAPVATANPARCLA LNVSLSREWTAHYGAAPAAPRC DALDGDAVVLRLARDLFNLSA PLARPVGTSFLQLTALRGWAV QLLDLTFAAARQPPLATAHAR WKAEREGRARRSALLRALGIRI VSWEGGRLEWFACCNKKNQRC
14626	44994	A	14712	225	980	VPSRTWAELYRTRFPVHSLGQPR SSHIPQSPQTDQTAQGQQQALAP PAGRSQQ*GRPGRRARLGPGER HS*APPPLSQLLLQTFPHLQALP SAHARPSGQPHADRGHHSRSPSG /DLSTSSSVLKVVPRQAGGPQKA RCPQAGRVCCHCPRGRRGPE/Q Q/GG*RPEAPQASPEKGSTGLRP SAKDSKNQGTGIFLRCQVAPR EALCCPPPRGADTPVSPCLWVA GAGIPLQPPEGAEGAVGLSLCT LCPGSPDSPPTS
14627	44995	B	14713	405	893	
14628	44996	A	14714	178	499	
14629	44997	A	14715	231	436	
14630	44998	A	14716	141	393	
14631	44999	C	14717	97	351	
14632	45000	A	14718	119	358	
14633	45001	A	14719	21	614	PPCTSLRPLHAFSGKMTHLNRG TLSLLDSQLHNLLALQMTCFKD VEIPNFFWEPSVTPTSHRNINMYF PAAVFGFLPISGTLFSYCKIVSSI LRVSSSGGKYK/AFTTCGSHLS VVC*FYGTGFGGYLSSDVSSSP RKAAVASVMTYVITSMLNPFYI SLRNRIKGVLRQPHGSTVQFQ YLLICSIPTVVVVKKGSKVK
14634	45002	B	14720	162	1263	

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14635	45003	A	14721	696	1791	VWIALKSENITCELLFKMQTQ CQVLVYLFPFQPSFLGKRCPI TDPQNLTVDVSIFLLVEVSGDPEL QPSPCWAVPCPCA WVTVLGNL LIIAISPSDSDLHTPMYYFFLSNLS LAIDIGFTSTTVPKIMIVDIQSHIS RVISYAGCLTQMSLFAIFGGME EDMLLSVMayDWFVAICHPL YHSAIMNLCSVGFLVLLSFFF LSSLSDSQLHNLIALQMTCFKDV EIPNFFWEPSQLSHLACCDTFTN NIIMYFTTAIFGFLPISGTLSYY KIVSSILRVSSSGKYKAFSTCG SHLSVVC*FYGRGVGGYLVSSD VSSSPRKGAVASVMTVVTPTM LNPFIYSLRNRDIKSVLRRPTEH CLISKK
14636	45004	A	14722	1	1971	MTRKVTLRLRTWRRGCGRLA MGMEAATPOGSLHPLFQEHWIR AEDFGVLSPMHPNSVQGVDDM IRLDGLNEAGMVHNLLIRYQQ HKIYVSLPSPVSTGEPLTGANLL DREKKMMHGRGHCPIALTEGVSS GPDNPMEGRARAKAKAKARAEL PLPAGETGDHLLPSQTYTGSILV AVNPFPQVLPLYTLEQVQLYYSR HMGEIPLPHVFAIANCYFSMK RNKRDQCCISPQNVRGAQTD VLKVFOQHLLISLICKTTLQACCI PSHPYISSLASAPGPPPLTTQCRSYS DSLLGPQLFGDVCYNCSHVIEG DGEALCSDLPHPTCSPGAWVLQL VSPLNKAWCVSCFSCSTCNNSKL TLKNKFVEFDMKPVCKRCYEK FPLELKRRKKLSELTSRKQAQP KATDLNSAEQPLAQLGAVGA/V TGITHEPHIPQVENGSQLDDV PALGV\ENWRIFMAERMEAQG GQRLLLSTMHEEYEFVSPSSV AELVALFLEGGLKERSIFAMALQ DRKATEGGPVGLTKKQGLLAS ENWTIQLQNDRTGKTGLVPH CLYTHTVTKHSDSCCTAVPTL LEASSGCIFMSYKKHITLTPKSA DSNKRPSTLGSQFKQSLDQLMK ILTNQCPYFIRCIKPNEYKKPLG FSDSFMLIKLIRIDKVQYDSFSYI

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14637	45005	A	14723	1	1197	MNNNIKKIVKQATVLTFTTALL AGGATQAFAKENNQAKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSRKTLTMTHQSTCPKH RASRVGPSNSLQNKTQVKKGD QTSVRRKRNDLKVEERHKNNH LARELTSSAAAASPHTGHAATA QAPQRHVEVGRAAAPAGDLGE GIVGEQVLGAERLVPGDASRAR ALCVLGLDRREAGHTAEMTAAP PAQVPGPGGPTALRRPSSYGL GVDEQNPMSVGDGEDDVRVQ HQELRDCLIKHTILIRGEFVTRS LNIAQAADRRDAFKVGIYGALF LWIVKKINAIAIFTPPAQDPKNV RRAI/GLLDIFGFENFENNRIJRT LCWRYREARC
14638	45006	C	14724	1	1032	
14639	45007	A	14725	1	4960	MSTTSIFQQQLNLLLSSHHKQKQ QIQLPQGRSRYRSCLMAAFRMQ YFLSLPMKSLLIVGFERLQAIAR SQPLARQYQAMRQRTVQLQAL CRGYLVRQQVQAKRRAVVVIQ AHGQGMAARRNFQQRKANAP LVIPAEQKSGQALPAKKRRSI YDTVTDTEMVEKVFGLPAMI GGQEGQASPHFEDLESKTQKLL EVLDLTVPMAAEPEEDVDGLA EYTPFKFAVTYFQKSASHTHR RPLRYPLLYHEDDTDCLAA
14640	45008	A	14726	86	370	RTWMTHVWRRRRVQAAPTAY SSFRPGTSPCPAQPRAGARA*TR SGTSIMPTGFSHTSCLTVPPFT ASSAGQHQRQRHKTTAAGHPT TTGAASF
14641	45009	A	14727	3	455	MOSVLPAGHSVSTRASSRSVTL SSPSTLNCRGRKSSRVTSPVG SGPGGGGGPGSGRFGIDPPRK FAAACGSFSTGAPSSVMVVRVSG MPSLSW*QYP*SCSTLGCRSRSS STISLSSLWA/VQPIAAPPYPELA TQLPISCR*SPSPCAPS

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14642	45010	A	14728	338	1782	NQLSK*KAHSIRT*TALQQSSGR SQICIVQSSADALPSSRCTNPSST FTPTPLPPrPPrHPTCSTLGCRSR SSSTISLSSLWAASR*QPLRTPN SRTQLPRSWPLKSTALSPPPPGQ ATRLCWWMVSSK*RTWMTHV WRRRRVQAAPTAYSSFRPGTSP CPAQPAGARA*TRSGTSIMPT GFSSHTSCLTVPRLHCVLCWTA SSTPQESSPGGWTRPWPWSWRRC CTCTGAGRYLQNSTAS/T/PVPS TSVSQTA <sup>PSK</sup> EDYRCWPSVYHH GSLPPFSVQPG*GCGMSVRAMP SVGPLWSPTTRPGQIKRQNYLL NYWSCWKMTLLAGIIPSST/GS RPADLDYFLGSSQCPRDERTLK GHVSCDPTSSISITGEKLKQKLE S/SSTLADTKSAFLQDSWT/SSLP TLGASA  <sup>RTT</sup> SAS*TDDQCPAP GPLHVSF/SLNSTYPSRLCSSTCS TVDSFQIIPMPN*MPFSTCGAFC WCLWFSAITALYFVM
14643	45011	A	14729	148	1040	WCTGQSFSKGTVWEILLRKPSL GNVGA <sup>L</sup> PCVATACLTTEV <sup>K</sup> R <sup>A</sup> PRGHPLAPVLD C <sup>P</sup> KGMSSS STSEL/CTWGNFEFWGRNKYNH WF*WG <sup>W</sup> ALLHQFKMGKGQAQG LQEASFYRKDTY*ATMP*NPIG ISEFGT\ALPGPCKNVFERFMS RFELPGKAAMTDNTNVYVR YKGDYYLCTETNFNMKVDIET LEKTEKMWKPRFRGICPQLQG CSVTEQQGFEFSDDAKSWALQH PKRPAQQDWAMSRGNQGWAN LGLKIRGEAVTTRAKEVS <sup>V</sup> V <sup>L</sup> KVLEVTDGKVW <sup>A</sup> REKKLRDSR
14644	45012	A	14730	189	507	AAGAD TSQGP <sup>GGGG</sup> PPPSQSR\  PKPSA <sup>G</sup> RKG <sup>G</sup> QLSPQPKKGL PSPQGTRKSAPSSKATPQASEPV TTQLLGQPTTQEEGSKAQGMR* PPQRLGASTQQQTNQEAA
14645	45013	A	14731	2	356	DGVSLCHPGWSA <sup>V</sup> ARSQ <sup>L</sup> TAT SASWA <sup>V</sup> CWQGCGETGILLPCW WECEKVQPLW <sup>K</sup> QYGR <sup>L</sup> SCEDH LNS*VQVILTTQ <sup>Q</sup> P <sup>L</sup> FP <sup>L</sup> WLH <sup>L</sup> FTFPPTGQKDSSFTTLP <sup>H</sup> CPG GRGCSELRSR <sup>H</sup> CTPAWVTE

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14646	45014	A	14732	1	408	FFFFFYTTFFLFFYFYFFEMESH SVTQAGVQWYNLSSLQPPPPRF RRFSCLSLPS*DYRCPPPHPAN FLCF**RQGFTLLAKMVSIS*PH DPPTSAQSAGHVLTSKWELENI EYTWWIKMGTDATGEHKNGEG WE
14647	45015	C	14733	262	536	
14648	45016	A	14734	179	745	TDCLHNRCHRSPRSPPPGPPG*R SRADWWRRGRCWGGSWCASSR RVC*RCAPSASFSCCRSPRGRQ GRTFPSPCPAPD*TQPVSPGD TRPCPPPSSPPAHRAT/GCCGRR RLPGNASYLASPGKEAGEFPAS QGDS*PGQYGYIGDSSS/RPTRG TWMKA <sup>ST</sup> PRHIAPIQICGA*G FGEHQEVPVREK
14649	45017	B	14735	1	1164	
14650	45018	A	14736	35	542	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAAVPRAAFPLSPLLPL LLGFLLLSAPHGGSG\LHTKGAL PLDVTFTY/KDYGDKLNMELSE KYKLKDKE <sup>S</sup> YPVFLFRDGD芬 PV <sup>Y</sup> PTGAVKVGA <sup>I</sup> QRWLKGQG VYLYGMPGCLPVYDALPGEFIR ASGVEARQALLKQQQDN
14651	45019	A	14737	11	908	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAAVPRAAFPLSPLLPL LLGFLLLSAPHGGSG\LHTKGAL PLDVTFTY/KV <sup>I</sup> PKSKFVLUKF DTQY <sup>P</sup> YGEKQDEFKRLAENSA SS\DDLLLVAEVG <sup>I</sup> SDYGDKLNM \ELS\VEKYKL\DKES <sup>S</sup> YPVFLFR EGDFEEPSSHYTGG*RLGAIQ RWLKGGKGVYLGDELVCT V*LTPWSGEFIR/ASGVKARQAL LKQQQDNLSV <sup>K</sup> E <sup>T</sup> QKKWAEQ YLKIMGKILDQGEDFA <sup>E</sup> SMTR IARLIEKNKMSDGKKEELQKSL NILTAFQKKG\AEKEEL
14652	45020	A	14738	3	227	
14653	45021	A	14739	1	424	
14654	45022	A	14740	1	207	
14655	45023	A	14741	2	352	
14656	45024	A	14742	1	441	

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14657	45025	A	14743	1	461	MTVDYRKFNQVVTPMAA/AVP DAVSLLQEINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAFLPQ GYINFPALCHNLRRELDFFLL QDITLVHYIDILLIGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPPEQKSHEQTLPWEQVP
14658	45026	A	14744	1	928	
14659	45027	A	14745	283	1074	
14660	45028	A	14746	450	1970	VRVLSPVEKELKLWKNTHKLL SYPTVGAATQLQNLNTAMGV GSHGARGQVVALNRQRQGD QPFTRTVTWKGKGYDRTFWGL LDTGSELTLTGDPKHHICGPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGIMVKGAKWKQ LELPLPRKIVNQKPYCIPGGTVE ISATIKDLKDAGVVIFTTSLFNS PIWPVQKTDGSWRMTVGYRRL NQVVTIPTAAAAPDV/VVSLE QINTSPGTWYAAIDLNAFFSIP VHKPHQKQFAFWQGQQYAF VLPQGYINNPALCHNLIQRNLD HFPLLQDITLVHYLNDIVLIGSA IKWVMHSS/DSIIKWKWHVHDR AQADPEGTS*PGYGHFWCPIC QQQRPTLSSQYDTIPWAISQLPG DRLIIGPLPLWKGQKFVFTGIDT YSGYGFAYPACNASAKTTIMES QNTLSTLMVFHTALPLTKALTS WLKKCSSGLMLMEFTGLTMS

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14661	45029	A	14747	1	2589	MGPPYKPPPTWPPQTLTSYHSTTPVKLQLSLLPPTAARGATEPCHLQAPASSVQQMTPPAAGPLKHLGGKSQMCLEQDGRSGSVRGSPCHAGHWVAGAGFGKGKTTTRIWGHVNLIJVPPNCTASSAARDSAPNQPLLGVVTAQIVPPTCPPAMTVQELIAPLTLPPAAGCRRGVPRPFQTRVWLLAQLLRAVLGGPGEGVVTCHSWRLERVAPRLASLWWALAAETAARLDWAAKRP SAWGSIKAAEFSKATPRLEGA SSRTLWVSYIQAKETTTGKNGPVEPSHLWEAYCRATAPHPAVHSPSAEVTYTCGIVNLLQGLVPKSHLEHTGCHVVVELICSVVLPLISRLSDPPDWHLVLMVIFSKARDPTPCPASGPEQPSVPTSLPLIAEVQQQLPEGRAPSPVAAAPGFLSKQIQDALCALEGSQALEPKGEGSEGVEAEGPGTETETVLPVSTLNFCPEIQIDIADKEIEQGEVTTSVTALLEGLEKTCSRSPSCKLDLTNDVYLDPTIFSFEPLSSPDGPVVVQNLHITGTITAQELSGTGLQPCTRTVKCETSLDGENSSLQQLAYHTVNHYWEFLNLQ/SHQEKKPDL*KF1KNUIEKMVVS1VDNLKTAFPCESESQGPTEELSEAEETSKSQTEGKARKSRLRFSSSKISPALSVTEAQDTIYLCLQEGNVESKTLMSGMESFIEQKQT
14662	45030	A	14748	478	3507	SKILRAVIWGSHLVRSAMKTETVPPFQETPAGSSCHLNNLSSRKLMAVGVLLGWLVIHLLVNWLLCLLSALLVVLGGWLSSLAGVASGRLLHLERFIPLATCPCPCEAERQLEREINRTIQMIIIRDFTVLSWYRSVSQEPAFEEEMEAAMKGLVQELRRRMSVMDSHAQSVLTLGGCHLQSYIQAKEATAGKNGPVEPSHLWEAYCRATAPHPAVHSPSAEVTYTRGVVNLLQGLVPKPHLETRTGRHVV
14663	45031	A	14749	1	417	
14664	45032	A	14750	34	350	RERGQEGGVAGRVEMDVSVVERGAYADQIWRPKGGESRGEKRKGRWVQRVRALRARVTPAGLGECKWGRGRGD*VRVVKPRALRERWGDGSTVSDSTPMKPGLE

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14665	45033	A	14751	1	1604	MASKRCIRDFRSRGGLKLSFQL YATFRKEGCGPVLANGNPGGG RGQEVSATQDLRRGWIASSAS RFPWRQSWPGRPRLGNYDSGA PGEAKMPSKGKDGGKGSKKG DTKKLILKTDESVVDRAKANASL WEARLEVTELTSRIKYRDTSRIL AKSNEDLKKKQCKMEKDIMSV LSYLKKQDQEKKDNMIEKLKQQ LNETKEKAQEEDKDKLEQKYTR QINELEGQFHQKAKEIGMIHTE LKAVRQFQKRKIQVERELDDEI NDLLVKEKIMQLVQQRSQIQL QKKVVNLLETALSYMTEKEFSE VLKLQQHAMIEQNAGQVIEIDK LQHLLQMKDREMNRVKKLAK NILDERTEVERFFFLDALHQVKQ QILISRKHYKQIAQAAFNLKMR EHVQEENIPKSEHLMMAESTAPI V*IRIFWRPKNGHILKEMWILEI *PGSRRKYCYCDCSLQK*MAVLL GNTTQSSRPSSSRMTMLFLDSGET KEFGDESKLQDKIFITQOIAISD VFW*SGATHYSKRTSGV*HSGK SESLQPRGQRLL
14666	45034	A	14752	95	473	
14667	45035	A	14753	168	449	

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14668	45036	A	14754	1	2000	MAFEQAKQVVKLALDWPIGD GPVELQVTVLQDHANWSLRQE QHGKRGPLQFTDVAIEFSLEEW HCLDTAQRNLYRNVMLENYRH LVFLGIVLSKPELITCLEQGKKP LTVKRHEMIAKPPGQKNWEKQ ALPLTGCLTKYPSWAKNIDIIVT CSHFARDLWPEQSIKDSFQKVTL RRYENYGHDLQFKKGCESV DECKVHKRGYNGLNQYLTITQ SKIFQCDKYVKVIHKFSNSNRH KIRHTGKPKFKCIECGKAFNQS STLTTHKKIHTGEKPKCEECG KAFNWSHLLTTHKRHTGEKRY KCEDCGKAFSRFSYLTAKHJIHS GEKPYKCEECGKAFKRSNNLTT HKIIHTGEKPYKCEECGKAFKR SSILTAHKIIHSGFKPYKCEECG KAFKHPSSLTTHKRHTGEKPY KCEECGRAFKYFSSLTTHKIIHS GEKPYKCEECGKAFNWSHLLT THKRHTGEKPYKCEECGKGF KYSSLTTHKIIHTGQQPFKCEE CGKAFKCFSLTTTHKRHTGEKPY YKCEECGKAFNSSSLTAAHKRI HTGEKPYKcerCGKAFKRSFIL TRHKRHTGEKPYKCEECGKGF KCPSLTTHKTLIEHAGKKPNK *E/ECSKAFKDTSALTRHKIIRTG EKPCFDECRAFQNQLSTFTKY
14669	45037	B	14755	269	1131	
14670	45038	A	14756	2	149	ALFRAGRQECLSLLKLCPQPL SPTCFVPGR*GFYLYHFFQRCAA QRGGI
14671	45039	A	14757	2	175	

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14672	45040	A	14758	1523	2667	PLLVHQRQTGSGEDLQQTPADL QQRDLLERKLTNRNE*HQHQQ KRHPLKNPTQMSP/CIDKQRYIN PRSTIKLELGKLLTENCTTTWK LNNLLNDCWEKQERSKTDTL TSQLKELEKPEKTNSKASRRQE TKIRAELEKIGTRKTLQKINKCG SWFFEKINKIDRSLARLJKKRE KNQIDTIKNDADITDPMIEQT TNREYYKHLYANKLENLEMD KFLDTYTLPLRNQEEVSLNRPI TSSEIEAVINSPLTKRSPGSDR FTAEMYQRYKEEL\VPFLLKLFO TIEKEGLLPNSFYEDSILIPKPG RDTTKKEN\RPISLMNIDAKILN KILANR1QQHIIKKLJHHNQIDFIP GMQGW\FNHKSINVIRHLNR
14673	45041	A	14759	640	1771	APVARMITA/PLFYTALLVFSAL GNILALCLTCQ\KRKINCTGIY LVHLAVSDLLFTVALPGRVVC YVLGSSWPFGKGLCRITAFLV YTDTYGGVYLMACVSVDHYP WVCAHWGPCRLTAGRARLVC VAIWTLVLLQTMPLLLMPMTK PLVGKLAOMEYSSMESTVGLGPL MVLVFAIGFCGPVGIIILSCYM KITWKLCSTAGRTO*PAGKDTT GGASPGGPBSDQPEKTPPAGAAQ EDPVTPRERTPPAGQPERTO*PA GKDATGGTAREDPTVTSRKGRH WRGCLLTLLMLVAVVVCFSFY HLNIKQFMARGMLHILPSCAER RAFLLSSLQATVALMNMMCIG/D PIIYFASTHYRKWLIGILKLKG SSSSSSSSSTLY
14674	45042	A	14760	1	401	MVLVQWLTAITSASFWTQNKG SLQFEDKWDFFMRPIVLKLLRQE SVTKQQWFDLFLSGLATLQDSSG PLLTGKLKKRKVSGTKY/IEAS SATSLKAATTDTTHHLLLYNPFWI PLTLI*HLCWLQRFA*SCDTDPH P
14675	45043	A	14761	184	2720	
14676	45044	A	14762	34	251	
14677	45045	A	14763	2	452	LQIEII*ALEELAAKEKANEDAV PVCLAADFPSAGMGS CIDGQE DELDIJKSRAA\YNTVLL/NFMDP PKIPHLLKEKPYFGMRKMAVRW HHAENLVDRPQ\EESEDDSHLE GRDLDTWHVGVKISWDVKTPG LATPQGD\CFMLGNLWRTKII

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14678	45046	A	14764	1	1701	MPFKCKKQHTFNKTSPEKEAII FTHGCLCTSPFNSELSEHGLNL KLSSWEHLHHRSSQQTLSVRLH VPTPQPVEHEFIQLIYIHTGAKL QASKVIIATKDGKRRKSPWLQQL KYPKLILREASSVSEELHKEVQ EAFLTLHKHGCLFRDLVRIQGK DLLTPVSRILIGNPGCTKYKLNT QLFTGPVFPVKGNSNIKHTEA*IA AVCETFLKLNDYLQIETIQALEE LAAKEKANEDA VPLCMSADFP RVMGMSYYNGQDEVDIKSRAA YNVTLLNFMDPQKMPYLKEEP YFGMGKMAVSWHHDENLVD R1QLQLWDPVDGTTASSAVPKQ GRDKRREVPTNLSPNNSQEGLI SAFHRSRCVHAFVFKLTSAPKTT SLPDVPSDLLAEGLAASRAGQA LWRCDKKSLLTLVRKINLQGK RDGGRSATNQQSQPHLDNTGL ERQLEQKVGRCRSPWRGLGHL EGNAQKGHLIHGVNKNGQHL LRRHGVSIIRAGRAFHAAADT APGRISCLGISEALKPRIQAGGL GAESIWQVLWEGGSNSSVFCR HDEEPAELPLPGKQASGGHM
14679	45047	B	14765	16	1462	
14680	45048	A	14766	89	566	MEQGSIIITQAWREDALVLTQKQ GLVSKSSPKRPHVCHILKVAAPFC CSCTQHVQGSSSPR*ANPHIRRE STPIAMSDQLQLRQYQFYQIPG TCLLPEVTEKNQGRICMVTLD ETLVHSSFKPISNADCLVPVELE GTMHQIHVLMRPyMDEFLT*M EEMF
14681	45049	A	14767	1	305	LSGLEMFQAGAGAPSSPGY*GS CWAISWSGPPDKHSNRGASC LETWAGAAATDTAGPHPAAGR C*A*AGSGGDQGTGSTAPLAT P*PLQLSLV*AAALPA

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14682	45050	A	14768	1070	2653	SLKPCMACL*HS*EKTLSDSSG RSWICAVSFQSPGAAAPLPEL SFPLRPGYTKLLPHATEEVSPFG SGAGRKKLGPMLPSTAELCPGTR ARWSEGYRDLGRQAQDLQAG RKSVVTWALEGHPREERAAA KVQQCQRMWEGCSDPQELIPR PGRNPDVVPDSAVALLPWGPSPR VPDLGPDESR/PAHSR/VQYWL HKAPAPPSPSPQLAEPATPQTRP SSPGSRSPSSWHLRSWSLNAD PWRPRPADLPGPNPAPPSSRGGA HGTWGKDVRPLGRGRSRLFSVV CGRREVQRAARRVGTTPGWR APGREREAAAS*QPPGTG/PASP MGRASSSGSRVSPGPIRRTAPW EGCSRSRRHHWGKGGLGPPDGE PGIPGSS*VAQPTVGGRRSLGPQ GAAPARDAAAATPPGDAARE GSGRHILRAPASRPQHQPRSRSR HPPASATTASLQKFRSASSEPPS EDRPFDFSPТАPPQCPVRAPSAG AR*^/AGRLPE/PR/RGPWGG GSRTNLTIPITSLHGPTAAARTS PHRKSR
14683	45051	A	14769	748	1073	SQHFGRPRWVDRRLSGVRDQP GQHDKTPSLLLEMQKVIAGRAGG CL*SQLLRRRLRQENPLNPQGGG CSELRSGLCTSVWATGRDSI^K KKKKKKKRKWPSSLLSLVILVQF
14684	45052	B	14770	59	466	
14685	45053	A	14771	2	3184	HRTGIPGSTISSPGGETVPE/MTA AMRERFDRLHFKNCMSDLA KLEAKTGVNRSFIAL/GVIGLVA LVLVVVGYGASLPLQPLLGFCY PAIYISIKAIQE/SPNKEDDTQW/ V*TYWVVVYGVFSIAE/FFSDIF LSWFIFP*LHG*KCGFLVGWCN GPEAPSKWGLKLL*QAASSGPF LSLEATKSQIGQVLVKDILKDQ GPKETADAIH^KKPKKSILP*ILL G*KKKKK
14686	45054	A	14772	14	455	PQFPCRRFRALSEEELDNEYY SLLNVRREASSEELKAAYRLC MLYHPDKHRVPELKSQLQARLF NLVHQAYEVVERRTPAIRE EFERLQREREERRRLQQRTNPKG TISVGVDATDLFDRYDEEYEDV SGSSFPQIEINKMHISQ
14687	45055	A	14773	328	479	

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14688	45056	A	14774	15	1095	KVAKMATALSEEELDNEEDYY LLNVREASSEELKAAYRRLC MLYHPDKHRDPELKSQLAERLF NLVHQAYEVLSDPQTRAIYDIY GKRGLEMEGWEVVERRRTPA\ EIREEEFERLLREREERRLQQRTN PKGTISVGVDATDLFDRYDEEY EDVSGSSFPQIEINKMHSISQIEA PLTATDTAILSGSLSLTQNGNG GSINFALRRVTSAKGWGELEFG AGDLQGPLFGLKLFRNLTPRCF VTTNCALQFSSRGIRPGLTTVL ARNLDKNTVGYLQWHICSSPLL QVQRPHRNTRACAPESPFRPFL HVPTWDAECSGARTPTSTA WTS AAVKLREACLSGP GSGSHQLL LTPRSKRTGGG
14689	45057	B	14775	508	1765	
14690	45058	A	14776	2	639	GRRRHRRRHDCSRGDCYLPT GTNTQQPLPPREPLPELPARTP DLSMQNSEGGADSPASVALRPS AAAPPVPASPQRVLVQAASSNP KGAAQMQPISLPRVQQVPPQVQ PVQHVYPAQVQYVEGGDAVY TNGAIRTAYTYPQEPQMYAPSS TASYFEAPGGAQVTVAAS/SPP AVPFHSMVGITMDVGGSPIVFS AGAYLIHGGMDRPELLANL

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14691	45059	A	14777	1	2091	MKPDIDNSTQNEGGQSFEERHE TLQRVKFRGGPKTAPGRKLIAF LGQMNSGTSGGQRVPGEEELM AGGATCLPNTEAHQPIRMKNL HTPAFRLCPLTLQDNEADAFW HQAFVWDGMPTGKKPQTLGLT YKTTIDLSMQNS/EGGADSPAS VALRPSAA/APPVAPSPQMLPLE LVILGVV/LDKCIPAQWSKEG QTNSTYTNPEPQMYAPST/AS YFEAPGGAAQ/MVGITMDV/GGS PIVSSAGAYLIHGG/MDSTRHSL AHTSRRSSPARSFRSNKAPSSRK FCC*LPTLSSKTL/SLFKNLLRK LPLGKIHSPDSVQWPWYGLLV AGSESLASLFPKASSGETLGF ATGQLAGESRLPSILLAFLVPID VAWGKEQLVTQTTVYRVQGS GQHLNKAWQEPAVLNVICGMGE KVDVQVGLCQHRAHLDGWNS SRAASVWPGETLTHHQDQCQA NLPPGIETSILGTTKGARYPSPQE QGGGRVWLERLDPRGIAVSGT DL*CLPQSDVPPGRA*SGGTGD KSISTHDKSGRGN SKYHY/YGIR LKPDSPLNRLQED/TQYAMMR QQPMIHQKPRWCRAELGGAGSP LQGMEDVSHVFPFEPAPD/LGSF LLQDGVTLHDVVKAL/QLVYRR HC/EDVV/MNLQFHYIEKLWLS FWN/SKASSSDGPTSLPASDEDP EGA VLP/KDKLISLCQCDPILRW
14692	45060	A	14778	94	3006	RTRSLTRKAMAEHAPRCCCLG WDFSTQQVKVVAVDAELNVFY EESVHFDRDLPEFGHVLDVHG VHVHKDGLTVTSPVLMWVQA LDIILEKMKASGFESFSQVLA LSG AGQQFHGSIYWKAGAQQA LTL SPDLRLHQQLQDCFSISDCPVW MDSSTTAQCRQLEAAVGGQA LSCLTGSRAYEFLN VCDRKHLK DTTQS VFMAGLLVGTLMFGPL CDRIGRKATILAQLLFTLIGLA TAFVPSFELYMALRFA/GL

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14693	45061	A	14779	1	710	MGPAAAGAPTSRASRGPRAPALR AAVGRRCPRPEMPCQCHPLAR CGLDPAWTQLPQETAGAPRQD PRCTNQLICEHLPLEGGLGFGYL GNKDSLHRHVVKVVAVDAELNVF YEESVHFDRDLPEFGGLASSAV TQSSS/DDLQQV*^SLQLSHAA* SLQTNASPTFEHSFLGKRHPK GAGQKRAESPTRPPRLRQEAAP GELOQRPLPYGTQVPAGLCPVS GLRLRARALLPYRTHSLSV
14694	45062	B	14780	1	252	
14695	45063	A	14781	73	198	
14696	45064	A	14782	762	1080	AGRAEMQQERESHEEAKDPSPLSPREGSQKQQQNVTNSTPSHCP/PLRMPPPAPRRPVP/CDHPR AEECERKAQHWQAAPPAAPVR DPLGEASWAPESGGDVESLYI
14697	45065	A	14783	1	309	MTKTEREQNEQLDGGGYGERLGEYSLFLCCVPSLNQGKCEVSSYFGMNLNSGVLKLLPFPPTRE SWPPPHTGTPHNHHGGVNSNGLGCAQRCSLIIHATNAGGWERGGVSNRSLFFFLLSASFSDAKIKPAPSPIDHRAEEC*/PPPLSQPPALVAWCREHLWAHPKAPLLTP
14698	45066	B	14784	1	471	
14699	45067	B	14785	1	1143	
14700	45068	A	14786	1992	2205	WRSMMSGLRKRQLASQISYCPCWSCP*EESHCRVSPAPLA*LLSPCPAPQQRSHSTDPPPFKHPFLPFSG
14701	45069	B	14787	389	973	
14702	45070	A	14788	287	525	TNPFNLLQH*KKP*CYTYISITDPTDACHKNKAFFSPAVSQLT/CIFFSTAGSFFVLSGHSCGHILAVFSLWPRSPQLPGTR
14703	45071	A	14789	475	616	
14704	45072	A	14790	1	704	MTKWKSNPQIHMELQRTLSNNNLEKSNVKTYYAKAKIFDDNLQLTFQHQRQDRDTEQEKKKEEREKRKQQQEPLRKKAQMOTVRPGFDLTQGPNCLTPHGKTKWSRLPPKNHRRPYTSRKPEGPRVKA* NHGPEGRRGTRLPPEAAKRAQ AEEAAQ*WPTRSTLRLEVTPTRAMPPSPSEDPRVAGVHPAPPGRPRSDS/APLRPQLRPPRSILFSLASEPAAAGNARGRHSVLA

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14705	45073	A	14791	200	408	SPHLMSINLITFANFLPFC*RNS QFLKS/SIFVMWMIHNGMKCRQ LDTCHCRHGTCKDSICPGEES PLP
14706	45074	A	14792	240	771	GRGMQSPAQVDPAAKRGNIAG HTAHLWPKGGLPLP/C/YHLLI MQIREQP*SSLEYPTF/RILSLVS GTKLNKILANRIRQHIIKKLIIHHN QVGFIQGMQGGLPTPGSEQGHL RVSPSSPSSTVTLKLFNFMEPFE NLNLSKGKASVHTITQENTDSL KVQGSQFSQGHEKRTLDLKVS
14707	45075	B	14793	1	1557	
14708	45076	A	14794	150	1668	ESDARQGPFPPLENTRPHPSCMQ NHGICRSLHPGLCGCPTTARD APATAGGVPAV/GPLTGAPP* LPGAGIGSKQSSTMGPAGGSC LGL*APSQPAD/PGSIQGVLVIA DTE*PLVGGDGGLAEHQWQ* EAQGP/GGLIPKHMNPQSRSQSLF GRRGYRDSSLRSLVLRGRTGQQT* HAELEGAGVGMGPGGNGR*GH/G PRGLPCLVQGRGPGVAAVA A GVSVAVPSGMLSENGPGCSK/P HSGDAGQRRLRENL*GVRALI WGAASSFLLT EQQLQELADCL HSGRKTCFFYFQGRGVDAPGPV APAHHLAGI STVVPEPGPGLCV GEDRQLPG/GNQRAEPPP*LVRS VSSLTGLPALGPRQMPNAGAG NGSGK*RGVRGSGPDWDCTGT HGGAGTGKLLWAGLSSLFLPSG KSEAHQQRAAGHGYGRGLGSP GRPPRSRKGRVLGSESAPA*GSP QPLRSARQKPSESSCPRQQPGVG RGPGAPLEAGHCSFPRPLGPAR SLHPDFPQGLQA
14709	45077	A	14795	3	374	RRPPSWG*RGCSQLPECAADGS LEDHGPPLPMVSCFSRHPAGR LRVFPSPPLLA VDCCWHNNSYV VAVDCCSATCSLLL YPSQEFP HKFLVYLVLSWHQLLGGLIC TQQPVNPVVS D G

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14710	45078	A	14796	73	890	MSLVRTTDGKVSFPHSRAASSPPRFA GSLPWTPKGHGFTSFPRLEGYCPS/REGPSDWGRNSFRVSS WAWRPSQGVSHHTPGQGP/PSPGNRDK*/VATRKSPGQPGSSPEP GWSLQSTSSPGATRTKGNLNTLKG*KQVVD*WVGVGTGWEGS GAPQSPQPSREWRLSPRGVGTVKETWPSPWSGR*APP CPGQPGQGQQTHMERGGR*G*QVGACGLG P*GQWSSVTNGKDTRAPWSPPP RQRNGRWPAPPPPFTHYYYYY YYYYYYYYYYYYFEE
14711	45079	A	14797	273	678	TEESTSVLSVPNQTGAGAARIGIVSLR LCGLYVTSPPRAARMHIRPHGP WPGGSHHENGEAGPES/EGAPASASGRGA PEGQAWPPRDAVLSSMLALFR TKSARHLVLTGTRQTAASPP FFSQPSWYCSLGVDGG
14712	45080	A	14798	551	743	PTRITRSAGSSSWGSCR PAPFSWSRPCLQGPRG*CRLGH SRFYAAP*VQGH PVHILPYSK RRAALRPRGQWGL DSVLGTA VC GCGP/RSESD CISGR*GPE/WY ISPPVPPH VHRGFQQL LN CARQVG KGGGGPGC PMLGNH HSSQVGL GLGGQD QDSLES PGRVSS PSGP SAASDP GG*GFQGNP DPVHP APPDW

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
14713	45081	A	14799	705	2299	KREWRPRRHPLGPPPCAGRSA PLSGPASPFS*WLPPGHGPCGR MCSRAARGGDVTYRTHNTRAP SCPSLHWVGGERG*DAHTRTPSC PSLHWVGGERG*DAHTRTPSCPS LHWVGGERG*GCPHSGLQLSFP PRSAGCCKALFEAEKSKGDTGL GKRGWAGGGAGGAARPCICNP TVPCPQSTQSPPV/PGTR*QLG SSASHSRAASSPPPRFAGSLPWT PKGHGFTSFPR/RGGVLPFPEGP SDWGRNSFR/GPAGPSMW*PAP PSDAQVGHGPGRAGLQRCRGR GGHTPFLAAAAAIDSAYFS**/D P*VFGSNFPHLSCFPGIGCGEGN Q*ARRRPLAGAAALPGPNLES WVCELSVAGPAVWDPVPSG/PD PTTGPESP/RNSAGACGAQGSM R+*GTPATWSL/GPPPELPGSR HQHQCECGPAHVQERMPGW ACMLKSVAQRGFQRRL*QLSKA QAAAWRV\PGGRIGAKD*GW RRWGVSRGGGLCCARGGGGS SVVRGEVEGS/GCARGGGGAG WRALSPSSLPISSGAQELGLS
14714	45082	A	14800	1	267	CSAGGPWRAPQPRRFHRRRRP AQLPPLPLPLPPLPASPRHNRFT\PRPSQRTPPPAAALGCPEPGS/RS QGRGHARPPGSSEGDPDTVSSPG
14715	45083	A	14801	218	430	
14716	45084	A	14802	9	201	
14717	45085	A	14803	1453	1936	EVEKHLQCG*ELLRAQHN*AA ACRRPRPPAPGPQCSAGGPMAR APAPQVPPPPPCSA/PPPLPLPP LPAS/HAHQPHFRHGRRSALLP RPPWAVRSRGALAGPRTRAAG GLRGGAGAAAPADARFPASSP AE*PKFQNSARALTGFPRTD PTVSSPGY
14718	45086	A	14804	1	580	TSGCSHLHKPAGVSTRPPTVA SICAPRRTSPRLRRGSLTLWPFP GGHLLTLETP/GFDSCPEEVEGP RFSTFKTS*ARGGRQRQCAPRG RREVGPPSAAESGRARGEPPRC RLLCRGGK/DPQPRAGEEAAA GTPEGSRAGASGSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR CVWGEPPGRRTLFPDE

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14719	45087	A	14805	279	1148	ALHEFAMSRSLHASLH*STC P*QQPAPAPAGEPRARPGKSSS ASSPGP/WPRPNHGKQLHLPAQP Q/QQGRISSPRVAGGSCTGRA LLLAAGLQNSTRSLNPRDPPTIL SHRPLQGM/PDAP/RGCSHSLHK P/SRS/TPLSGQL*PPSAPIHAPAQ APSAGPLPCGLSPGDT*RYWR LLRFDSCPPEVEGPRFSTFKTS* ARGGWQRQSRVWASARGASTL QASVQGR*NPQPRAGEGEAAA GTPEGSRAGASGSEGALPAAAS PGNSSGRSRPEAGANPKGAPRR FLGGCLL
14720	45088	A	14806	765	4270	SQDTPGDLQCHGDLL*DGAVLSEAPGERVPRDD*GGVCPEGVP HVSLRDSVAEALQPRGEAGGDQVPEAHPSSAQR*PAGAGLRLHPAAAGGVPGQSGHGLPKIQ DDLTSKS*TSNITKTLFPNKVTL SDSGRA*ILEGHRSTQGSLGLEADPGTVSHHQHPCPPNAATHF HRTARPGVQQGPGPASVQQPES DGDGALLRSPCSLLPQGADEVLLQPDGDKQGGRPRGDSESD*G YSERR*AQDEYQGH
14721	45089	B	14807	133	2943	
14722	45090	A	14808	1	814	MEEELLRELLYSENWWSIPYND TQEELCCWAVLKRTFINGNTSR KPGMKMVTGLKQERRSKQW GCEKEAKFVPMWIVLEVGRP EERGIDGKRWKGKCSVQSVW AFQNPWWSKAQTLNNSMK/AYE KGKEGVEEKFEARSWFMRKK AISHLHNMEMQGEAAASADVEA AVSYPEDLAKIIIDESDYTKQWIS NVDKTVFYWKKMPSRTFIATE EKSMPGFKASKDSLTPLLGTNA AGGF*LKPLLTYHSQTSRALKN YAKLTLMLYKWN
14723	45091	A	14809	123	515	PKQSAKTIWITSTARPEDVVTCS FKEEFLPGNTNHDFSIKNRSDPE LEVSRPLARPENFPANRSHSLL L/RPCCRGRWAAHWTGCSLLLD ASSAPRTDQPSLWRNLPASLG GPWSHINQPGIVFQNTYLMKWP

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14724	45092	A	14810	279	1136	VDVDLACVRGLLCSDEFLSW LALNRTVLATPALPSCLSQMAS SLPGLCARTRRGERADSQRGTC AFFSPARTASQAPLVASSVRKQ RVWAPNPLNCHTLPPSRGSQRG GYIGEEGVFGSRVVGIWVPGPN GSPWPLGVQR/PECVLLGVGSG S/SHELFSEADPISRLLAPSPSP APAS/MGNAIEEEAPELGPLGRV FVDDDFHYDYNFIHLHEDLCYGP LEGPDLDLAGTGDRTTPLLHSRP RASLSPSALRCP/*ALGF/WSTLA WGSPNSSSRVPEAQPPAPSLAE
14725	45093	A	14811	1	1597	GGRKAAVGVETRPQGSQPTW LPVHGDTCTTLLPCRAWRWL GGLPWAASVVGAKCVVTPPER GLLMLHCKPMPGWSSGYRVVLP AVAFFRLRAQVTKLGEEVSLRF LKREAKLCGFLQKSFLALEKR MKASESSRLKLEGSLRGELESR WEKLRGLMEERLRLALQQHKHEE SHLLEQCQGLDAAVAQQLTKFV QQNQASLNVRVLLAEKAWDA KGRLEESRAGELAAVYQENLE AAQLAGELARQEMHGEVLLR
14726	45094	A	14812	150	1625	CLGKAFCRELNAYLRLPTFFIV FSLRQPSLRMHSRAWVKTCGA MPCSCCRIRHCSSVTDMAVRSL ALLQLVNRTPLRRRQISAACQR MSTFLFFRACTF*PRNRSSSGRH /DLTAPRQAILRQNFLK/RAQ5 RNLTAPNPR*LLVKTYRQTS RPVSAAH*CPR*RGRAALAAAC HSGSPGARRQTAGPAEGPAT*T RRDFL**RAACLRRRWKWP*E *RSRSSSP*SQGSCPPALPAPP CSAGSRTGPAARWCAGAGSR RHAGSSA***SRR*GRSASGRR PRHGGTAGSGRWLWWARCPA *AGIPWPSWPCHSSWP/PQSVRV VSSG*RASLHSPPGLDSSGGLQ SFLLVQLPAQGKTSSQP/RHAA APSAACPHAE*CTLGSCPRSA TLSPTPPRASPPAG(RSAVSPC GHEGVVLVISKHLLLSRSRG LGGNNVVRPCSVQPMMDGVGQEL AVADRDQLPCLVCQDGECPNK ASGRPVVLGCP

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14727	45095	A	14813	921	1446	ACCISHGNLWHHLDQKHGLQ *GEKSRLFSRPNLQVPVHTGLD HRARYLTGPRKQGHLWPTGPS SVFDNEFCKLSVGM*TRASA RQQIQSPFAESGKAFSDICSVSL RLCVLPHPWNSRLRSPALRNSL KYSVTSSAAARRKLLPLASGPL RLGPRSLPTRLQVLRWEKVASA
14728	45096	A	14814	1	675	
14729	45097	A	14815	1	2341	MASDLVNRCEACDLPGPISVH QFPRLSNEVTITVGRNSEPNQ RSVSGPWTPREVRGVAAAAH GFSGQNAKWAHHIPATAMSFA LPYSVLHSPHALTTTPLNPGDA VTMPSWTSTVSAANASKGRSFS QCFQSTEEGQERRRPTSQAQKV QQGSTAGKVNELITLAGHIKSQ APHGKRKPPPRDSHVICSMLRK RKPDETPSPSSDAQFSGMLAV VSSLCPRSSPSQWCHCHSPSTT ILGSSDVSDTSFQPSTKLGPGHG FPPQSRDCILDFELIRKVTGAW SLTAGSWETKIQEFSSEIDLAP RITPGHSSKSPVHFLASLWGR KTKLYHHTIQDKEPRSVPEAGS SGRRDGGAAHSMLCMAPEPD HPGSNPNCRSPATLHDADGN LQREAAKCQGDGTQVSTHVDH TSAPRQAETGPATGENEKMESH GRSKRGLVGADQCPAETLDSY TLLVGHKRDKDRQTPGPAPQ VNSFPENYLLRGPLAPLGLSAIS MKTAGAVHIRPSGDLGRAPAP AVRPRPRPDRRPRRLPGPAHL GAPRPPAPAPLSRRAARQSPAA AAAPPPGCE/RRG/PAGPAGSAG PPAPAHGARPGGKPAANPPRAP QP*P/RRRSRRRAQPRPGPAPL SRMRAEGPARALRPPPHYQPEL GPPSETVGPVTELLAPISTARFP TRSHPYPVTPASPARSS*TSGLD*
14730	45098	A	14816	44	455	HLRNRT/PSQ/TPHYINHLLFDK /PLFNIWW/WENWLAICRKLLKD PFLTPYTKINSEWIKD*NIRPKSI KNLEENLGNTIQHLD/GKDFM TKTPKAMATKAQDIDWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP

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14731	45099	A	14817	1	279	IQDIGMGKDFMTKTPKAMATKAEFIDKWDLIQLKSFC <sup>T</sup> TLKEITIRVNRQTTENYPSDKGLISRMLPNF*RLFPAS*KKPPLFDIGKTEKTNYS
14732	45100	B	14818	1	2025	
14733	45101	B	14819	1	3570	
14734	45102	B	14820	1	1380	
14735	45103	A	14821	1391	2742	KKRESSLTHVMRPAF*YQSQAETQQKKRILDQY**TLMQKSSI/K/YLAKR <sup>I</sup> QQHIKKL <sup>I</sup> HDQVGFIPGMQGWFNIRKSINVIQHINRAKDKNHI <sup>M</sup> ISIDA <sup>E</sup> AKFDK <sup>I</sup> QQPFMLKTLNKLELEETTVKFIWNQKRAHI <sup>A</sup> KSI <sup>S</sup> QK <sup>N</sup> KAGG <sup>I</sup> TLRDFKLYYKATVT <sup>T</sup> KA <sup>W</sup> Y <sup>W</sup> YQNRDIDQWNRTEPSEITL <sup>I</sup> HHNYL <sup>I</sup> FDKPEKNKQWGTDSL <sup>N</sup> NKWC <sup>W</sup> ENWLA <sup>J</sup> CRKL <sup>L</sup> KLD <sup>P</sup> FL <sup>T</sup> PYTK <sup>K</sup> INSRW <sup>I</sup> KD <sup>L</sup> NVRPKTI <sup>K</sup> TLEENL <sup>L</sup> GITI <sup>I</sup> QDIGMGKDFMS <sup>K</sup> TPKAMATKAKIDKWD <sup>L</sup> IKL <sup>K</sup> S <sup>F</sup> CTAKET <sup>E</sup> TIRVN <sup>R</sup> QPTKWEK <sup>I</sup> FTTYSSDK <sup>D</sup> GLISRIY <sup>N</sup> ELKQIY <sup>K</sup> KK <sup>T</sup> NNP <sup>I</sup> K <sup>K</sup> WA <sup>K</sup> DKMNRHFSEEDIY <sup>I</sup> AAKKH <sup>H</sup> MKKCSSSLAIREMQ <sup>I</sup> KT <sup>T</sup> MRY <sup>H</sup> L <sup>L</sup> TPV <sup>R</sup> MAI <sup>I</sup> KKSGNNR <sup>H</sup> APFS <sup>I</sup> H <sup>H</sup> THIMFGSLY <sup>L</sup> QI <sup>Q</sup> KDLS <sup>L</sup> SIL <sup>G</sup> FW <sup>W</sup> YPRGILEPIY

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14736	45104	A	14822	1	1698	MEDEMNEMKQEGKFREKRIKR NEQSLQEIWDYVKRPNRLIGV PESDGENGTKLLENLQDIIQENF PNLARQTNIQIQEIQRMPQRYS RRATPRHIIIVRFTKVEMKEKMS RAAREKEIQTITIREVYKHLYAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRITVTGSEIVAJINSLPT KKSPGPDGFTADEFYQRQSESI MSEFPFTIASKRKIKYLGQLTRD VKDLFKENYKPLLNEKEDTKK WKNIPCSWVGRINIVKVMALPK VIYTFNAIPIKLPMFTTELEKTT FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLLDPL FLPTYTKINSRWIKDLNIRPKTIE TLEENLGTITQDIGHMGKDFMSK TSKAMSTKAKIDKWDLIKLKSF CTAKETTIKVNRQPTKWEKIFA TYSSDKGLISRIYNELKQIYKKK TNNPIKKWVVKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIK TTMRYHLPV
14737	45105	B	14823	91	1596	
14738	45106	A	14824	1	2757	

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14739	45107	A	14825	1	2677	MGKKQSGKTGNSKKQSASPPP KEHSSSPAMEQSWMENDFDEI NKIDRLLARLKKKGKQDNT TKNDIGDITTNPTEIQ/TIREYY KHLVTNKLLENLEEMDKFLDTY TLPTINQEEIESLNRTITGSEILAI INSLPTKKSPGPDGFTAECFYQRY KEELVPFLLKLFSQIEKEGILLN SFYEASILIPKPGRD/TTKKNFR PISLMNIDAKIFNKILANRQQHQI KKLJHHDQVGFIPGMQGWFNIR KSINVQHVNRKDKNRMIIISID AEKAFDKIQQPFMLKTLNKLGI DGTYLKIIRAIYDKIJTAIIHLNG QKLEAFPLKTGTRQGCPPLSPLL FNIIVLEVLAIRQEKIEKGQQL GKEEVKLSLFADDMIIHYLENPIV SAQNLKLISNFSKVSRYKISVQ IPQAFLYTNNRQTESQIMSELPF TIASKRIKYLGQLTRDVKDLDK ENYKPLLNEIKEDETKWKWNIPC SWAGRINIVKMAILPKNWKKT TLKFIWNQKRARIKSILSQKN KAGGITLPDFLYYYKATATKTA WYWYQNRDLDQWNRTEPEIT PHIYNYLIFDKPDKNKQWGKDS LFNKWCWENWLAICRKLLDPL FLTPYTKINSRWRWKDLNIRPKT KTLEENLGITQDIGHGKDFMMS KTPKAMATKAKIDKWDLIKQE SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRIYSELKQIYKK
14740	45108	B	14826	1	1186	
14741	45109	A	14827	1	2304	
14742	45110	B	14828	1	2995	
14743	45111	A	14829	1	3095	
14744	45112	A	14830	1	3654	
14745	45113	A	14831	1	3189	
14746	45114	A	14832	1	2064	
14747	45115	B	14833	1	3031	
14748	45116	A	14834	1	3192	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mol. wt in USN	SEQ ID NO: 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14749	45117	A	14835	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSSHTIUM GDFHTPLSTLDRSTRQVKVNDI QELNSALHQEDLIDIVYRTLHPKS TEYTFSSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDSAICL ELRINKNLTQNRSTTWKLNNLL LNDYVWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTITSQQL KELEKQEQTSHSKASRRQEITKIR AELKEIETQ
14750	45118	A	14836	1	3144	
14751	45119	A	14837	113	1336	PTLAGTGQETSHLGFNAIPIKL RMTFFTEL/EKTLKFIWNQKR ARITKSILSQKNKAGGITLPDFK LYYKAIVTKTWWYQYQRNDID QWNRTEPSEIMPHIYNYLIFDFKP DKNKKWGDLSLFNKWCWEN WLAIYRKLKLDPLTSYTKINS RWIKDLNVRPKTIKTLEENLGN TIQDIGMGKDFMSKTPKAMAT KDKIDKWDLIELKSFCTAKETT RVNRQPTWEWEKIFATYSSDKGL ISRIYNELQIYKKKTNNPICKW VKDMNRHFSKEDIYAAKRHMK KRSSLALIREMGIKATMRYHLT PVRMAIIKKSGNNSRSNIVHSVT QANALESSWIPFLPHIQYISKP QASSFKMYHVTDPILPPSSQHL DQAAINLCLQWPPLLWFECMCP SKIHLMLKLTPQ
14752	45120	B	14838	1	3127	
14753	45121	A	14839	1	2742	
14754	45122	A	14840	1	1998	
14755	45123	A	14841	1	3030	
14756	45124	B	14842	1	2558	
14757	45125	A	14843	1	3828	
14758	45126	A	14844	1	4134	MRKKQSRKTGNSKKQSTSPPPK ERSSSPAMEQSWTENDFDELRE EGFRRSNVSKLQEEIETKGQEVENLEKNLDCITRITNIKECLKE LMELKAKARELHEECRSLRSRC DQI.EERVSVMEDEMEMEMKQE GKFRERKRIKRNEQSL.QEIWDYV KRPNLPPIDVPESDRENGTKLE NTLODVIQENFPNLARQANIQI QEIQRIMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSG
14759	45127	B	14845	1	3555	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14760	45128	A	14846	1	3345	
14761	45129	A	14847	1	3451	HTKNPSVHHHRQRPKVDKTTK MGKKQNRKTKGSKTSQAFPPP KERSSSPAMEQSWMENDFDEL REEGFRRSNYSSELREDIQTKGK EVENFEKNLLEECITRINTEKCL KELMELKTKARELRECRSLRN WIKSQDPSLCCIQETHLMLCRDT HRLKIKGRRKIQYQANGQKKA GVALVSDKTFKPTKIKRDKE GHYIMVKGSIQQEELTILKLYAP NTGSPRFMKQVLSLDLQRQLDLS HTLIMGDFNTPLSTLD
14762	45130	A	14848	1	2606	MVASRSSRVGVFGGQNSVGD VSRRSDGSLNECLYRPPGTGAY LAYDTLDVLPSQFTVNTPPID VNGKSLALLWEHTSLLTSMG GGRWAMQPLGQLGQLEHLGD RRDQVLDRSGRSRRLDAAQHL RHRPDRRPQGMVGVLTNQKEP RTRWIHSRILPEVQGGTGTVPSE TIPIDRKEGILPNLFDEASIIIPK RGRDTTKKENFRPLSMLNIDAKI LNKILANRNQQHKKLIIHHDQV GFIPGMCGWFNICKSINVQHIN RTKDKNHHMIIISIDAEKAFDKIQ QPFMLKTLNKLIGIDGYTLKIRA IYDKPTANIILNGQKLEAFPLKT GTRQGCPPLSPLLFNIVLEVLR AIRQEKEIKGIGQLGKEEVKLSF ADDMMIVYLENPIVSQAQNLLKLIS NFSKVSAVKINVQKSQAFLYTN NRQTESQIMSVPFTIASKRIKY LGIQLARNAKDLFKENYKPLLN EIKEDTKKWKNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGILPDFKLHY KITVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGKDSLNFNKWCWENWLA ICRKLKLDPLFTPYTKIHPRWIK DLNVRPKTIKTLEENLGNTIQDI GMGKDFMSKTPKAMAACKAKI DKWDLIQLKSFTAKETTIRVN
14763	45131	A	14849	1	2862	

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14764	45132	A	14850	I	3724	MGKKQRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTAKRELHEECRSLRSR CDQLEERVSAMEDEMEMKRE GKFREKRIKRNQSLSQEIWDDYV KRPNLRLIGVPESDVENGTKLE NTLQDIHQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHII FTKVEMKLRAARQKAPH HTYSKIDHIVGSKAL
14765	45133	A	14851	2	2375	
14766	45134	A	14852	I	2376	MGDFNTPSTLDRSTRQKVNK DTQEELNSALHQADLIDYRTLH PKSTEYTFPSAHPHTYSKIDHIL GSKALLSKCKGRREII TNCLSDHS AIKLELRIKNLTQNRSTTWKLS NLLLNDYVWHNEMKAEIKMF ETENENKDPTYQNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRALELKEIETQKTQLKINESR SWFFERINKIDRPLTRLIKKKRE TNQIDAIKNDKGDTADPTDRQ TTIREYYKHLYANKLENLEM DIFLDTYTLPRLNQEEFFESLNRP ITRSEIVAHNSLPTKKSPGPDG TAEFYQRYKEELRKJYLGQIQLT RDVKDLFKENYKPLLEIKEIKEDT NKWKNIPCSWSVGRNIVKMAIL PKVIVRFNAIPIKLPMTTFFTELE KTTLKFIWNQNKRARIAKSILSQ KNKAGGITLPDFKLYKKATVT KTAWYWWYQNRDIDQWYRTER LEITPHIINYLYLFDKPEKNKQW GKDSLFLNWCVENWLAICRKL KLDPFLPTYTKINSRWRKDLNV RPKTIKTLEENLGITIQDGMGK DFMSKTPKAMATDKDIDKWDL IKLKSFCATAKETTIRVNRQPTK WEKIFTTYSSDKGLISRIYNELK QIYKKKTNNPICKWAKDMNRH FSKEDIYAACKHMKKCSSSLAI REMQIKTTMRYHLTPVRMIAIK

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14767	45135	A	14853	1	1576	MDKFLDTYTLPRI.NQEEEVSLN RPITGAEIVAIINSLPTKKSPGP GFTAEFYQLRISNFSKVSGYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLG\QLTRDVKD LFKENYKPLLNEI\KEDTNWK NIPCSWGRINIVKMAILP/KEL EETTLKF\IWNQKRARIAKSII.SQ KNKAGGITLPDFKLYYKATVT KTAWY\WYQNRDRDQWNRT SEIMPHIYNYLIFDKPEKNQW GKDSL\FNKWCWENWLAICRK KLDPFLTPYTRINSR\WIKLDHV RRKTIKTLLEENLGNQD\IGMG KDFMSKTPKAMATKAKIDKW DLIKLKS\FTCAKETTIRVNROPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKED\IYAAKKHMKCKSSLA IREMQIKTTMRYH\HTFVRM\II KKSGNN/R/CAPGTPERQNHSL WKGS*SQEP\SGLAQW\IPLPWSP AS*DPLA*NSCCQHSCLKSTWD AQACARKLRLTIKGYRNQCLE
14768	45136	B	14854	328	1467	
14769	45137	A	14855	3	3412	
14770	45138	A	14856	1	2907	MDKFLNTNTLPLRLNQEEVDSL NRPITGSEIVAI\NSLPTKKSPGP DGFTAEFYQRYKEELRIKYLG\I QLTKDV\KDLF\KENYKPL\KEIK ED\K\N\W\K\N\I\PC\W\G\N\I\W\K MAILPKV\YRFNA\PI\PKLPM\T\FFI ELEKTTLKF\IWNQKRALIAKSIL SQMN\RAGGIMLPDFKLYYMAT VTKTA\WY\WYQNRDIDQWNRT EPSEITPHIYNYLIFDKPEKNKK WGKDSL\FNKWCWENWLAICR KLKLDPFLTPYTKI

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14771	45139	A	14857	1402	3004	TEPKTKTF*LSA*MQKGPLTKF NNPSC*KLLIN/IVLEVLLARAIRQ EKEIKGIVQVGKEEVKLSSLFADD MIVYLENPIVSAQNLKKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPTIASKRKRYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNILCSWVGRINIVK MAILPKVIYRFNAIPIKLPMPPFT ELEETTLKFIFWNQKRARIAKAIL SQKKKAGGITLPDFKLYYKATV TKTAWWYQNTDIEQWNRTEP SEIMLHIYNYLIFDQPEKPKQW GKDSLFWNCWCWENWLAICRKL KLDPFLPYTKINSRWIKVLDNV RPKTIKTLLEENLGITIQDISMGK DFMSKTPKAKATKAKIDKWDL IKLKSCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELK QIYKIKTNPIEKWVKDMNRHF SKEDIYAAKKHMKKCSSSLAIR EMQIKTTMRYHLTAVRMAIIKK SGNNSLIVGASMDTSLLSGPIPY DIQHFDRFGSVTVRRGCAIEFY

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14772	45140	A	14858	884	2925	GIKYLGQLTRDVKDLFKERS/Y EPLLNEIKEDETNWKWNIPCSWV GRINIVKMAILPKVIYRFAIPIK LPMTFTELEKTTLKFIWQNQKR ALIAKSILSQKNKAGGILPDFK LYYKATVTKTAWYQWYQRNDI DQWNRTEPSEITLHIYNYLIFDK PEKNKQWGKDLSFNKWCWEN WLAICRKLKLDPLPTYTKINSR WIKDLNVRPKTIKTLEENLGI QDIGHMGKDYSMSKTPKAMATK AKIDKWDLKLKSFTAKETTIR VNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKKTNNPIKKW VKDMNRHFSKEDIYAAKKHM KKCSPSLAIREMQIKTTMRYHL TPVRMAIIKKSGNNSPCTVQSD WKLTOAVGLWSAEAEAPKSAQ RRPLAEGHRAAVQRDGSGLQL LCTVKLQVLPCHIAQGNGGRKA TSSLEAELTSWRPLCLEDGTGF RGEDTLETVNAEGRENRKAG HRAAGSSASRRCRNTGRSVQRL RPQKTQAFPTHCHFCLILVVKA TQLNPKSRVRKVPFAPMKHGK ALAGPWNANICAGKSSNEIRTC RHGCCQYSQRSQRPHQGVDI LCSAGSTVYAPFTGMIVGQEKP YQNKNAINNGVRISGRGFCVK MFYIKPIKYKGPPIKKGEEKLGTL PLOKVYPGIQSHVHIENCDSSDP
14773	45141	A	14859	I	2577	

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14774	45142	A	14860	3019	5574	RETRGEVKNSKNQSTSAPPKDC SSLADPKKIQITIREYYKHLYPN KLENQEEMDKFLDTYTLPRLN QEEVESLNRPITGEIVAIHNSLP TKKSPGPDGFTAEFYQRYKEEL VPFLLKLFQSIEKEGILPNSFYE ASHILIPKLGDRDTTKKENFRPISV MNIDVKILNKILANRIQQHIIKKL IHHHDQVGFIPIGMQGWFNIHKSI NVIQHINRTKDKNHMIIAHEK AFDKIQQQHFMKLTNLKLGIDGT YLKIIIAIYDKPTANIIHNGQKL EAFPLKIGTRQGCPLSPLLFNIV LEVLRALARQKEIKEKGIQQLGEV VKLSLFADDMMIVYLENPVSAQ NLLKLISNFNGKVGSGYKINVQKS QAFLYTNNRQTESQIMISELPFTI ASKRICKYLGQLTRDVVKDLFKE NYKPILLNEIKEDTNWKWNIPCS WVGRINIVKMAVLPKLPMTFFT ELEKIVTLKFIWQNQKRARIAKSI LSQKNKAGGITLPDFKLYYKAT ATKTAWYWWYQNRDLQWNRT EPSEITPHIYNYLIFDKPDKNKQ WGKDSLFLNWCWENWLAICR KLKLDPLTPYPTKINSRWIKDL NIRPKTIKTLEENLGLTQDIMG KDFMSKTPKAMATKAKIDKW DLIKQESFCTAKETTIVRNQPT KWEKIFATYSSDKGLISRIYSEL KQIYKKKTNPIKKWAQDMNR HFSKEDIYAAKKHMKKCPSSLA
14775	45143	A	14861	1895	6140	
14776	45144	A	14862	I	2875	MKAEIKVFFETNENKDITTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTSQLKELEKQEQT HSKASRRQEITKIRAELEKIQTQ KTLOKINESRSWFFERINKIDRS LARLIKKKREKNQIDTIKNDKG DITTDPTEIQTIREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPITGAEIVAIHNSLP KKSPGPDGFTAEFYQSWAETQP KKENFRPISLMNIDAKILNKILA KRIQQHIIK

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14777	45145	A	14863	2843	4460	HQHQQKPHPHRNPIQKSPSTS KVLEVLRALARQEKQGS/GIQIGS QEVKLSSLLEDDMIVHLENPI KNLLQLISNFTKVSGYKINVQK SQAFPYTNKTQIEQIMSEL IATKRIKYLGIKLTRDVKDLFK NNYKPLFKEIREDTNKWKNIPC SWVGRINIVKMAILPKVYIYRFN AIPIKLPMFTTELEETTLKFIW NQKRARIAKSILSQNKNKAGG LPDFKLYYKATVTKTAWY QNRDRDQWNRTEPESEIMPHIY YLIFDKPEKNQWGKDLSLFNK WC*ENWLTIICKRLKLDPFLTPY TKINSRWIKDLNVRPKTICKLEE NLGITIQDIGHGKDFMCKTPKA MATKAKIDKWDLKLKSFCTA KETTIVRNQROPTKWEKIFATYS SDKGLISRIYNELKQIYKKKT NPPIKKWAKDMNRHFSKEDIYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPTVRMIAIKKSGNNR WRRCEIGTLLHCWWDCPKVQ PLWKSIVRFLRDI.EI.EIPFDPA PI.LGIVPKGYKSC
14778	45146	A	14864	1	8335	MGKKQNRKTGNSKMQSAPP KERSSPATDQSWMENDFDEL REEGFRRSNYSSELREDIQTKGK EVENFEKNLEECITRINTEKCL KELMELKTAKARELRECRSLRS RCDQLEERVSAMEDEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDHSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDYRTLHPKSIEYTFFS APHTHTYSKIDHIVGS
14779	45147	A	14865	1	3166	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSLQLRDLDSHTL MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDISRTLHP KSTETYTFSAHHTYSKIDHIVG SKALLSKCKRTEIITNYLSDHSA IKLELRINKLTQSRSTTWWKLNN LLLNDYWVHNEMKAIEKMF TNENKDITYQNLWDAFKAVCR EKFIALNAYKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELEKIEETQ
14780	45148	A	14866	1	3912	
14781	45149	B	14867	1	2832	

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14782	45150	A	14868	1944	3531	LRDCKRINQHPVKTDQSAFCKM/API/MQDVVLEVLAIRAQKE EIKGIGLGKEEVKLSSLFADDMI VYLENPIVSAQNLLKLJSNFSKV SGYKINAQKSQAFLYTNRQTE SQIMSELPTIASKRICKYLGQLT RDVKDLFKENYKPLLKEITEDT NKWKNIIPCWSWVGRINIVKMAIL PKVIVYRFNAIPKLPMTFFTELE KTTLKFIWNQKRAMAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWWYQNQNDVQDWNRTEP SEITPHIYNYLIFDKPDKNQW GKDSLFWNKWGWENWLAICRKL KLDPLTPYTRINSRWKIDLNV RPKTIKTLEENLDITIQDGMGK DFMSKTPKAMATKAKIDKWDL JKLKSFCAKEETTIRVNQPTKW EKIFATYSPDKGLISRYNELKQI YKKKTNPIKKWAKDMNRHFS KEDIYAAKKKHMKRCSSSLAIRE IQIKTTMRYHLLTPVRMIAIKKG NN/R/CF*WQKPGPFG*ALRSWK EDIAGTSYVGMNQCQMRKNTK TLI
14783	45151	A	14869	1182	3891	KMIKGISTTDLTEIQTTRYYK HLYANKLENLEEMDKFLDTY LPRLNQEEVESLNRPITGAEIVA IINSLPTKRSAGPDGFTAEFYQR YKEELVPFLKLFLFQSIEKEGILP NSFCEASIIILIPKPGRTDKKENF RPISLMNIDAKILNKILAKRIQQ HIKKLIHHDDQVGFGIPGMQGWFN IRKSINVIQHINRAKDKKNHMIISI DAEKAFAFDKIQQHFMLKTLNRL GIDGTYFKIIRAJYDKPTANJLN GQKL
14784	45152	A	14870	997	1161	CTSTVIMSICTKLQNKEHVIJEAL RRAKFKFPGHPKIHISKK*DFT KFNADEFED
14785	45153	A	14871	1	1458	
14786	45154	B	14872	53	1468	
14787	45155	A	14873	1819	2235	

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14788	45156	A	14874	707	1613	VRARAGERARVVRENGKAELP VALVLPSRALSHTFTCTDLKVQ FHQRRLRQEKGSKFQGSNSMSQE SDNNKRLVVALVPMPSPDPFNPTR RAYTSEDEAWKSYLENPLTAA TKAMMSINGDEDSAAA/HRPA *LLQENQSEPIPREGVGVG*GE ERERMRMTEEEQEGEGGGGRRG GEGEEEEEEDVEEEEEEEEE EKEEEFKGGEKEEENEEKEKQR EGRRGKETSNGQMVRPRLLPP HQEHSSRNLYLVFIMDSNIEICF REASISPKAQAYVLIPDFKNCIY GWEEDSIEILWGLPGSHV
14789	45157	A	14875	3	346	QRSKCKVPGGLGKPLTLPPKPE KIPQGQKDRRPTGFKP*N*RRR SEKSLRFPPPGS/PQAVPIPVGFS FDTNL*HFL*KPLIFIMGGTVSL PHPRSPSAPPGTQQRPMTFCHLK Q
14790	45158	A	14876	1868	2666	GLLLSPFQGLQGVAPRKTRSNL HPGSLAHLSHQPPAWPPRGLW PPQETSCCHCASGRALGTGSPR PPHAPWLHLEPQRAHSGAPSP GSSPSAHLIPVAPENLQLSLGHR SPPNPSGPDCYPSPSGP/PPSSL SPGLQTAGAMFLSPRSVGQSA CPTPRSLDLRNSPASTPDQSVCP TPLSLAWLWPPPSPTSAKSLFFT LTSEVQSFSPTRIPPGSSDPPLSK QVPSGSCLSSSHLSLSPSPVRHSP WPRSSPQNPHSWTLPSS
14791	45159	A	14877	762	1528	AIPGGAAWPFRAEGAQGPGR LTKPLGAQRQSVSGSEVPPL PLHLKMAPEMPMVAL*SPGTGV HPSLLPPT/GPKVPPGRIDRGVP TLAPQVGTAPIQWHCRGSRCP G/SRPFGWR/RPCQAPAPPLGQ HLPRLLPPPTGPQGPRLPTSEP PPWCSWLPASPPAGPGSRRVGG GPGTCQGLLRS*G.I.LLSPFQGL QGVAPRKTRSNLHPGSLAHLSH QPPAPWPPRGLWPPGQETSCHC ASGRAVGTGSRRPRA

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14792	45160	A	14878	1	963	MARKDCCSPPGDSSPGRPLVL PAQCLVLLRLQITAFSSIHVAAN DMMSFFLMAQDSIAKYRJFF IHSSVDGHARPLSPSLVVENGC GKQVFVLLCSDNASPEVSTVALA SCPGTFFPRHCAGAESTHICATG LGEELTPQGHGHIPNKLACCAT GLEELVPRDHGKLGIISWFGIA GAYLNLRARVVGECCQGSYGYLS LHHYCYCHYYHYCHYHYHAA TY*NHYYHYYH/HHNNSYHHH SYYHYSYHFYHYYNNCYHHH YHCRHYYHPHDYYHYHA/RHY SLYYCIIYLCHYYYRCYHDHSS HQHNHHECLP*VRHSAEHLQY
14793	45161	A	14879	105	1448	CHQPPASPFSRREP GGEKPPER GCPAWEPAAQGPVQPLGEDGP RLCQPPPSPDHALG\PYGHQRS GRPTLPGPRK\PAKKRGR*PSSS TGQ*SHRPIT\GTPGGQAGGSG* VTAQGQ*PPQNL*AKISCPEMP GPSPGMQQGVKHPSLFSHQTV AKGFTTRWNCRQVCPHRGERK WISSVRPCGGALAPSCA/DGLR GRRTLSGSQPLW/PPAAVSAVG QLQPPCHTLTPHPLQNSTQHAE PQRGSVYSL*EGTSPLAAPVFA PHIEKRFSTFPAGDA*PSEAHA/ PGPACCHSPGGLLEGPVSRAGPG TSAGRIPGNGRERA WPPHSGPS TPPDTS CG/SPGPQLARAGSRRA NGSTLPPTRQGFPLGRKDSAGA CGQP*AE GAAGAGPSRSPA AER AVLPLPR\GRRKCRGGGPGVET GVSGARRGGDRSGCSPAA ALDA EAPASLAGVSI REG
14794	45162	A	14880	1	2421	

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14795	45163	A	14881	1080	2571	VHCRFWILALCQMSRLQKSPLL FNIVLEVLA KAIKQEKIEKG IQL GKEEVKLSLFA DDMIVYLENP1 V/SAQNLLNLISNFSRSVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKR KIYLG IQLTRDVKD LFKENYKPLLNEIKEDT KKWK NIPCSWVGGRINIMKMAILPKV1 YRFNAIPIKLPLTFTDERTTL NIFICNQKRAPTL P QVQSLSIQKN KAGIGTLPDFKLYLQGLQ*PK TAWYWWYQNRDIDQWNRTEPS EIMPHIYNYLIFDKPWEK/HKQ WGKDSL FNKWCWEINWLAICR K1.KLDPFLTPYTKINSR WINDL NVRPKTIK/TLEENL GITNQD/IG MGKDFMSNKTPKA/MA/TKAKI DKWDLI/KLKSF/CTAKETTIRV NRQPTK/WKKI FTTYSSDKGLIS RIYNELKQIYKKKTNPIKKWA KDMNRHFSKEDIYAAKKHMK KCSTSLAIREMQIKTTMRYHLT PVRMAI/IKKSEN SRCWR
14796	45164	A	14882	136	420	RESRNLSRGE ESEDPAEPS/RNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHF RFSICQVN RNFLERGH/ SPSPAPPETHTGSPRPPSGRSR IRAYLH
14797	45165	B	14883	1	1197	
14798	45166	A	14884	3	538	GAGTDGGRT PAPRAFP DPLGEA RTSAPTPARPGGSASAARPA A VRPAEPAAEETQEQPRAKGKRAI HEYRYVYYQQRKTD P QPAVA VFGIPADGD*VSRTAYH AHOPL AWSGR/E*MCLSMAMWNT*ST MKK*ISIRVISRC SGPVHRTN*QI PEPVRAWRFLICRCICFSPGRW1 KT

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14799	45167	A	14885	1208	2765	KMAPTDKVMSSAQMGFNQ ALLEQLSQDELSKFKYLITTFSL AHELQKIPHKEVDKADGKQLV EILTTHCDSYWVEMASLQVFEK MHRMDL SERA KDEVREAALKS FNKRKRPLSLGIGTRKERPLPDVDE MLERFKTEAQAFTETKGNVICL GKEVFKGKKPDKDNRCRYILK TKFREMWKSWPGDSKEV/RGY G*EQDADPPIQQPOGASRALPY TVVLYGPAGLGKTTLAQKLM DWAEDNLIHFKYAFYLSCREL SRLGPCSFAELVFRDWPELQDD IPIHILAQARKILFVIDGFDDELGA APGALIEDICGDWEKKPVPUV LGSSLNRPVLCIENKLGVGGED WGDQLRVYWWNPSCREGGSG WSHGSE DANQSLKHLRLSANV LLDEGAMLLYKTMTRPKHFLQ MLSPWETTLAQIIMLDWAETS SDKLKYYAFYCSCRELSRLCPN FEELVFRDWPELQDDPHILAQ ARKILFVIDGFDPLGGRTLWTL TRGHLRELGNRRKCPSSWV
14800	45168	A	14886	213	625	EPGIDTSCLCAGRCSRPGKGRA CGGSSPCSWPGQPPAPPAAA PACPSGGRGAGPIQSGTCCRS ADSRCTSWTAW/WPPGLGAAT VQTVMS*TV/WPMMPHQAGW LALGOGAAA AKHPLTSATRS WCLGVGP GPWM
14801	45169	A	14887	1	375	MCNAQVLEYMGKSSLLTSDL QLVRDALRSLRNSFSGHDPQHH TIDSLEQGISSLMERLHVMETQ KKQERKPPLVIPRQT/WVWSGP PANSNRPAAEGPDC*KEN*RDA LRSLRNSFSGHDPQHHITDSLEQ GISSLMERLHVMETQKKQERKP PLVIPRQTGSGVDLQQPTDLQ LRDLTVRRKTNEQKGIASASTK RTSTPKPHL

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14802	45170	A	14888	1	750	MGELNQGSWRQGHPLDAAN GIAIRVPRRRKDESRNKPTRKPH SWKPTKNFEDDVEMVKRMSMI RIEDTHSGPSAAGVLEFAGGPL QTLFAWVSPAEAAEQQRLLPVP /CLWKLCPRGAPARCVQRNPSK LPSGFVYTVRGKLPTQASVVVD APPATKLCPRSTSDCCAGSKN FKPVDSLLASVGPRVNLQQES SHYGKISVTVAGHCPTTHATGR LGKQALRWSPMCMSMFIGRALG LVPVEGGLLQIA
14803	45171	A	14889	81	164	VGKQGLEWTPANSSRPAEAGP DC*KEN
14804	45172	A	14890	1	674	MVVYACSPSYLEAEVGGSLSE VEATNPKNSSKKFLDLISEFCK VSGYKISVHKSVALLYTKNDQ AATQIKNLIPFTTAAKQFKYFGI YLTKEERLKPSPRKITKKHTK KRTASLILHAMICSQIPKQQQNE KYQVPOFDQSTIKNIESAKGLD VWDSWPLQNAADGTPPLVIPRQ T/WVWSGPPANSRPAEAGPDC QKEN*QTERNSINIKKDIHTKT PLCI
14805	45173	A	14891	619	931	YLLMDPPLLHSWLVSLGDKV HEFWRGCPSCSFGRFWAVG LVL*APKL*LRQVRSAGKRCGQ KW*IK*/SDRLCVD*NK/WSDSD LKPATSCSLIVTCHSLLGF
14806	45174	B	14892	1	658	
14807	45175	A	14893	48	288	LCSIKKPEKSLLCW*YPGNRVW SGPPAKSNRPAEAGPDC*KEN* QTERNSININKKDIHTKTPSEGH QHQRPKTPKGRI
14808	45176	A	14894	801	1157	QSGPSAAGLLDFAGGLQTLFA RVSPAEAAEQQRLLPFPSGKL RPRGAPARCPQPELSCMRCR*SL LGGVQSGBYMGVRDPFEEAAC PLSELECSAGRSAALLRMVRQG HLGLLKLKP

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14809	45177	A	14895	1	1891	MPVWVTVVKSNTQIGRPGH VSALGFELTKNPWPLTYESGDG RSLGKPGAVSRRGGRHGPHQ QAECDLPAGRIAGPCERGLERQ EKLPPAPQGGAWHRLRSERFK SEDAPKIHVALGGSLFLNLNLA LVNVGSGSKGSDAACWARGA VFHYFLCAFTWMGLEAFHLY LLAVRVFNNTYFGHYFLKLSLVG WGLPALMVIGTGSANSYGLYT RDRENRTSLELCWFREGETTMY ALYITVHGIFYFLTFLGFMVLA LVVWKIIFTLSRATAVKERGKN RKKVLTLLGLSSLVGVTWGLAJ FTPLGLSTVYIFALFNSLQAHKQ LKDRKVGPHFMQGAVFLEGKF WGVDIASFEPQEQQFWWTNLGK EDEDKSFDMPHFSWVEQIEISPEE EAMGSAQMVRGVSGPERGSKK RPQLTVSTAFETRCPNGKKVIQ YKRAKLEKWA PYLNSNGLVSR LTTYEDLQCTNILEIKEWYQNR EDMLELKHNKTTDLKTDYFKP GHPQALRVHSYKSMQPEMDRV IEFYETARV DGLMK REETPRTM TEYYQGRPDFLSYRHASFGR/PS QEAHSEQCRVKPPAHCAKPAE DDV/RKSAFCWSSRRSASSCATT AVRTTSRPPSASSCGA PRWTAK
14810	45178	A	14897	1	425	HVQQTEISRTVSTGSPiLSCSVP VTLPGPVLWFKGN/AGPNRKL iYNFKQQGNPVRVKEIGDTTKPG NTDFSTRIREISLADACTYYCV KFKGRAIKEYQSGRGTQVFVT VSYSSRSQKSEICISGLKSRHQQ NCSFWRF
14811	45179	A	14898	1	393	RQGNFPRAKQIGDTIKPGNTDF STRIEISLADVGTYCCVKFIKG RAIKEYQISGRGTQVFVTEQNP RPPKNRPGAGRSRAHHDAHT CLSALEPERNSTNYFVQPCCLR LLGLTGFAVKIIQTGKERTSK

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14812	45180	A	14899	1	753	MGSSLSPVLYVALPVRQPLIRS VVEERSTKMRVGSPGFAQKFRF YSQGLSWARGEEGLVPAFWL QPYPRPLNPKAEMTEQKENQT YVDGGFRPYIIRRKNLTEGHK AEKEMEPWDGFSDESCRTHCQ VHDYAKHGGEVQRRERVDEQK EHLGRRQDCQQQHLNRRLLHC /TVSGEAPSEASGSVRGHGRAH GLAGSERHGHDAAPEHQQLLQ SVDADHVVPAWYQFWDEG RGILSPGDHKPDRRGAALY
14813	45181	A	14900	6	726	VEGISRTG1QAEQAPGFTT1MP1P VSVPNGDVLTACNMSALSPE GPVLWFKS1GPGQQQ1FSCNGS HFPRVTVENTMVDQTDY1S1LS CSVPTLPGPVLWFKGTGPNR KLIYNFKQGNFPRVKEIGDFTK PGNTDFSTR1RE1S1ADAGTY1C VKFIKGRA1KEYQSGRGTQV1FV TGEVSYTPYPLVYNS1PLWDE ASRGRSRQQS1LFCSLHW*YPR KQDLEWTSSKLQQTCCRVA
14814	45182	A	14901	760	978	KKLLLLLCG1EWHOFSSDGS GGWVPEG*K*GCEH1LLPEDVP SCFGWAECWLVRRTLPLHYV ELCYSFHG
14815	45183	B	14902	772	1165	
14816	45184	A	14903	1	2133	
14817	45185	A	14904	1	1311	MATTPGRALGSLLPTLLLGLTA GQPFI1TG1PSHRTSPGDVPN CTAVPFSNQDFSRDFNVTWLK DSDEHPASAQRLVPDNGGNDFI TSKAWVT1TRQDVSS1ETCEVT HRALAEPLKTTMNLQS1TRNP DGTYSLEHTWQAEAT1EEREF ACWVVHDEQPP1KANV1LQAQ VRRQKGQGSVQPYKLQGQLQR SEPGTR1RLTYASSGFSTHQVT TWLKNKHELNPQTSVQYSGH TYNVTSSVLVPLMDDDVFSHV VCHVEHKLTWFFQKTTGLDQY L/QG/DP*QLCGGHLTLPSSPRAP PQLPGLQHP/VVFHSQVLLFSCL VAVTCLVQRFY1PQN1VHLAWLE DCHTLKGTEQPTLKNNNDRSY TLEKLLL1VNASVQGPERVLTC MM1HEGQPPKRANLVLSTA1AH TAY1PIGSTES1MVT1I1T1SQM

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14818	45186	A	14905	3	341	RRATRPGN*GGRHNAGRSSARL ETGRPAMAPQGRPRLGCRTPQ HPGHWPSSAPGLLPPAPGPVAG MTQAQRWCPEPDAHFLQYTLV FVRHIPQLPKQTPHHYIATRLPC ATQ
14819	45187	A	14906	154	679	GVCCPPLLGGVSS*ATWGSIT* GGNTHLJ
14820	45188	B	14907	1	2554	
14821	45189	A	14908	387	826	ARAACLPRGSARGTAGAGEPP DPAPLHLRGEGPAP/HPRSPRGC MGWPAAAPSTRSPSP*RRCPPLP RPRWSP*SHPGPRASARLPL*LS *RASRSSEAPSPGSLGSVAGQD CSRTGTGFSPPAFPSDGQQTPPP APSSVPTLNSLG
14822	45190	A	14909	86	2223	GQEPCQVREQKACHHILGSSPPPS WEL*EQRPAGP*N**PLTITGT GSTTT*QIRMKVN*MGN/DSPQ GKNTPKMYSGEFSPVVRHVPPFS LSDLKQIKIDLGKFSDDPDGYID VLQGEDILAKAGAIRHLNIGEG THVCCPLLEEGINPEVWATEGK YGRAKNAHPIQVKLKDSASFVY QRQYPLRPEAQOGLQKIVKVL KAQGLVKPCSSPCNTPLILGVQK PNGQWRLVQDRLRINEAIVPLV PAVPNPYTPLSQILEEAEWFTVL DLRDAFFCIPVHPDSQFLFAFED PLNPMSQLTWTVLQPGFRDPSY LFQQAQADLSQFSYLDTHVL WYMDLALLAARSETLCHQATQ ALLNFLATCGYKVSKPKAQLC LQQVKHRLKLKGTRALSEER IQPISAYPHPKTLKQLRMFLGIT GFCQIWINRYGKIAPIPLTILKE TQKANTHLVRRTSLQPVAYL KETGTSLSQPVAYLSEIDVVAK RWPHCLRVVAAIAVLVSKAVK MIQGRALTWTSHDVNSILTAK GDLWLSDNHNEEKIEHNWQQV IAQTYAAQGDLLEVPLTDPDLN LYTDGSSFVEKGLRKAAYAVS DNGILESNPLTPGTSTQALELIA VTQALELEGKREPENPADNASY SCEPLEDLRLLFRRQPIEAVKLQ MVLQMEPQMGSMTK1YRGPLD WPASPCSNVDDIEGTPPKISTA

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14823	45191	A	14910	929	1324	RRYQVQRPSEGTLVYLFWPV/*PVVGVPWLPPTGPD*YSLVPPIP PPRARTPRWA*A*MKGCRRSAT A*WCMC*SCRVPCPSTCPMFHS PCSAMTAVTPSLARP*THGSPPKAQQAPQGVKGPSGGLAEPPWA
14824	45192	A	14911	2	286	
14825	45193	A	14912	220	249	P*N**PSTLTTGTGSTTT*QIRM KVN*MGN/DSPQGKNTPKMYS GEFSPVPRVHVPFSLSDLQKIQID LGKFSSDDPDGYIDVVLQ
14826	45194	A	14913	1	163	EPENPADNASYSCPEPLEDLRLL FRRQPIEAVKLQMVLMQEPQM QSMTKIYRGPLDWAPSPCS*DF LGRGAFAVNINIGAWASRPVQGS AVDLHGLHLGLHLKNHL
14827	45195	A	14914	1	287	
14828	45196	A	14915	2498	2788	
14829	45197	A	14916	112	333	
14830	45198	A	14917	329	1666	
14831	45199	A	14918	1	756	
14832	45200	A	14919	1256	1651	RRYQVQRPSEGTLVYLFWPV/*PVVGVPWLPPTGPD*YSLVPPIP PPRARTPRWA*A*MKGCRRSAT A*WCMC*SCRVPCPSTCPMFHS PCSAMTAVTPSLARP*THGSPPKAQQAPQGVKGPSGGLAEPPWA
14833	45201	A	14920	1	987	MLVLGYNRKNTEGTQKQKGT NASDFHFLSQVLEQVQVSPKGSK EAQCCVLRLHGCESSESAPGIPP NLGIQLLTWAVMWDPFPITLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLKGKERR QREGERRERKREREKRERERESQR KERKREKKGKKREREKDRSDL KQKIDLGKFSJTDGYIDVVLQ GLGQPYYLTVRDIMLLDQTL TPNERSAAITA VREFGDLWYLS QVNDRKITEEREQFTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGRLKTRKKP*IN*SMISTI TQGKEENPTAFLERLREALRKH
14834	45202	A	14921	473	1015	
14835	45203	A	14922	3	937	
14836	45204	A	14923	530	612	LQAKVFFLLRPAILRG*NYGPRGVPH
14837	45205	A	14924	101	430	

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14838	45206	A	14925	1	1587	MAALTLRGVRELLKRVDSLATV PRRHRYKKWAAATEPKPPAVR LALQNFDMTYSVQFGLWPSIR VSLLSEQKYGALVNNAFAAWDH PGDIVLDLCAAPGGKTLALLQT GCCLTWSRKRCALSMFSRPA RCLCRARTTAPRAVRRPDQRR ATAAAATKQQARATPEAPGSAA HSSYCTMIPSACCLPRLKPPH AQPARSAAKPGLDQPGSHARL RGRGEARQSLEAIRGGPSGIA PSDIPLPAKPSRRVIAQTYAARG NLLEVPLTDPDLNLVYIDGSSFVE KRLRKAGIKAVKLQIVLQMPEQ MQPMTKIVCGPLDQPSAPRSNV DDIEGTTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLGKFSDTDPGYIDVILQ GLGQPYYLTVRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPPTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGRLKTRKKPUN*SMISTI TQGKEENPTAFLERLREALRKH
14839	45207	B	14926	1	939	
14840	45208	A	14927	1	4317	MQSMTKMYCGPLDQPSAPCSN VDDIEVKLEIMLLTERDDGKEV LDVGEERRYEIEEYDGSWTRK YNCLAVLVRHSGSQITTMKLIL WYLVVALWCFFKDKGIAASRS GGFSYVGSSSGDLDRKPKLFSL EFGSPGETEDKSQRQRQDAGSPK SEDTAGGFFNSSSSGSDSRTK PFSSLGLGAPGKAEDKSGDSQD AGGSKSEDTPPGGFFYGSSSSG DSDKKKPLFSFEGATGEDEDK SRERWDAGNSRSEDS
14841	45209	B	14928	110	269	
14842	45210	A	14929	1	561	EVFPACSQLVYWGKPITIYPLCE NNVYMLSPNASVCLYSP*LAEQ FSHQFSPSHDLPSPVLAKFSLPVSL SEFRNPLAPAVQETOLIQMVM WMLQRRRLIQLHTYVCLMASP SEEPPRPREDDVPPFTARVGGRS LSTPNALSGSPTSSDDMTLTP SMDNNSAELLPSGDSPLNQRMT ENLLASLSEH

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14843	45211	A	14930	1891	2522	GLSNQNQQPGRCIPDAHPVQDL VQDLVHTWCRVPCTSYYPCV* VPGAYLVHTRCIPGAGPGAYPV HTWCRTWCIPGAGFPAL/RPYH ALLLLSDEKSLLGELPIDCSPAL VRVIKTTSAVKNLQQQLAQDAD LALLQAMGSAVAIVMWAWP RATGPLKYCLRVGAGGACGWR PRLVAVSRAILLVWRCGSPWG PALAWQKSPEYSTKVLEKQ
14844	45212	C	14931	113	274	
14845	45213	A	14932	1	1634	MEIPAVILTVAPILHLTSCGFPV TGDGLKQAEKGKCAPEEWNPTK FIKLTDNQACFACGGLWPLSEIQ RRTSRTVIIHSRISALREKGNGR KPTSiSGSVNEMRQVLVKDQVS MPRVLPITIIFVPEAGFSAGAV WPCAAPLWGSSWTPLKVENC FYIRLSFAISVGGDELKIAKLV AFPERAYDLVGHQHQRPKVDK TTKMGMRNQSRKAENSKNQNM SPPKEHNSSPAREQNWWMENEF DELREVGFRRSVITNFSELKEH VLTHIKEAKNLEKRLDEWLT INSVEKSLNDLMLKTTLREL EAYISFNSQFDQAEERVSVIEDQ ISEIKQEVKFREKRVKRNEQSL QEIWVDYVKRPINLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QANIQI/QGKLQRPTPKVASSRT ATPRHIIISVGSPKLNMKIEKILR AAQRERSGLPTKGKPFRLTAAD LSAETSTSQKTEWGPiFNLKEK NFIQPRISYPAKL.SFISEGEIKYF TDQAKCLRDFTTTRAFSCLP*K STRPALKELLKGST

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14846	45214	A	14933	1	1429	MVLAAGDPVEKGITWARENAGIYISCTMMKLSMIPIGDQSYRNLIPLKFVACILIEGNAKCPWLPFEDPSQIRLIVYQDCERRGRNVLFDSVKKRNEDISVSRKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWEIRINIVKIAILPKKLGSDAQVKVFGKCCQLKPGGDSSSLDSSVTSSSDIHKDQCLKYQRTVDLSAQQLSSSGKGQTSSSGSLTPMTPHWEIIPSSGGQQTSSHTGELRLASGRGSSGMKLPPEEGTDRNLCCSAASSGDTQANRDWSGPANTSRPAAEGPDCRENGTKI.ENTLKDIIHENFPNIARQANIKIQEIQRTQQRYCSRATPRHIVRFTKVEVKEKMLRAAGEKHWVIHKGKSIRLTVDSLQARREWGVPIFNVLKEKNFQLRISYPAKLSFISEGEMKSFPEKQMLRDFVTIRLALQELLKEALNMARE/NR*QPLQKHM
14847	45215	A	14934	2320	2811	ESKLTRGVKDLFRENYKPLLNEIKRGHKQMEEHSMMLMGRKNQYREKWPYLPKVNL*IQCHPHQA TNDCFHRIGKLL*SSYGTKKEPALPSQS*DKRTKLEASHYLTNSYTTRLQ*PKQHRYWYQNRDI DQWNRTEASEIMPHIYTILWLTNLRKTSMGERHP
14848	45216	A	14935	2	872	
14849	45217	A	14936	769	828	
14850	45218	B	14937	1	669	
14851	45219	A	14938	1	807	
14852	45220	B	14939	35	212	
14853	45221	A	14940	235	837	QQAHKTPQRRHSAFTEYVRNNRLPETVIRVKQPALAIIFSPDIAPLFVHFRADDVTATARVIIHAIJIMIFWCDRVEKRVSDAVACFTLESEIAEVGVLCRTHIRQ*RQVTPARM*ALSRILHACRSEDVRHNRPPYPIVVKQPAIRRDLAPTT*PHCSSIAQTITSLPGCMREVIT/ELRPEFFK*RKTVLRPTPIMRARAERRCK
14854	45222	C	14941	1	1755	
14855	45223	A	14942	1	747	
14856	45224	B	14943	1	2466	

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14857	45225	A	14944	1	333	LNLVLFQQRAELMIS*PQ*FSRA LLVIFPLLQTELQQLFFLLHVNP AAVEAPPSVPIGLYSENVRRNNR LPETVIRVKQPALARFSPDIAPL FVHFRADDVTARRVEKCK
14858	45226	B	14945	1	1794	
14859	45227	A	14946	1183	1899	LNRRDSDYVEYLADKVADREED AEEYLEAIMEARVTAGMGLV MEVQDYFDGEADRLAKAWLA EYTPQIKSLKDERKEAQRQIVE MSTEPQDVLDLVRPANKFEMTR VREGEKEADLPVWKKHHL/SV^R KRELSGSVEPLGNQVFEIETKRE NS*EL**KSLKDERKEAQRQIVE MSTEPQDVLDLVRPANKFEMTR VREGEKEADLPVWKKHHL/CDE SGNYPALLNHWETrFLRSKPN VKIHRSDDKSPTYFVFFISQYDL PAFYPINGHFLVERVVKVRIVF EEFADHHHLAIFQFNRLQRHA FVVTLANVTNQPFSSVVVNL
14860	45228	B	14947	1	3099	
14861	45229	A	14948	1174	1545	
14862	45230	A	14949	1	945	
14863	45231	A	14950	62	576	
14864	45232	A	14951	1	1642	MLANIGFYNSNVHRSKGAIGE GPPDPRGIVEQNLGGDISPCYN GPRPRSAQKTTLGPLNQPRIPS AQCAAGAFTPRAVAAAGAGGGGG GGSGGSGFCLGWRLRRRRQR RRWRRGEGEGDGDAIGHMRPR PAGRAEARRRRRLRGNPPIPGAR LPNREGNGSGVSWAAEVSGDG RGARTEAARTRRPGGADNYP GAVPPVQLLTGWCVTAKAPPDI SAISALTAVKHGNCSSTPLLLNP PGSDVIVCAEMDEQWGYGVAK SRQRWLFYAYDSLRTKTVVAHV FGERTMATTGRLMSLSPFDVV IWMTDGWPYESRLKGKLHVI SKRYTQRIERHNLNLRQHIALR GRKSLSFKSVELHDKEELAAL FSELKQEQQKKVDELIAKLVKNR TRIVNESDVFSWVIRREFQELR HPVDEEKARCLEGGGHTRLGV ASLDMQLEQAGTTRERLAQAE LCWNNSSEMRTTMSSSGSSTPWP PVSRRRPWTERRLGSVRGDR ERSPAVNTRPRMSRVPAGPR GTPSRWWMMKCDHQMRG LVEEEVG

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14865	45233	A	14952	1	1513	MIIALQKESLMSLQAQLDKALQ KEKHYLQTTITKEAYDALSRKS AACQDDLTQALEKRTGRDWNP PPFRTQQRGSKSLTAIRPLCLFR KLNHVTSETKSLQQLTQEQK KAQLEEEIAYEERMKQLNTEL RKLRGFHQESELEVLVYEEEMG NHNENTGEKLHLAQEQLAAG DKITSLERSLNLYRDKYQSSLS NIELLECQVKMLQGELGIMG QLSKTSSDLSKM/RCY/TTW*W WTKLQFIHSILTSVIFHLLSFSSM GSI*KWIMALSGSSFLDAHYIS QFGPQLPSPVCAEPEKEATDG VVRNGKSTAGHQRYLCSHCRK TWQLQFTYTASQPAGQ*RHRL RGIMDEQWGVYVGAKSQRQRWL YAYDSLRKTVVVAHREQQSIK CKLEEDLQEATKLLLEDKREQLK KSKEHEKLMEGEALRQEFK KKDKTLLKENSRKLEEEENLR AELQCCSTQLESSLNKYNTSSQ VIQDLNKSPMEIRFOLYIFTPDQ
14866	45234	A	14953	125	363	INVSVWSQPFPGG*QPEKGLKE HPADARPSCCPPAGRPVQGRA EVASAAPPGRGSSPAAAPGQSHP PSCLRAPLYWSFSS
14867	45235	A	14954	306	583	TCSTRRKNDLSVKYVSVWSQ PFPGG*QPEKGLKEHPADARP SCCPPAGRPVQGRAEVASAAPP RGSSPAAAPGQSHPPSCLRAPL YWSFSS
14868	45236	A	14955	225	407	LRGMVTFSPFSSILNGQFEPNSG CPL/CPVCWVCLREP GDPKEKLG EFLQKDNISVHYFCLVS
14869	45237	A	14956	484	722	NTCRGHHNRSPENVNSRRGGLRS IPRMPDAGSCS/PPAGRPSAGPG RRSPPPLPRGSSPAAAPGQSHP PSSSQGAAVLEL

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14870	45238	A	14957	434	1790	GNFFRKTSACIISVLSVLSCLR GASPTEASMDFCLKTSKREAAR ASRKICFVCKKKGAACNCQKDQ CLRNFHLPQCGQERGLPFTIFWR VQIIL*QTSP/EHRTSNMGHVG ESCLCCEDLSPTECLRTFQSPC CSQAIYHRKCIQ*TNMPTHQSK HFFKCPQCNRKEFPQEM/REN GNSYSRQRQCLGTRARGFLRLI SALSAL*CPHLVCMNKAETALR MKGGGASFCVLHADPTPEPTGT APLLDLTVRNGSVRSHL/PAA TDYIPENSGDIPCCSSTFHPEEHF CRDNTLEENPGLSWTDWPEPSL LEKPESSRGRRS/VLLEVQGCQ NH*QLQKIQVTPSE*LLVPHNR V*TCAPPSSGLGREHSGTVRQGS RASSETMS/LSKEKSQWSMRRE QSRCQQGNAFMATRVPLLSPLL LPPRILPP*SCFHMPLLTSPMFV VMQIKVFSPKKKKK
14871	45239	A	14958	146	484	
14872	45240	A	14959	228	353	
14873	45241	A	14960	214	722	TARELPGRVLKEMYIQQK*EGA ALGRPTRPGRQGQRVRAECR RLFRGVLRPCNRC
14874	45242	B	14961	1	951	
14875	45243	A	14962	241	517	QSCGQLPVTVLR/PLRTPWILPM YPQPLPAGGPTPCLRSRPYINITI LKGDKGDPGPMGLPGYMGRE GPQGEPPG*GSKGDKGEMGRP RRPVP
14876	45244	A	14963	748	1055	DRKQTSPGDAYHTIPGSLSSSSD HVLSEPD*GEGSHL**SVQHDD VPPTA**RLQY\RAVVLFPTATL PAILIM*GMRCPLVPRNCSRTW TAQIRAYIEVQQT

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14877	45245	A	14964	1	832	MPHVCAQRRLPVAAVLPPDGQNCILLAGLSAGTFCHHGVHILLSNPVTSLVVAIDRVGQIPPPP PPPPALPYDCCCPPPSRHTEDREHVPIPLHWKLMVNWRFLPVPTEWIA TLSNSSRSSRTCSMQGLSF LDSQVHLKAMIEDLRGNVSKES SPCLADNA DVGQFPMEGQKQDK PKQRIIPFCQGVNTLNSGPHGP VCGGSHYQKQFSEISLSVGVQWTSSRRMSQVGSSSHCRGARL GPNVPRRDGVQDEFSLQPEE DAG*QTSVDPMVLEQYVVVA/ NYQKQESSEISLSVGVQ/VDIJE KNEGWFWFV/STAEEQGWVPA TCLEGQMGRMSFLCSLKKML DWIQRRLVSL
14878	45246	A	14965	1	346	
14879	45247	A	14966	157	413	ALVCS/SSLAI REM QIKTTMRYH LTPV RMAIIKKSGNNRC WRC GEIGTLL HCWL DCKL VQPL WK SVW*FLRN LEIP FDP AIP ILL
14880	45248	A	14967	1930	5781	RAKSPANII MTGSNSH ITLTN VNGLNSP IKR HRLASW IKS QDP SVCC I QETHLM CRD THRL KIG WRK IYQ ANGK QKK AGV AILVS DKTDF KPT K RDK KEGH YMMV KGSI QQE ELT ILN MYA PNT GAP RFIK QV LSD LQR LD D SHT LIM DFN N TPL L TLD R ST R Q K V N K D T Q EL N S A L H Q A D L I D I Y R T L H P K S T EY TF FS A PH HS YS K I D H L G S E A LL SK C K R T E I I T N Y L S D H S A I K L E R I K N L T Q S R
14881	45249	A	14968	1	2235	
14882	45250	A	14969	1	2148	
14883	45251	A	14970	1	1821	
14884	45252	A	14971	1	1248	
14885	45253	B	14972	4	2121	
14886	45254	A	14973	1	1137	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
14887	45255	A	14974	1	1240	MNIDAKILNKILANRIQQHKKL IHHDQVGIFPGMQGWFINCKSI NVIQHINRAKDKNMIIISDAEK AFDKIQQPFMLKTLNKLGIDGM YFKIIIRAIYDKPTANIIILNGQKLE AFPLKTGTRQGCPPLSPLFSIVL EVLARAIRQKEIKEKGQLGKKE VKLSLFADDMIVYLENPVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNRQTESQIMSELPTI ASKRLKYLGIQLTRDVKDLFKE NYKPLLKEIKEDETNWKNIPCS WVGRINIMKMAILPKVYRFNA IPIKLPPMPFTTELEKTTLKFIVE KRARIAKSIPSQKNKAGGGITLKD FKLYYYKATVTKTAWYWYQNR DIDQWNRTEPSEITPHIYNYLIF DKPEKNKQIQLKAFILHKEPVW MWNGMGTNVR
14888	45256	A	14975	1	2241	
14889	45257	A	14976	1	2802	MYGTGYRDVAGKWAIDPDSK REFLDVTQEGIQGCDFSGTCRQ TLSILTQPLRQWGLEGIKKPN WIISEESVSNNGGPPLIPRQTA GVDLQQTPTDLQLRVLTVRRK TNKQKGIASTSTKRTSTPKHL YVTIHKDQSYIKPQRWGKNAIE KLKILKIRVALSLQRNAAPHQ WNKAGRRMSLMSQQKKASEV ESQMNEIKGEEKFREKRVKRNE QSLOEWIDYVKRPLRLIGVPD SDGENGTRLENTLQDI
14890	45258	A	14977	1	2739	
14891	45259	A	14978	1	2478	
14892	45260	A	14979	590	727	
14893	45261	A	14980	1	3255	
14894	45262	A	14981	1	3810	
14895	45263	B	14982	1	3127	
14896	45264	A	14983	1	3325	
14897	45265	B	14984	1	1734	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met #	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, ~=possible nucleotide deletion, ^=possible nucleotide insertion)
14898	45266	A	14985	I	2067	MELKTKARELREECRSLRSRC QLEERVSAMEDEMNEMKREG KFRERKIRKRNEQSLQEIWYDV RPNLHLIGVPETDGENGTKLEN TLQDIIQENFPNLRQANVQIE IQRTPQYSSRRATPRIIIVRFT KVEMKEKMLRAAREKEIQTTR EYYKHLHANKLENIEFMDKFL DTYTLPLRNQEKVESLNRPIG AEIVAVIIN/SLPTTKSPGPDGFTA EFYQRG\LPNNSFYEASIIILIPKG RDTAKKENFRPISLMDNIDAKILN KILAKRIQQHIIKKLIIHDQVGF PGMQQWFWNRKSINVIQHVNRT DKKNHMIISIDEEKAFDKIQQPF MLKTLNKLGLIDGMYFIIIRAIYD KPTAHILNGKKLEAFPLKTGM RQGCPLSPLLNFNIVFKVLRALAR QEKEIKG\QLGKEEFKLSLFADD MIVYLENPIVSAQNLKLISNFS KVSGYKINVQKSQTFLYTNNR QTESQIMSELPTIASKRIKYLG QLTRDVKDLFKENYKPLLKEIK EDTNWKWNIPCSWVGRINIVK MAILPKVIYRFNAIPKVPMTFF TELEKTTLKFIVWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEITPHIYNYLIFDKPEKNQ WGKDSLFNKWCWENWLAICR KLKLDPFLPTYTKINSRWIKD
14899	45267	A	14986	I	1293	
14900	45268	A	14987	I	3229	
14901	45269	A	14988	I	3352	
14902	45270	A	14989	I	1419	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
14903	45271	A	14990	1	1716	MKAЕIKMFFETNENKDТTYQN LWDTFKAVCRGKFIALNAHNR KQERSKID/SQLKELEKQE TYSKASRRQEITKIRAELEKIE ETQKTLQKINESRSWFERINKIDR PLARLIKKRQKQNMQMDTIKND KGДITDPTEIQTTVREYYKHL YTНKLENLEEMDKFLDTYTLPR LNQEEVESLNRPITGAЕIVAIINS LPTTKSPGPDGFTAЕFYQRYKE ELPGRDTTKEENFRPISLMNIDA KILKNILANQIQQHIIKKIIIHHDQ VGFIPGMQGWFNIRKSINVIQHI NRAKDKNHMIMSIDAЕAKFDK QQPFMLKTLNKLVLEVЛАRAIR REKEIKGИQLGKEEVKLSLFA HMIVYLENPIVSAQNLKLISNF SKVSGYKINVQKSQAFLYTNNR QTESQIMSELPTIASKRKYLGI QLTRDVKDLFRENYKPLKEIK EDTNKWKNIPCSWVGRINIVKV AIPKVIYSFNAIPIKIPMPFFTEL EKTLKFIWNQKRARIAKSILSQ KNKAGAITLPDFKLYYKPTVTK TAWYSYQNRD\IDQWNRTEPSE ITPHIYNYLIF
14904	45272	A	14991	1	702	

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14905	45273	A	14992	473	2385	HSFLSFIVLMLTMDLTRSQKH GWASSPSHGTPWPVRLRTSLA KPCKWVQVSLCWVLSASPGSSF SLVRSSLLIIVPHAESVSRPSSL SRVGLFPARY*HRVWQRSPSQ TRDHLIKRNPSQDV*RRQQPRG TRVSNKCSLHTSALGIGRQPSC DATL*GQQGLP/VK*KRQQPAP/ MSQQQTGAALAEVLARAIRQE EIKGIGLQGKEEVVKLSFADDMI VYLENPTVSAQNLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPTIASKRITYLGIQ LTRDAKDLFKENYKPLLKEIKE DTNKWKNIPCSWSVGRINIVKM AIPKPEGWARSVLFQARGLQG QGRCGQSRRGGGSGCLGGGGST ENWQHREPSARKTGSTEENRRH REPAAPRTGSTENQHREPAAPR TGTENRHREPSARKTGSTEENRR HREPAAPRTGSTENQHREPAAP RTGTENRHQEPAAPRTGGTENR QHREPAAPRTGTENRQHREPAAP RTGSTENRHREPAAPRTGSTEN RQHRESAAPRTGSTENRQHQEPA APRTGTENRHREPSAPRTVGTE NRRHRELVAPRTGTENRPREP PAGTRPRHTPMRGGSEGALFH QRRFLEPTPDREQLEGIRYPPVA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14906	45274	A	14993	687	2274	LRDCKRINQHPVKTDQSAFCKM/API/MQDVVLEVLAIRAQEK EIKGIGLGKEEVKLSLFAADDMI VYLENPIVSAQNLLKLIISNFSKV SGYKINAQKSQAFLYTNRQTE SQIMSELPTIASKRKYLGQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPIPCSWVGRINIVKMAIL PKVYRFNAIPIKLPMTTTELE KTTLKFIWNQKARMMAKILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNARDVDQWNRTEP SEITPHIYNYLFDKPDKNKQW GKDSLFWNKWGWENWLAJCRKL KLDPLTPYTRINSRWKDLNV RPKTIKTLEENLDITIQDGMKG DFMSKTPKAMATKAKIDKWDL ILLKSCFIAKETTIRVNQRTKW EKIFATYSPDKGLISRYNELKQI YKKKTNPIKKWAKDMNRHFS KEDIYAAKKHMKRCSSSLAIRE IQIKTTMRYHILTPVRMIAKKSG NN/R/CF^WQKPGPSG^ALRSWK EDIAGTSYVGMNQCQMRKNTK TLI
14907	45275	A	14994	1	3189	
14908	45276	A	14995	1	3351	MGKKQRKTGNSKMQSAPP KERSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRINTEKCL KELMELKTKARELRECRSLRS RCDQLEERSAMEDEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDHSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIYRTLHPKSIEYTFFS APIHHTYSKIDHIVGS
14909	45277	A	14996	1	3192	
14910	45278	A	14997	1	2742	
14911	45279	B	14998	1	2313	
14912	45280	A	14999	1	1542	
14913	45281	A	15000	1	3300	
14914	45282	A	15001	1	1824	
14915	45283	A	15002	1	2982	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hd	SEQ ID NO: in USSN 09/S40,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
14916	45284	A	15003	1	2375	MSGFLISPCKHKGHTNSGIVSWADVQSQLRHIEAAFDQEAALVMARLGVFRAESEEEGPDVLRWLDRQLRLHSLLTLDIVPAGKGEVVKGPMISISQQAKGCQKFGQYNNKEDPTSFRLSDSFLYQPQMFHLRRSPFLQVFNNNSPDESSYYRHHFARQDLTOSLIMIQPILYSYSFHGPPEPVLLDSSSILADRILIMDTFFQIVIYLGETIAQWRKAGYQDMPEYENFKHLLQAPLDDAQEILQARFPMPRYINTEHGGSQKKREKNQIDAIAKNDKGDDITTEPEITQTTIREYYKHLYANKLESLEEMNKFLDTYTLPLRNQEEVESLNRQITGEIEAIINSLPTKKSPGPDRFTAKFYQRTNDQKHMIIISIDAEKAFDKIQQQPFMLKTLNKLGDGTYFKIIRAIYDKPTANILNGQKLEAPPLKTKTRQGCPSSLNFNIMLEVLARAIRQEKEIKGIOQGKEEVKLSLFADDMIVYLENPVLAQNLKKLISNSFSKVSGYKINVQKSQAFLYTSNRQTESQIMSELPTIASKRICKYLGQLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWSGRINIVKMAILPKVIYRFNAIPIKLSMFTFTELEKTTLEFIWNQKRARITKSILSQKNKAEGITLPDFKLQYKATVTKTAWWSYQNRDIDQWNRTEPSEIVPCIYNYLIFDKPDKNKKWGKDSLNFN
14917	45285	A	15004	1	1428	
14918	45286	A	15005	2	1975	

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14919	45287	A	15006	1	3891	MKPEIKMFFETNENKD TTYQNL WDTFKAVCRGF KFIALNAHKRK QERSKINTL TSQFKE LEKQEQT NSKASRRQ EITKIR AELKEIETQ KPLQKIN ESRSWFFE KINKIDRP LARLIKKR EKNQID AIAKNDKG DITTDPEI QT TIREYYK HLYAN KLENLEEMDKFLDMYTLPRLN QEEVESLNRPITGSEI EA INSLP TKKSPGPDGFTAEF YQRYKEEL VSFLLKLFQSIKCEG ILLNLFY DSIILKPKPGRD TTKENFRPISL MNIDAKILK I LANRIQPHIKKLI HHDQVGFIPGMQGWNRK S VIQHINRTKDKN HMIISIDA EKA FDKIQQP FMLK TLNKL GHGTY LKIIRAIYD KPTANII L NQKLK AFPLKTGTRQGCPLSPLVFNIVL EVLA WAIQ EKEI KGIQLGKEE VKLSLFA DDMT VYLENPI SAQ NLLKLI SINF SKVSGYKINVQKS QAFLYTNNQTESLIMSELPFTI ASKR I KYLG IQLTRDVKDLFKE NYKPLLNE I KED T N KWK NIPCS WVGRINIVKMAILPKVIVYRFNAI PIKLPMTFTTDLEKITLNF WNQ KRARIKTSI LSQKNKAGGI TLPD FKLYYTATVT KTA WYQNS MVLVPKQ RYRSMEQ NRALRN NAACIQLSDL
14920	45288	A	15007	1	4215	MHSCLP DTA GEGELY NLSGLST WSFLSMIGVLLWVDFSGDSIDL CSPLWNR TN.EALQKKLE ELEI DEQQQRKRLEAFLTQKQKV GEL KDDDFKEI SELGAGNGGVFK VSHKPSGLV MARKL IHL EIKPAI RNQI RELQVLHECNSP YIVGFY GAFYSDGEI SICMEHMVLLQER PCPGFLWMEN SDYGLLPLD L I CLSFSFSK VLSDLVSD I L HGM KARNR SIHGDVV VV VELLPKNE WKGR TVALCENDC
14921	45289	A	15008	1	2823	

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14922	45290	A	15009	1	3253	MGDFNPLSTLDRSTRQKVNK DTQELNSALHQGDLIDITYRTLH PKSTETYTFSAPIHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRKNLTQSRSITWKLN NLLNDYWVHNEMKAIEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQALKLEKQEQTHSKASRRQE ITKIRAELEKEIETQKTLQKINESR SWFFERINKIDRPLARLTIKKKRE KNQIDTIKNDK
14923	45291	A	15010	1	2816	MEDEMNEMKREGKFREKRIKR NEQSLQEIWWDYVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIEQIQRTPQRYS SRRATPRHIIIVRFTKVEVKEKM LRAAREKGHCHNCNSGKSHRSLWE QNKGIFITTCICDDAEDLQSPSTA GPWFGVLYTKGGVPQDIFSE EVHTGPKLRKKIQEQYQLTQSKWS KSDVQSVERRMAGGNPNQCH IGEVLLDGFTAEFYRKYKEELV PFLLKLQFSIEKEKG
14924	45292	A	15011	1	3347	MGDFNPLSTLDRSTRQKVNKD TQELNSALHQADLIDSYRTLHP KSTETYTFSAPIHHTYSKIDHILG SKALLSKCRTEIITNYLSDHSA IKLELRKNLTQNCSTITWKLN LLNDYWVHNEMKAIEIKMFF TNENKDTTYHNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELEKEIETQKTLQKINESR SWFFERINKIDRPLARLTTKKKS EKNQIDAJKNDK
14925	45293	A	15012	1	3855	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSSELWEDIQTKGKE VENFEKNLEECITRJNTNEKCLK ELMELKTKARELHEECRSLRSR CDQLEERSVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWWDYV KRPNRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMPQRYSSRRAPTRHIIVR FTKVEVMEKEKMLRAARQKAPH HTYSKIDHIVGSKAL
14926	45294	A	15013	1	2559	
14927	45295	A	15014	1	2956	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
14928	45296	A	15015	1	1853	MGRNQSRKAENSKNQASSPP KDCSSSPAMEQSWTENDFDELT EVGFRRSVITNFSELKEHVTNL KEAKHLEKRLDKWLTRIKSVE KILNDLMEALKTMAQELHDTCR SFNSQFNQVEERVSVIEDQINE MNIDGTYLKIIRAIYDK!PPRNII LNQQKLEAFPLKTGTRQGCPLS PLLFNIVLVEVLARA!RQEKEIKGI QLGKEEVKLSLFADDIMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLG!QLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMFTFTELEKTTL KFIWNQKRARIAKSILSQKNKS GGITLPDFKLYYKATVTKTA/W U/YHTPLSCLP*WNRTEPSEIIIP HIMAVAQIQQVKLLLLLQGQHA SSRLQPTSSTKCGGTASSASP RSMGLSSWKGNLASAIHYFPCK PLTLPRISTSSSWGCRQAHAV LEVLRWPPGLGWPGWHHLTL HVPPVRITKSNGPRACTRASAS HARHHQYNQFPLSPLHSPLP PEQVLVSTAERTEDRSYHRTLC RHSPYFKNEAADLRGEGYSS
14929	45297	B	15016	1	3276	
14930	45298	A	15017	1	2274	
14931	45299	B	15018	440	3383	
14932	45300	A	15019	1	2646	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
14933	45301	A	15020	1	2229	MGKKQRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSSELREDIQTGKE VQNFEKNLEECITR/INTEKCLK ELMELKTKARELRECRSLRSR CDQLEERVSAMEDEMEMKRE GKFREKRIKRNEQSLSQEIWDDYV KRPNLRLJGVPSDVENGTKLE NTLQDIQENFPNLARQANVQI QEIQRTPQRYSRRATPRHIIVR FTKVENMKEKMLRAAREKEIQT TIREYYKHLYANKLENLEMD TFLDTYTLPRLNQEEVESLNRP TGSEIVAAINSLPTKKSPGPDGFT AEFYQRYKEELVPFLLKLFQSIE KEGILPNSFYEASIIILPKPGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIIKKLIIHHQVGQFPIG MQGWFNIRKSINVIQHINRAKD KNHMIISIDAEKAFDKIQQPFML KTLNKLGLDGTYFKIIIRAYDKP TANIILNQKLEAFPLKTGTTRQ GCPLSPLLNFIVLEVLRALARQE KEIKGIGLGKEEVKLSLFAADDM IVYLENPIVSAQNLKLISNSFK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRKLYLGIQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVK AILPKIGKTTLKFIWNNKKSRIAK SILSQRKN/KAGGITLTLQYYKA TVTKTAWYWWYQNRDIDQWNR
14934	45302	A	15021	1	960	
14935	45303	A	15022	1	2928	MEDEMNEMKQEKKFREKRIKR NEQTLQEIWWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRMPQRYS SRRATPRHIIVRFTKVENMKEKM LRAAREKDRSMRQKVNKDTQE LNSALHQADLDIYRTLHLPKSTE YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEIIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNNNN DYWVHNKMKAIEKMFETNEN KDTTYQNLWDAF
14936	45304	A	15023	1	1782	
14937	45305	A	15024	1	4881	
14938	45306	B	15025	1	5962	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
14939	45307	A	15026	1	2053	MKAEIKMFFETNKNKDTTYQNLWDAFKAVCRGKFI ALNAHKR KQERSKIDT LSQLKEQEQTHSKASRRQEITKIRAE LKEIETQKTLQKINESRSWFFERINKIDRPLARLLKKREKNQIDAIKNKGDITTDPTEIQTTIREYYKHL AYNAKLENLEEMDKFLDTYTLPLRNQEEVESLNRPITGA EIVAIINSLP TKKSPGPDPGFTAEYLQRYKEGAVLEV LARAIRQEKEIKG IQLGKEEVKL SFLAGDMIVYLENPIVSAQNLKLISNFSKVSGYKINVQKSQAFLYTNNRQTESQIMSEL PFTIASKR KIY LGIQLTRDV KDLFKENYKPLNNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVYIYGNAIPIKLPMTFFTELEKTT*KFIWNQKRARIK*ILSQKNKAGGITLPDFKLYYKATVTKTAWYWYQNRDIDQWSRTEPSEIMPHI NYLIFDKPDKNKKWGDLSFN KWCRENWLAICRKLLKLDPLFTPYTKINSRWIKDLNVRPKTITLLEKLSNTIQD IGMGKDMSKTPKAMATNVKIQKWDLIKLKSFC AKETTIRVN RQPTTWEKIFATYSSDKGLISRIYNELKQIYKKKTN NPIKKWVKDMNRHFSKEDIYA AKKHMKKCSPSLAIREMQIKTT MRYH LTPVRM AIIKKSGNNRC
14940	45308	A	15027	3	3229	
14941	45309	A	15028	1	3907	MGDFNTPLSTLDRATRQKV NKTQELNSALHQADLIDIVRTLHPKSTEYTF SAPHHTYSKIDHILGSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNR SITWKLSNLLLNDYWVHNEMKA DIKMFFE TNENKDTTYQNLWDTFKAVCRGKFLALNAHKKQERSKIDT LSQLKELEKQEQTHSKASRRQEITKIGAE LKEIETQKTLQKINESRSWFFERINKIDKPLARLKKREKNQIDAIKNK
14942	45310	A	15029	1	4005	
14943	45311	A	15030	287	2708	
14944	45312	A	15031	1	4602	
14945	45313	A	15032	1	4806	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met ind	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
14946	45314	A	15033	965	5928	TWKGTTTSRCKIMPKYRSTRQ KVNKDQTQELNSALHQADLIDIV RTLHTKSTEY/TFFSAPHHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRINKLNQSRSTT WKLNNLLNDYWVHNEMKAE IKMFFETNEKNKDTTYQNLWDA FKAVCRGKFIALNAHKKRKQERS KIDTLTSQLKELEKQFQTHSKA SRRQEITKIRAELEKIEIETQKTLQ KINESRWFFERINKIDRPLARLI KKKREENQID
14947	45315	A	15034	383	8708	
14948	45316	A	15035	2	3257	WRKIYQANGQKKAGVAILV/S DKTDFKPTKIKRDKEGHYIMVK GSIQEEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSTSHTLIMGDFN TPLSTLDRLLMRQKVNKDTQEL NSALHQVVDLIDIVRTLHPKSTE YTFSSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTQSRSTTWKLNNLLLN DYWVHNEMKAEIKMFFETNE KDTTYQNLWDAFKAVCRGKFI ALNAYKRKQERS
14949	45317	A	15036	1	3508	MELKTKARELREECRSLRSPCN QLEERVSAMEDEMNEMKREG KFRDKRKRNEQSLQEIWDFVK RPNLRLIGVPESDENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSRRATPRHIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIITN YLDHSAIKLELRINKLTQNHST TWKLNSLLNDYWVHNEMKA EIKMFFETNEKNKDTTYQNLW TFKAVCRGKFIALN
14950	45318	B	15037	1	4760	
14951	45319	A	15038	1	3110	
14952	45320	A	15039	1	5546	MELKTKARELREECRSLRSPRN QLEERVSAMEDEMNEMKREG KFRKRKRNEQSLQEIWDFVK RPNLRLIGVPESDAENGTKLEN TLQDIIQEDFPNLARQANVQIQE IQRTPQRYSRRATPRHIVRFT KVMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSTSHTLIMGDFNTPLSTD RSTRQKVNKDTQELNSALHQ DLIDIVRTLHPKSTE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
14953	45321	B	15040	1	4534	
14954	45322	B	15041	1	1826	
14955	45323	B	15042	1	1626	
14956	45324	A	15043	248	1212	NSKHYRSGQKKKLPTLPRAN SRWRSLSKI/GFTVSFDETLKPFV RDVSGSRLKDLPKPNKSDDETR ANDAVNRYKLLKKDARTIAAQ QVARLESAMCLRRRWSLENFQ LFLVEHPLVRHLTRRLIWGVYS AENQLLACFRVAEDNNSSTADD DLFTLPEGDISGTPHVLIESPTD AAALLFADYELLPPFRQLDRNS YALTEAERNASELTRWAGRKC PSGRVMGLANKWIKGEPODG GWIGWMIKPLGRWLSLIMEIDEG FAVGMSPAELSAEQLLSKLWL WEGKAERYGWGSNSTQEAQFS VIDAITASELINDIEALFE
14957	45325	A	15044	1	1788	
14958	45326	A	15045	1	3048	
14959	45327	A	15046	1	3546	
14960	45328	A	15047	969	1205	SPVRCCISAVHRTYHRRTSALL RRAELIIRLLEKCASTRQWMYEN I*SPFRQIA*CLPYSDHKNQLRH GLDSIFLARLLW
14961	45329	A	15048	877	1248	WPLTVPYCGVGYAS*A*VADN HRAVGYLSRWAAGRKCPSGRV MG/LANKGWIKGEPOQDGWIG WMIKPLGRWLSLIMEI/DEGFAV GMSPAELSAEQ/LLSKLWLWEG KAERYG/WGSNSTQEAQFSVID
14962	45330	A	15049	854	1313	DHGVASAATCVYTHEGHRQSY VRVCEYASRTRVSHHCSV*RVL RCEAIRIVSPDRSC*RDPEFSYLV ALPENYNRFLPNSTNQTNRNI KTLNSIAIGKLLAAGGVYNGNI EGFRDTAEKLKDGRITDGYDQIL NEKTAVIAKATA/SILLTKRS
14963	45331	A	15050	1010	1396	KPFGKLTYKLFEGHAWLVKA KVRVGYRILGRLTYPFDIRFPAL PFGLV*KGAFHTVPRIWAGHA C*LMPMALPMFRWKVTGLFIP ICLVKPSFLTLTIIAIRRISTSTN CRKTPKQPSRWCKPR

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14964	45332	A	15051	361	837	DGQQLIALHRLALRELQQAVH AGLPQQAKIL^DGGSEIKGKIPSEI YFCQLVKLILCPVLFCPCWRVVA ILWRRRDVLFFGSFSFSALVSPH LCG/SYLPFVFDVGDRL*LSVG WSKEIWPKCK^GFGHLMMSVLNT PMKSLVEGFKHPLAGFGYEYL SFFCR
14965	45333	A	15052	1563	1652	
14966	45334	A	15053	2756	2995	AMRSAHRCVTFSALLNCWQITP HILTPSVMICGQLLTNVNRC*PSS TIFSILPLSKQVARMFRSAMSPL NRARCWKVPCN
14967	45335	A	15054	762	2184	WRAVPSEPIFILKADTEKYVY L^NSSSAQYSGSCTRAYYLDTQ HPTPLCLIPGGKDSLMLHLT AELARQMGKKICVLFIDWEAQ FSCTINYVQSLRELYTDVIEEFY WDALPLTTQNSLSQYQPEWQC WEPDVEWVRQPQPDQAITDPDF CFYQPGMTFEQFVREFAEWFSQ KRPAAMMIGIRADESYNRFAV ASLNKQRFADDK^PWTAAAGG HSWYIYPIYDWKVADIWTWYA NHQSLCNPLYNLYQAGVPLR HMRICEPFGPEQQRQGLWLYHVI EPDRWAAIGSPADREEDAEYYL EAIMEARVTVAGMGLVMEVQ DYFDGEADRLAKAWLAEYPTQ IKSLKDERKEAYRQIVEMSTEP QDVDLVRPANKFEMTRVREGE KEADLPVWKHHLLCDESgnyp ALLNHWETKVFEIETKREGFAF WYRNPOYTGQSSLGIAVEAE QYKIVRPDFLFAEQDGKMVV
14968	45336	A	15055	2069	2586	PWLENLPVGICWSAVKKMGGT RSLVSCL/AVTLVSPQLMNAYL LGQQLPEVWDFGMFSIAKVGY QAQVIPALYLVVVPVCSLILAV FLAHALIGPFGRMIGDGVAFAV RHLMTGSFAPIGAALFGFLYAP LVITGVHQTTLAIDLQMIQSICG TPVLPVNALSNDLWHISILV

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14969	45337	A	15056	356	1205	APASMTFEQFVREFA/VMVFTK RPAAMMIGIRADESYTVLSPSP V*INNVPLTTWTFPQTIYDFLW LIGEAIFF/YLPVGICWSAVKKM GGTRSLVSC/AVTLVSPQL/MN AYLLGQQLPEVVWDFG/WCSLII/ AVFLAHALIGPGRMI/GDGVA FAVRHLMTGSFA/PIGAALFGFL YAPLVIT/GVHQTTLAIDLMM QSMGGTPVWPPLSNAQGSA VIGHISSRKHNEREIPGEVFPRT GVGKGKSLG*PLH*LOPYRQHL GAGSYSQTLKKQIAESAVRLSIP
14970	45338	B	15057	1	435	
14971	45339	A	15058	2	1785	WLLYRAHVKG/E/STEALPPNM VATSLAKLPIPKLMRWGATYV HFVRPVHTVTLLGDVKIPATIL GIQSDRVIRGHRFMGEPEFTIDN ADQYPEILRDSGVIAIDYEERK AKIKADAEAAARKIGGNADLSE TLLEEVASLVEWPVVLTAKF/E EKF/LAISRTALVPYSADNMYQ LVNDVQSYQFLPGCTGSRILES TPGQMTAAVDVSKAGISKFTTT RNQLTSNQSILMNLVDGPFKKL IGGWKFPLSQEACRIEFHLDFE FTKLIELAFGRVFKELAANMV QAFTVRAKEVYSASMRYIYIVV YISYRPPNLLDSHIIIGFSSTTHC AVTSHHYNSCDMTMTIHSYVT PYISVRSVSLTQTYAPSPSRNLRI TDLTIYRAISSEKSIDDTRHIHTI ESRCRVCGAHDSRDAERLDRF AQTADEIRIADRGFSSRPECIRS LAFGEADYIVRVHWWRGLRWLT AEGMRFDMMGFRLGLDCALIS KTRLSENRRKGRVVVQAEITLE AAGHVLLTSLPEDIYSAEQVA DCYRLRWQIELAFKRLKSSLHL DALRAKEPELAKVGIFANLLAA FLIDDIQPSLDFFPRSAAGSEKKN
14972	45340	A	15059	1	993	

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14973	45341	A	15060	1	5621	MSEKTFI <sup>VEIGTEELPPKALRSL</sup> AESFAANFTAELDNAGLAHGT VQWFAAPRRLALKVANLAEAQ PDREIEKRGPAIAQAFDAEGKPS KAAEGWARGCGITVDQAERLT TDKGEWLLYRAHVKG <sup>/VEGETA</sup> LLPNMVASSVAKLPIPKLMRW GASDVHFVRPVHTVTI <sup>LL</sup> LGDK VIPATILGIQSDR <sup>/</sup> VRIGHRFMGE PEFTIDNADQ <sup>/</sup> YPEILRERGKVIA DYEERKAKIKADAEEAARKIGA KAWGTV <sup>NEFHVNQNP</sup>
14974	45342	A	15061	82	732	
14975	45343	A	15062	1	3849	MDLGANGWQTFRYVVLVPNLS ALLAGGMLAFALSFDEIIVTTFT AEQVDAAVRAADAFAEWGQ TPKVR <sup>A</sup> ECLLKLAD <sup>V</sup> IEENGQ VFAELESSNNNTAFARASSNGDL PTKADLQAQLDSL <sup>N</sup> KQKDLSA QDKLVQQDLTDTL <sup>A</sup> TD <sup>L</sup> DKIDRI KEETVQLRQKV <sup>V</sup> AEAP <sup>E</sup> KMRQA TAALTALSDVDNDEETRKILST LSLRQLET <sup>R</sup> V <sup>V</sup> AQLDDLQNAQ NDLASYNSQLV <sup>S</sup> LQT <sup>Q</sup> PERVQ NAMYNA <sup>S</sup> QQLQ <sup>Q</sup> IRSLRDG
14976	45344	A	15063	219	1186	PPKLGKRG <sup>I</sup> FLPSHSNPNTNRI CPNCMNGV <sup>ST</sup> ANTTSKSSLV <sup>I</sup> CAWTKH <sup>A</sup> LLNAILQ <sup>P</sup> EQ <sup>L</sup> WKS GSRW <sup>I</sup> RLN <sup>L</sup> ALP <sup>R</sup> GY <sup>R</sup> ES <sup>L</sup> QPW QAER <sup>L</sup> TD <sup>K</sup> GEW <sup>L</sup> LY <sup>/</sup> RAHV <sup>K</sup> GESTE <sup>A</sup> LLPNMV <sup>/</sup> ATSLAKLPI <sup>P</sup> KLMRWG <sup>/</sup> ASDVHFVRPVHTVT LL <sup>/</sup> LGDKV <sup>/</sup> IPATILGIQSDR <sup>/</sup> VIAA TGKAKIKADAEEAAR <sup>/</sup> KIGGNA DLSE <sup>S</sup> IL <sup>E</sup> EV <sup>/</sup> ASLVEWPVVLN AKFDEK <sup>/</sup> FLAVPAEALVYTMKG DQ <sup>/</sup> KYFPVYANDGK <sup>/</sup> LLPNFI <sup>/</sup> F VANIESKDP <sup>/</sup> Q <sup>/</sup> QIISGN <sup>E</sup> KS <sup>F</sup> V <sup>R</sup> LADA <sup>FFF</sup> /NTT <sup>*</sup> KRLFLPHQKL PPSQLH <sup>H</sup> QQT <sup>R</sup> NYAS <sup>F</sup> CHR <sup>H</sup> R <sup>D</sup> NWTSA

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14977	45345	A	15064	1	1496	SGGCAGLHGGI.CSKEPFQASV QQGVAGHACAPAALQVPVCGT LSDCGSRAASLCENPSFLSYLGR LVATSLAKLPIPKLMLRWGASD VHFVRPVHTVTLL\LGDKVIPAT ILGIQSDRVIRGHRFMGEPEFTI DNADQYPEILRERGKVIADYEE RKAKIKADAEAAARKIGGNAD AKFEKFLAVPAEALVYTMKG DQKYFPVYANDGKLLPNFIVFA NIESKDPQQI/DRIQALAGWIAE QIGADVNHATRAGLSSKCDLM TNMVFETTDTQGVGMGHYAR HDGEAEDVAVALNEQYQPRFA GDDLPSPNVACALAIADKMDT LAGIFGIGQHPKGDKDPFALRR AALGVLRIIVEKKNLNLDDQLTLT EEAVRLYGDKLTNANVVDDVI DFMLGRFRAWYQDEGYTVDTI QAVLARRPTRPADFDWDHALG RAGTGDVVVGVGRGLAIVPLT DGLDEAGHSTGVLQGEVPQRL ERAATPGVTLQPOALQARGL
14978	45346	A	15065	134	384	VTPTGWRKRRIRQWCSDAGCG VNALSGLRFSHSLALFSAAAMFI LGVVSGITMSISP*ILSCVRSKNP LLVSGSGPLSCNSTIH
14979	45347	A	15066	1	723	TKSPKIAERSRHIPLCHFIFERRPI MTNSNRKLTWISFLSYALTGA LVIVPGMVMMENIADYFNLPVSS MSNTFTFLNAGILISIIFLNAWLM EIVPLKTQLRFGFLLMVLPVAG LMFSHSLALFSAAMFILGVVSGI TMSIGTFLVTQMYEGRORGYR LFLAASLFSMAGMIPPMIAAFL LAPSS*W*WVYACLGLAYVTIF IMTFGCEFPALGKHAKPSYAPV EKVKWGLGASSFRAV
14980	45348	A	15067	422	1045	LLEGKLTNRKQ*HQH*QKARPC KKPIQSQAQN/WNREYYDELTEV GRRWVITNSFELKEHVLTQWK EAKNLDKRLQEGLTRITSLEKKI NDLMVLKNTARELHEAYTSINS RJDQAEERISEIEDDQLNEIKLED KIRGKRIK/RQTNKQSL*KMWD YVKRPNLRLIGVPESEDEENVTE LENTLQDIIQENFPNLRQANIQ IQEIQTLR
14981	45349	A	15068	1	1131	

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14982	45350	A	15069	383	756	LNPSNKLALINPAASPIIKGVDT TANQI/PCIADIPLYDADVQQE* CFPATVEALGEQIRQADGVVIV TPEYNYSVPGGLKNAIYWLSRL RQILVFLDAMVMNKPEFMGGV IQNKVDPQTGKVIDH
14983	45351	A	15070	343	924	
14984	45352	A	15071	223	308	
14985	45353	A	15072	57	5546	NKMARKKKFSGLEISLIVLFVIVT IIAIALIVVLATKTPAVDEISDST STPATTRVTTNPNSDGGKCPNVL NDPVNVRINCIPEQFPTEGICAQ RGCCWRPWNDSLIPWCFFVDN HGYNVQDMTTTSIGVEAKLNRI PSPTLFGNDINSVLFTTQNQTPN RFRFKITDPNRRYEVPHQVVK EFTGPTVSDTLYDVKVAQNPFS IQVIRKNSNGKTLFDTSIGPLVYS DQYLOQISARLPSDYIYGIGEQVH KRFRHDL
14986	45354	C	15073	1	1818	
14987	45355	A	15074	493	576	
14988	45356	A	15075	381	498	
14989	45357	A	15076	48	514	LLLFLLLQSYYDWSESGKRQSA HGRQKGLPKSPTAARGGSDPW PSCRHP*GPNRKRRKS/R*PMET APRRPSVSPALTPARPPGLTATP RLHPRPP/RSPNPSANLRRPTP DT*AHATGPGGRSRHIFPGQLS TE/RRRSAEGGRSRNEASRRE GGE
14990	45358	B	15077	1	1116	
14991	45359	C	15078	249	332	
14992	45360	A	15079	710	1326	RAAGNCFPEPGFVKQLAAAA VVAPAAAATEGSIPDTGKSPSSI SHWPNPQKVNICKRRGRVEQE QAWEKGR*RVVFGI*KSMRCP VDLLPQSCLCQRFLHQ/GKWIL TKDYIHSAKSGRWLDAATYYE WGYKIEKDOSRYSPQMOSAPKR WREELKRTGAPGAFHRWKVVL LVRTDKRSDSLIRFSDFGDCDI RMEEKTFRTLMES

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14993	45361	A	15080	602	1257	FGKRGRTITLCLAVGMLCCRKGHTKPRRRPGASPITHLHSSPPISTHLHTSPPPHRREEARSGQ*RQSCGAAAAR*PWWWNCDGWGPKCQRFSKH*DIAQPDDEVSWGQ*PWAVGALAGPHP*PQASEGPLGCTPASICGSTRKPSKPLSKKPPQAARTSSSRIVFTPISTRPTTQGQPEAKASATPTNDLEGPSAKVFKVNFLMDETFPEPSFFF
14994	45362	C	15081	140	175	
14995	45363	A	15082	2295	3089	NLLGYQEINPPLQIFWDKLLAVSERDSSVKEESGDVESDDTML*MLPCP*ETTEFSS*PFRSS*LSS*STAQIPAAETCFAGGGWYSIFCPQRIEQETMCLL*SWQSEVAVSCESPWPTALHHSHPNNSRAPPPCY/SKSTSSSLSSPLENSG*QNRPPSSLITSVLPLRITCLP*VSFIPPIMLQGGSFLSNDRL*QSFILPKNVSLEFVSFPLI*GAVSKPAISFNTSVSPLVSDIFFALSLLP*GLGTWLISSSLLLVRGF
14996	45364	B	15083	143	1727	
14997	45365	B	15084	307	1017	
14998	45366	A	15085	1	959	MSRMGLLGFGERKELPNHPAVSEWPLTLVTGCGSGTVAAEGEGNLTTSGLFSIVPLHPDGVAAGQRHSSLPRWGSQAEALLTSQTVDGQAEMLLTPQTMGQOEMLLTSQTTGEDFTIRTSGESGTHSKSHKGDEGEPRWMLGWMLWVCDIAEPLVKAKLLDCCKHTCCSVCLQQTRTSQKDVRCPWCSCGVTKLPPDFSVSQLDDPEVLAUTIPHASEHMPVFIIRLPGSGCY\SCPCPSPRS TRCCPEI*AATCCPGTGRSPSL\CDIHCWTAASARQGSPGGGGAGQAGHGEKLHVVEGVHCHLGGIRLGLPPQHRAP
14999	45367	B	15086	112	672	
15000	45368	A	15087	2	530	SGRSAALLSARVNRSQSFAVGLGSHERGPRSFVFSPPGPPRKPPALSRSVRMFSVAHPAAKVPQPERLD\WVYTALKRGPDGLLGAVHQQEQEKLQGQIRESKRNS\RLGEWREGFLYDLDKQVKSIERFLRRLEFHASKIDELY\AYCVQIRRRL\DGALHMGRAYTTGSPGSR

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15001	45369	A	15088	216	1369	EPVLLRRPRQPRAGAQGFPVFS PPGPPRKPPALSRSVSRMFSVAH PAAKVQPQPERLDLVYTALKRG L/QAYLEVHQEQ/DKLQGQIR ESKRNSRLVMAGGVLTWTVV*E RGAVTSLASAAGVLLIPPKYLPPL LPTPAGIALLYDLDKQVKSIERFL/ RRLEFHASKVRVQHVCRWWD ELYEAFCVQRRLRDGAYNMV RAYTTGSPGSREARDTSLEAETR GHREYTE/DEGWGPMRQRHRS MCLLES/ELEAQLGFEFLRMKG CAVDINDLGTIKLSLEVTA SVNKASTVTKRSPPIARAHRT PHFGNSFLSTRKPNTYTA RPIEQHPDMRTTPPPHARTNT GRKDVKRAHEGEKATPTTRG APHGKAQRRLRPLYQYVNTIATLS
15002	45370	A	15089	1	940	MSYN SKNYVETITTMNSVKFG ETTPRN RTHYLSTNEKKI KIFLSGV FSNAYPAGLSRGWDSWGSTP WVRHFCYLSSTQLCDQNCSSL SLLPAGPSVCNRLLASA WQKSS SSASSEASETCQSVSECSSPTSD WSKVVGSHQPSGATLQRKDR VEVPCETQSPGPASGGTLGP SEAPR PRMSPATIAAKHGE VSP AASDLAMVLT RGM SL*HQKSS RDSLQYSSGYSTQTTTPCS EDT IPSQGRPA GLGPTKPV SIESTYL QSPQR LKQEWATE GKIQKLPPQ IQVNNFQV DSSPSLPLIMVPEH MHVS
15003	45371	B	15090	1	777	
15004	45372	A	15091	26	336	KISPMINVFCSESSPSGERRGA* TPPSQSPPCGPKPSSPPCS NYFLLFQGLCAEHPALA AAAS VGTCPSPASGTHAAAP SGPWRG RCVHSGPGRLW
15005	45373	C	15092	46	423	
15006	45374	A	15093	1773	2219	ELDYL YCSNSSAQC PGALLPSL ALPGPAGSARQAGSPARRLC AP VQPSGRW PAPGGPGFP GSSCPA SPT RQ*LLTSGSGC P RCHPSG PPQ*QSTQAWD WVILGP GAHG PSGQR CERCLPS RSPG PQTHSG VGSE PRA VRGPG GVSFV
15007	45375	B	15094	1	7916	

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15008	45376	A	15095	16	545	GLPWRQHVRVEECCGRS/PLRPC SPGTPSPS*PLPAATRGPATCQS LSGLQPEKTT/SPS/CAVAHER PPGPVPCPAQGTGLI^*EGWT QPQQIRQGPHPHVAHECAHDLQ QAAPGPGGAHQG/PSQPG*PDR QPDAERA VVHPGAQ*DAEIQPG LPGEFGGPLATRTERSPAQRSP QARG
15009	45377	A	15096	320	1167	MDLKTAVFNPARDGKLRLLLTK *IMASKSKEEVSSLISEKTNGAT PLLLMAARYGHLDLVFELLEQC SASIEVGGSVNFDGETIEGAPPL WAASAAGHLKVVQSLLNHGAS VNNTTLTNSTPLRAACFDGHL IVKYLVEHKADLEVSNRHGHT CLMISCYKGHKEIAQYLL^KG ADVNRKSVKGNTALHDCAESG SLDIMKMLLMYCAKMEKDGY GMTPLLSASVTGHTNIVDFLTH HAQTSKTERINAELLGATLFT QKEISCDESGRTRDLSPRRKPPH
15010	45378	A	15097	187	623	KLKTQKNNIGPQACNSLASVS TRSPPTTLSVPIIMTDDSQASQL LLAAVTIRKLWSRMAPMLALP TGQSGQTGAEGQQGKEGERGQS PCWKPRLDPKLC/EPRQPAQLL* ADVCTGP/CGVRGCPADCRLPC LSPSSAQPKEASRSA
15011	45379	A	15098	789	1041	
15012	45380	A	15099	707	1373	SAWPSCHCCHLDILSR/PGDDA CSVQLVPGLKGDAEGKGDKG APGRPGRVGPTGEKGEKGDKG DIGPPGPNGEGLPCECSQLRK AIGEMDNQVSQLTSELKFKINA VAGVRETESKIYLLVKEEKPYA DPPLSWQGRGGTLSMAQDEAV HGLKGAYLGOARLGRGFIGIHR PWKRRAPILLF*TLSPLRSF*KG DGGGNTQKGSRKKKRELAGQW GPCIRR
15013	45381	A	15100	79	420	WRRLFLLGVFRGYLGCLRS VLGRLKVSDMRIFFFACCGCGHL STLPSWPLRPSLWLRL*EEQELP SLSVPSSGRSASRLL*LGWRGF GPSPSRLLTVQFSGGRRQAQGPs
15014	45382	A	15101	3	284	
15015	45383	C	15102	83	112	

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15016	45384	A	15103	84	303	EEQELPSLSVPSCLWGPCRAG WLHSLHWPVSHFSATSTFGM AIWT*SLASGIKPQSSSKVSSRIQ VPPTM
15017	45385	B	15104	112	462	
15018	45386	A	15105	326	1323	DRKAINLQVKLEGAVAL*KP\G EAQLEFGKALGLFQ\STLGHHF VNNKEKILGDFQEA\TLQAA\TK L\TRGRSLVMENMEQ\LLSMRME DQSQRNMP\LSVVLIREKAHSPF ENRKQE\QGEGAS\PNFRAR\QG *FLAFKAAPP\AASGP\AAQER SVQEP\SVNAPG\IPEGGLHTLA GVH\H\*ALA\WC\SP\LN\KPRFLW KRLP\SR\TFHFP\VEDE\SPGSKP SGD\LLTLLGGNAAGDF\KLK\UP CLVY\PS\EN\PCFLKG\SF\KP\NLPL VWCSH\KK\AWV\QPG\QSE\TPFQ KKKKKKKK\AWV\TMSL\QEW\FL LH\FC\ST\VE\AR\CT\QY\DL\PKGL PILD\ST\PG\HP\GC
15019	45387	A	15106	3	375	HASAHASGLLQQSYQAVKEKSS EALEFMKRD\LT\EF\TQV\QHDT ACTIA\ATASV\KEK\LA\TEGSSG ATE\KM\K\GL\SD\FLG\VI\SD\TFAP SPD\KT\T\STAM\SS\Py\DG\TK\AR\LY S\Q\SD\PA\TY\CE\N\EP\DG\PP
15020	45388	A	15107	184	377	YCTNNQKV\N\TKE\I\TK\RK\TP\SR QKKD\SA\FS\PS\H\PL\TE\GL\W\ND L\T\LS\VS\LT\HD\GF\W\RR\G\K\GV
15021	45389	A	15108	3	816	SWEDVGW\W\RS\WL\QQSYQAVK EKS\SE\AL\EF\MK\RD\LT\EF\TQV\Q H\DT\ACT\IA\ATASV\KEK\LA\AA CSR\GAC\FLC\PC\PS\I\Q\TE\GSS\GATE KM\KK\GL\SD\FLG\VI\SD\TF\AP\SP\SD KT\ID\CD\VI\TL\MG\TP\SG\PA\EP\YD G\TK\AR\LY\SL\Q\SD\PA\TY\CE\N\EP\DG P\PE\LF\DA\W\LS\Q\FC\LE\KK\GE\I\SE LL\VG\PS\I\RA\LY\TK\VM\PA\AV\SH SE\TF\W\H\RY\Y\FY\K\V\H\Q\LE\Q\EA RR\DA\LK\Q\RA\VS\G\DS\CT\*SG\VL T\NE\*KG\SW\VR\DT\ER\VR\SL\PL\QT F\SEG\VG\W\RE\C
15022	45390	A	15109	1	281	

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15023	45391	A	15110	1	1194	MGFLHLGQAGLEFLTSGSSTD SEDWEKDFDLMTEEEVQMAL SKVDASGEPCFWKGYPGEL ETLIRLLQKLFFLKTDPAFVLSP STLVKLLHWGNEGLQESLESLV LHDAALVILVPNLEKGEISELL VGSPSIRALYTAKMVPAAVSHSE FWHRYFYKVHQLEQEARRIA RLKQRAEQSISEEPGWEEEEEE LMGISPSPKEAKVPVAKISTFP GRTLAPQSPCEENLVTSVPE EVTPESSESIPKSLPITRALGD
15024	45392	A	15111	213	1031	AGNKPDFPWAGRNRATAVLPDVS VFHREDVGWWRSWLNQSYQA VKEKSSEALEFMKRDLTEFTQV VQHDTCTIAATASVVKELA TEGSSGATEKMKKGLSDFLGV SDTFAPSPDKT*^RDVITLMGTP SGTAEPYDGTKARLYSLQADP ATLLY*^PDGPPELFDAWLSQFC LEEKKGGEISELLVGSPSIRALYT KMVPAAVSHSEFWHRYFYKVH QLEQEQA^P^RDALKQRAEQSIFE EPGWEEEEEEELMGILPIFPKEAK FPLAKISYIP
15025	45393	C	15112	414	557	
15026	45394	A	15113	98	467	
15027	45395	A	15114	1	155	
15028	45396	A	15115	16	94	RCPIASEASWTID*RCPIASEAS WTIDALGNSYSGGMAF
15029	45397	A	15116	95	115	IIRHLCND*^TPREGCLPSP*PAW SDTFETWVNQASLQ
15030	45398	A	15117	3	282	LKPVITCLLQLGLLKPINSPYNS PTLPVQK^PDRPYSKPNPLP*LNP SLLQRNNTYSIFLLTLNMPISCT TMLLYGQKEISSLHKGPPSLMP
15031	45399	A	15118	548	1401	SCTPCWHLTGRWLWGITAVRK RHVLSPVDPKLRHQSRTKAAFP WCLIIAGTPL*LYTHVSRVSDH AGMPALVLHPLQQVPLFWGRG NTL*KD*SLLSLACVQHGLLKP INSPYNSPILPVVKPDPKPYKLVQ NLRLINQIVLPPIHPVGEAPVPLE TGGKSGKDCILWFECHLHSHTI EHQVSSSTFRIVVATGVVLVSLH PQLYMAQNRRERHAECLGESKG REQESLSGNPENSRSFSLLTTSRRY LYKSTRTIVLLGLAGPLKQKKL RSQHPSLYKYLQSFRNKSYR

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hid	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
15032	45400	A	15119	144	298	WQVPLFWQPFPEPLELWPKA/H LTDSFPDLLGLAAED*RCPIASE APCTQVI
15033	45401	A	15120	449	667	
15034	45402	A	15121	2	111	
15035	45403	A	15122	323	401	LLLGLAAED*RCWIASEAL*TIT DAK
15036	45404	A	15123	2	593	CTLPSH*NLLTLPNLNIPSHG ML*KD*SLLSLACYSTAF*GL*T PLTIPPFYLFKNQTRLTG*FRICP LSTKLFCLSTPWQCQTHILSYPCQY LPPQPFLFWISNMLSLLFLCTL YPSLSSLSLGLTLTPIRLSKLPGP YCRKPSQTAPTSNHPSSFSGSW YSVETSYPLSSSIFRKGRTDSW LKDTPHQAQPPT
15037	45405	A	15124	354	630	
15038	45406	A	15125	29	354	RFLVSLMLPPAVVMLNHCYSLI FTNALVKRLFAWNMLSELATC AGNLATGPRNARSPGFLLSCVP SVRDPGTGNQTVQLTWQQLPPEPL ELWPKA/HLTDSFPDLLGLAAE
15039	45407	C	15126	1	576	
15040	45408	A	15127	377	624	RDQLQCLQLWDAGACYTCWK SATGPRNAHSTVFLSHVPSVV DPTENRTVHLTWQPLPEPLELW PKA/HLTDSFPDLLGLAAED
15041	45409	C	15128	1	462	
15042	45410	A	15129	44	340	PCQTTQGRLLTAGTPL*SFTHVS RVSDHAGTPALVLHPP*RQVPLF WGRGNHISGTQELPNT*TAV/V QAF/LPEPPPTG/CLLHVPEIWPL GQGMPAGQDSS
15043	45411	A	15130	242	522	RLVWPATATQRAWSQSEAAA TVDLALSARNSATGPRNACSPG FLLSCAPSVWDFGNRTVQLTR QPLPEPLELWPKA/HLTDSFPDL LGLVTED
15044	45412	B	15131	1	1080	
15045	45413	A	15132	1	642	

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15046	45414	A	15133	245	1033	TALLLTQSLFGLLTQTRMKFG AVTRIGGPPGLDQSPVLLFFVPR ERSTYDLDGPQTQPKKKHLTNFK STSFVFSSCIPPP^PSSISLLPPW/T TDHAPLTISL/T/*SPLPCSMPI/AS HISML*KD*SLLSLACYSMAF *SL*TLLTIPPFYLS*NQRRTG* FRICALSTKLFCCLSTPWQCTHIL SYPQYLPPQSIIWFWSNVLSLLF LCTLHPSSLSSLSGLTLTPRLS KLPGLYCRKASQTA[PITSVPKP FLPYLLPISA
15047	45415	B	15134	146	556	
15048	45416	A	15135	1	555	LTSLFLHCCLSHIIYHGQAIIHPRH FLHLICRCHCHQYCHAYLDPC PQDSHHLHWCPWQPLPEPLELRP KA/HLTDSFPDPLLGLAED*HCP IASEAALPPCFPRPDIMTSRLQL QRRRQTA[GVRYRNATYRTRT ASTNSLRPGSPFPFLALVTNDR QVRSQLALWKRDRLLQLSPINR AISESSFT
15049	45417	B	15136	1	555	
15050	45418	B	15137	499	769	
15051	45419	A	15138	752	1111	MQPTIGNSQSWSRPTA*MPLAE SHPITQLVGTVTTPRVTPLSIRH PWRCR SANAGA MILT MKQLAI VMRVYQHQVRRSMRPGRNA RSGMSA VGAYYSSCIRVMTAL QSCTGDDEAVLL
15052	45420	C	15139	1	632	
15053	45421	A	15140	1	375	PGVRGAQGGPSIPRQCEESAIGP KFAWISSFHWKQGMFNMEAP SSLFFVNMCNAVKKQTTWGRPD RGFIWQPLPEPLELWPKA/HLTD SFPDLLGLAED*HCPIASEAPA LVYTAGLHCFSKPSQ

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15054	45422	A	15141	1	1340	CSEYEDSSPAPVPA[TDLSSTLSS SVPQPQDTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAEH EHAGLGVQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSAFG LLNLHQWVFSGFQAFSDRLKA ALSASLLRFGDSDWLPSSAC KCLMLGLH[VIVGNICATLKEK YSSMLHLDVTMKKNGEKRTRL QKRKKGMPPHPAYEDLNIAAIT LPANVVLHQPSGFRTSGQLDPV WWSLDTDAHEIWCDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQTIDQPKKHILTNFKSKTKE GFIHGPKTPAPVTDWEGSLPLV FNHSGTPL*LFTHVSRVSDHAG MPALVLHP*RQVPLFWRRGK!* LTSPSRCTIIEKSCNSLPLP*DKP QPHLQHTRTSKCLNRSQQAF/L PEPPPTG/CLLHVPEIWPLGQGM PAARDSS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
15055	45423	A	15142	2	2107	IDMIFTPGPPSTPKHKKSQKGSA FTFPSQQSPRNEPYVARPSTSEI EDQSMMGKFKVVERQVQDMG KKLDPLVDMHMHQHMERLQVQ VTEYPTKGTSSPAEAEKKEDN RYSDLKTIICNYSETGPPPEPPYSF HQVTIDKVSPYGGFAHDPPVNLP RGGPSSGKVQATPPSSATTYVE RPTVLPIIPLLDSRVSCHSQADL QGPYSDRISPRQRSSITRDSDTP LSLMSVNHEELERSPGSFSISQD RDDYVFGPNNGSSWMREKRYL AEGETDDTDPTPSGSMPLSST GDGIDSSTVPLFLSSEIILQKQVG QSITSMLGFLSRGPMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSSKKFFSLLSVTSY SFAFKFVSVAVNISNLKTVDP AKFPTRYCYCLNNRTNDLSDFT ALLVDIIGNSTSYLTEIFKSTSIL SVNQSNESDCIFCIVMTKGSGR NLSDFWEIEEKYPINYTFTSGL SGVLLALLTQSLSFGGLFTRTRM KFGAVTRIGGPPGLGNQSPSSCSL LHEKDPPTTSGPQTDQPKKKHLT NFKSAARPTFLGGQGVPLNPF FTLS/EQVLLS^AARTPQSLISTP QPLISVPQSLISVPQPLLYFSGG QEPPPPPPLLCVSSLFSRLASFTM GAFTHGTQTPSPTKATAPRYPQ TGDLSAEWPTFAGEEPLVLPVR
15056	45424	B	15143	1	930	
15057	45425	B	15144	401	1093	
15058	45426	C	15145	1	843	
15059	45427	A	15146	1	498	
15060	45428	A	15147	112	669	SLOGRLSDYPTFQGCQTTQGC LPWSFTLCSKSRFSGEGETRFKR IKACYHSPATAWPFKAYKLQLS FPHFTCRKTRQALQVSSESAPY QPNCFAYPPRGAEPIHSPILNTS LHNPLFCSGSQTCFLY/SFLCTL HPSLSSLSLGLTLPIRLSKLPGL YCLKSSQTAPITSVKPKFLPHLL PISA
15061	45429	A	15148	957	1100	

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15062	45430	A	15149	303	2028	LGSGDLPWEINPLSSCSLLREKD PPTTSGPQTHQPKHEHLTNFKSD KGDMFYPWTON/YQCRSRTGK AAFPWCLITAGTPL*LYTHVSR VSDHAGMPALVLH*PQVPLF WGRGKLLLARPS*VPILPQPLLL HPIIFLSPPLTTPGPAVSFVL*LA LPHLPSNLLLKRWLEPKA*SSM/ TLKGLKPVITRLLQHGLLKPNT SPYNNSPILPVLKPDKPVKLVQD LRLINQIVLPICHPVLGIIGLTSSV RRDAQDQLKRDRAEFLLGDEV HHPHRRRIAERRLLLGQHFDP LHRLIGQVLEGEARYVAPPVEQ HHRLAPARRTGQRLHPLEQFG QAGRAQRNRNLGIEHRDRLDRP DDGAGNAALAGDGDFFRGCLFA GIGIRPRYCRYRQSDDDRPSH AAPRPRALPIPHRATPIADVM VMFSVIAIMSQLRLVLRHIDGIS RWPPAVVIFTDVKILWLYPSDD CRIRSNDRDDDMQGEAPAMSMN AAARVGDPIGHISFSQGLFGEAL DGLFFARRSEVDMRAGNLGRLI ARGLSSGGRWTPADQQLTGSR DVFINGPPATMTIRSTGQCRRQH
15063	45431	A	15150	653	1076	RSKYPNLVSLCPSPLFPRPDLLS LWPNPFLHPNLLYLCAPIPYFH APTSYLCPTPTPYHFDPFPFLFW KELATSARNLATPRRNACSPGF LLSCVPSVRDPTGNRTVQLTW QPLPEPELWPKA/HLTDSFPDL LGIAAED*CCPIASESP*TSDELG RDTLLLALKVQTQVQLTACGE GHVAGNCGRPLETEGSQLQTAT KKLRDSVLQPKSPEFCQQFTRA WNRTQVPDETEAPAGTYAAQS GDLPWEINPLSSCSLLHEKDPP ASGPQTDQPKHEHLTNFKSGFRG VRPRRDACLGPSPLAASPAFLG KGQVQPILLSVSLPILLRLSGGQ ETPNPFSFTLSGKSAFLEEQVPQ PRISVQSLISTPRPLISVAQSLIS APQPLISLCPNPFLFPCPDLLSLHP NPLFPFPNPFPALEGACYKQCQ KSGHQAKECLQPGIPPKLRPICA GPHWKSDCPTHLAATPRAPGT LAQGSLTDSFPDLIGLAAED
15064	45432	C	15151	234	449	

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15065	45433	A	15152	2095	2663	LGLGDPWEINPPSSCSSLREKD PPTTSGPQTYQPKKHLTNFKSA CFERIKACYHSPAKAWPFKAYK LSLQFPFHFTCLKTRHAI/PS*FSD LCLINQIVLPIHPMVNPNVYTL SIPPVTMHYSVLQLIRAAFTIPL P*PSLY*VSLGLTLTPIRLSKLP GLHCRKASQTTPITSVKPKFHP HLLPIST
15066	45434	A	15153	678	1189	LGSGDLPWEINPLSSCSSLCEKH PPTTSGPQTDQPKKHLTNFKSE TKETCFIHEPKTLAPVTD*GRQP SLGV*SLQGRPL*SFSHISRVD HAGMPALVLP*RVQVPLFWGR GKYPNPFSPCCLLPLLCFSGDRG KYPNPFSPCLYSFSAFLGLTGQV QPLLSSLPLLCF
15067	45435	A	15154	649	1428	QCISEQFLLASTVRQTPATSPA HKNFQTPELQRPGVPPEPPPTG ACYTCRKSGBHWAKECPQPGIPP KA/HLTDSFPDLLSLAA*ED*HC PIASEAPETITDAELPVTLTVEA HLHPGEINSHVAHTKPVWWSL HRDAHEIWCCDSDRGTSLLRRPI PCPPALCSVTKIHLRPQVLRPTS PRNISPISNPAAQHQAELGPNP/ SSLCSTL*SFYHLPPSHLWVLT VSFRD
15068	45436	A	15155	240	1208	LRSGDPWEINPLSSCSSLREKD PPTTSGPQTHOPKEHLTNFKSC KQ/DLFLSSPSTS/ITQPLSPFN LGATLQSLSPS/NFNSFHFVLET ETRFIRGPKTPAPVT/VLGRQPS LGV*SLQRCLSDYTPTFQGCQT TQGRLPWSFTLSKG/CPLFWGR GNTL*KD*SLSSLACYSMGLLN PINSPFPSSHFTCPKTRQAVTS* VQDLRLINHIVLPIHPPGAQPH TLFCPQYRPVVLPIILFVYVKA FFTIPQPLIPSLPSLPSLRLTLTPI RLNKLPLGLCCKAFRDSPHYLN QAQISSSSVTYLGIILIKAHVSL PIVSDW
15069	45437	A	15156	1174	1623	KFGLVQLTLGKPLPEPELWPK A/HLTDSFPDLLGLAAED*HCPI ASEAPYTI/DAELRVTLTVEGK SVPFLINTEATHSTLPSFQGPLSL ASITVVGIDGQASKPLKTPQLW CQLRQYSFKHSFLV1PTCPVPLL G*DTLTKLASLTIP

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15070	45438	A	15157	1	1610	MGLGKSLCILKDAVLALREIKG ISFQYAPNTNRLWGYRQAKQT QHLSGISTLDCPQRYNQDDUTGS VWALEPSCMLWACPLVFPSEIY YFISEDVWKHLDQAEKFAAVM GPSRRTSVRAVWKGNVGLEPP HRVPTGALPRVVAKRGPLSSRP QNGRSTYGLHCLKDPTQEDW LVSVLPEGSRVGVDPCLIPTALG HGRRTFLKVLDFQGPAPCPAA MGVRILMAGPQCVSSDYWKKM AKVLRSAHHHLIPVKENLVDKI WTDRPERPCPKPLTLGLDYTGJ SWKDKVADLRLKMAERNVM W/FV\VTALDEIAWLFN\LRGSD VEHNPFFSY\IIRD\*ETFLMFLI DGD\IRIDAPS\K\EHLLLDGLE AEYRIQVHPYKSLSELKALCA DLSPREKVWVSDKASYA/V\*SE TIPKDHRCMPYTPICIAKA\VK NSAESEGMR\ISDEKASAGNLTED PFYVIDRTLITTVGVVCNSTEKSS LMSVASADTAENLWHLFFHILP SERALTRKLRLVULKLGPNYSVQ NPTAQLHQQGPHLGVA
15071	45439	A	15158	1	756	
15072	45440	A	15159	1	1677	
15073	45441	A	15160	1220	2620	GPTEPHTGELWLESGGCPGKTK LPEEGTGSNLCCTASAGDTQA NRVCSGPPTNHSRPAADRPVRR KINKQKTTATSTKRTSTQRPH PKVTNDHSSPAREQNWMENNE FDELTEVGFRRWVITNSSLKK HVLTQCKEAKNLEKRHSLGTK EPAALKGRTQY\WQDSSPADLR PWLCATLLKQYKPTVFSHSTVA VHPRAGFLNLSTVDQHPVLDEP IAEAVCIADTNKWSVQVATSQ RKVPHINLKLQGDVLVSSQVSSL LQSILQLYKLHLPA\DFVGDILL NNLKCVFQLGSILPVTRSHDP YDGEGETDELRTAACSPDTEQLA RQSGTYPVSLGQATVLEDSKA ALPGLGPTLMAVTVVTEAAV DMVVGDRGEERGGTLVAPGTR GLTEEEIWFVVPVPSPSRWWSHPV VAFITLAKYGTSSPPVFHGPNIIRHGAQGAASAGDGSSSRCD RLPCRQNA

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15074	45442	A	15161	666	1536	FSSAGDTQANRVCSPVPTNHSR PAADRPVRRKVNQKQTATSTS TKRTSTQRPHPKVTNDHSSPA REQNWMEN\EFDELTEVGFR WVITNSSELKKHVLTOQCKEAK NLEKRVRVNCLTVRIT*P*RTT\  KTLMEALKNTARE\LEHAUTSINS WINQAEERLSEI\EDQLNENIKRED KITEKMKNSTTVRAASMQSK LLQGVAAEGLPLRLTRSAFSAE\  SMCHQWLFSFTFGNGKSRNRYH CEKAHIEGNQLVEETGRAFKSR HRYGTGPLHKFEIHEYTELHHV LMLQGKC
15075	45443	C	15162	104	364	
15076	45444	A	15163	162	467	
15077	45445	B	15164	1	1122	
15078	45446	A	15165	188	456	
15079	45447	A	15166	485	1580	GEGYKADLAAATVECPICQQQ RLTSPQYSHIPQGDQPTTW\Q VDCIGPLLKQGQRFLTGIDTYS GYVFAYPVVCNASAKTIISGLTE CLIHCHIPHSIASDQGTHFMA KEVWQWAHVHGH*SYHVAD YPEAAGLIEGWNGNLLKSQLQC QLGDNTLQGWGKVQLQKPMYA LNQHILYGTSPATIHGSRNQD WNGSSLRGWTTILFTAPRREP GTYIASDQRTHFMAKEVWQW AHAHGHWSYHVADYPEAAGL IEGWNGNLLKSQQLCQLGDNTL QGWGKVQLQKPMYALNQHLY GTSPATIHGSRNQGMFVEVA PLTITPGDPQAKFLLPVPMTLS AGLEVLPPEGGTLPPGHTTIPN
15080	45448	B	15167	10	2352	
15081	45449	A	15168	2	497	WKPIAMRKSRQQEKLIPVQK EGQPKLEGREEGGPVQAKQVP NRLHLHWTT/HLPSFFQLPLLD SLWRALKFVVLEAIVKMIRFNG VLGKCEAIRAQUALHEGGPPLPL AVFHNRRLQIVACSRISARLRGS PPPKNNEQSSLSTDLRDTDSQLR PPLSRNAQQKG
15082	45450	B	15169	1	1911	

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15083	45451	A	15170	1	1569	MPIGKVGEYYIKGTLRATKESE QQSSALELSSDRVYLNKEPGD QPWNAAFFVFRGCGVALALRPP HLGWGEPRWAGFRGAFGFPFS TLNPSNWSLTLIQQGCKQEGFYS PSMRPRVVPKRGSAKPVRAEEN AALPSRCPPGPLPV/AQPRGLLM GAHVSSAPAAGVGAASCHRLC PGFDFDRPRPTLRSICMNAVGG CDLRQQVYDPTGGWANEGR DLSAVQGVNPNGPGRCPCTPQS SRQLPVSRRPVVRPGGEAPP LDILPAALAHQSLLTPQDPRE DRPSPADLWAQDSWVQGPQFL PVGSRVRTGTEPDTHSGSVCTS RQGKDGSGLARESSVRVILQG PSSAWMMFPEYTPGPRARAGT AVVGAMARQTVNVCLTKVRL QHPEGIPGGGRGPLVPKPVCTC/ IVDVKGSRVWHVHICMSMG RHVCLCGRSVGSWRMCTAGQT PKLARQASIELPSMAASSTKSW WETGEVQAQSAAKTPSKCDIV AGDMSKSLWEQKGGSKTSST IKMDSVTT
15084	45452	A	15171	328	641	LLMRWSLPSAPRGFSCSCLQP QYPCRTESWPQTEPVPSVPSHR LLVLATAMLGSSME/RLAG*LG GPASGLDGGLGVLFQPLNLDG QVWLGLFLHTVTLLYGA
15085	45453	B	15172	120	1458	
15086	45454	A	15173	1	440	IQQDSQAPLYS\IKETQRANTYL VEWEGAETAFKTLKQALVQA PALSLPTGQNFSLYITERAGIAF GVLTQTRGTTQPVYVLYKIDGEP IEHDYQQQIAQTYATQDDLLEV PLANPDLNLYTDGSSFVVNGIR RAGYAIVSNTVLE
15087	45455	A	15174	288	376	NHWLLLTMDPRIQQDSQAPLY SIKETQRA

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15088	45456	A	15175	777	1548	SKIQRDSQAPLYSIEETQRANT HLVEGEPEAEIAFKTLKQALVQ APALSLPTGQNFLYITERAGIA LGILTQTREITPPQPVAYLSKEV DVVAKVWLHCLRDGEPIKHDC QQIIVQIYAAADDLLEVPLANP DLNLYIDGSSFVENGIRRAGYAI VSDVTVLENS LAAVT LQNRQG LDLLTAEKGGI.CTFSGKECCFY TNQSGISSL LEDTTA GPFHLPI QQEVARAIIHQFPTAGFVSCLE GRLRGEASWTSWVE
15089	45457	A	15176	1	1359	MGPEPKNTHPGSCTCPLACSSS HKGFECLAVEQGSYTPVAPIV GVKENQEILDLLKYNQTRSA VTRCVLGAASTARIKQAAEGR SRLAESSGLRLPFPVLEPALEHQ TPSSSGFELLDDHQRLATWSQA FNYRLKDTLLASLLLRFWDSD WLPCSSVCSWPIVGLHLVIIERN YSYQQGTETVSSWATGVSA ASVSA TIPINRVQGHCGFLGKR CFYCCIGECNHSIDHQPGPTVAG SWARGVSATASQIQV DVLGKFS DDPDRYIDVLHLTWRDVMLL DQT LAFNENNVALAAQEFGD TWYHRPVNDRMTAEQRDKFP DIKTAAGIPWNHWLLTMDPQ TQRDSQAPLYS\*ETQRANTYL VEWEPEAE/TSFKTLKQALVQA PALSILTGQNFSLYVTERARLAL GVL TQTCGTTPLYQDELRKKT RHRDSEGSGFNQLEASAD
15090	45458	A	15177	368	5192	AAPAPQLGLGPCKLASHLQS HLSQS VSEAEQKAGASPASSI QREPLFKDQLKAPLPEQKRRSL LTVPPLTFRAQKCGPGSPSLVAR GGATDWSLVSEEFRLSDSTAPP TELRGQEATGITKPPASLHPQPH AWDWARGRDRPRRHLI LGTPELQ EHSEKTTTETLPADMGKLR TW ERKEATAGQAEGAAAGGIHFE ATSLLRPSSYV PQTQ GALSTTY KEAKMDRDLH LTPILA QRAR GPRIHSFPSDEMI EPS

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15091	45459	A	15178	76	969	KKSTALVIDNGSCMCKAGFAG DDAPQAMFPSTVGFPGHQGV VDMGGQKDSYYVNEAQSKRSIL TLKYPIKHGIIITNWDNMEKIWH HFYNELHGAPE*QPVLLTEDPL NPKDNREKMTQIMFETNTPA MYVAIRDVLSLYAAGRRTGIVM DCGHRVTHTVPIYEGYSLPHAI LHLDLTGWDLTEYPCILLFSEK SYELPDGQVITIGNEWFWCPEV LFQPSFPCMESCRIHQTTSINKK CDVDIRKDANTVLSGGTTMYPG IADRMQKEITALAPSTMKIKIA PPERKFWSVWIGCS
15092	45460	A	15179	1	451	
15093	45461	A	15180	130	227	LMKMKKVM*RA*KEEERRTPP AEDDFEKDLEWLINENEKSDAS IIEVYIANSIHNHYITKCFAIL
15094	45462	A	15181	104	1715	KEEERRTPPAISVPAAAFYTAY FLHQKQMNENKDTDSKKSEY EDDFEKDLEWLINENEKSDASII EMACEKEENINQDLKENETV EHTKRHSPPDKSLQDEVSPRN DIISVPGIQPLDPISDSDSENSFQ ESKLESQKDLEEEEDEEVRYI MEKIVQANKLQQNQEVPNDKR ERLLKFKDQLQVVDLEVPPLIEDIT TSKNYFENERNMFGKLSQLCIS NDFGQEDVLLSLTNGSCNEENKD RTILVERDGKFELLNLQDIASQ GFLPPINNANSTENDPQQQLLPRS SNSSVSGTKKEDSTAKIHAVTH SSTGEPLAYIAQPLNKRKTCPSS AVNSDRSKGNNGKSNHRTOSAH ISPVVTSTYCLSPRQKELQKQLEE KREKLKREEEERRKIEEKEKKR ENDIVFKAWLQKKREQVLEMR RIORAKEIEDMNSRENRPQQA FRI.WLKKKHVEEQMKERQTEEL RKQEECLFLKGTEGRERAFKQ WLRRRKMEKMAEQQAVERT RQLRLEAKRSKQLQHHLYMSE AKPFRFTDHYN

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15095	45463	A	15182	881	2040	MKAGWRQTQHLHIDAGQLLHLI LPGEQGVARVQLRRDAAQAPH VNIGHVVGVQAQDHFWGSVEPA LDVRYYCGGKTGGKQRERREG RCGVEILMVGGERKMENENKETD SKSEEEYKDESEKDLLEGTLNEN EKSDASIIEMACEKEEENINQLDK ENETVIEHSKQLSDPPDKSLQDE VSPRRNDFISVPSIQLPDISDSD SENSFQESKLESQKDLEEEDEE VLPRSSNSCVSGIKKEDSAAKID VVTHSSTGEPLAYI/ASTKLAY IPPLNRKTCPSAAISDRSKGNG KSN/HGQSAAIISSSVTSTYCLSP* QKEL/QKREQKREKLKREEEQQ KIEEEEKKRENGIVFKAWLQK KREQVLEMRIQRRAKEIEDMNS RVSKTSLKKNKFIQI
15096	45464	A	15183	873	4292	MVVSGLRVVSSLSESDPDTGRVG R*VDCKVDRSIWAGVWISEDAP SEA*ELGGGLGRK*MLSGGPQSPS KHVHIL*DQDSSSIPEPMGPQCCP PHAPGKEPGTCSIDTDGKLSG VSGDDS*T/GTDGGESEEILLPQ *QLPVTLPSLPLPG*VRYTTSR SRSRSTRDPGRKSRSPIGLRGLC GDGAT/S/PLTPRHAPARDVQ/PG VSMAFAGDR/GDGGRRGGASQ/ PAPPPGA/VPRPCAQYSARAMPA SGRRES
15097	45465	B	15184	1	2214	
15098	45466	A	15185	3	361	
15099	45467	A	15186	1	1035	MKIHKSGGLKATPQLYASQFSG VAILATWGPHPRPRNSSTSFSSTOS KLRRPDESSVDFQKLMCLKEAT KKSKKEPGMAFFQQGHILFSDV AIKFSVEEWKCLNPEQRALYRE MMLENYRNLES/VG*LFIKIHDG VLINRARQYRSVPHRDIGKT*FL LPRNQERYSGL*VSVARN*KK WP*STHDRNQRVN*VHTGEKP QKCNCECGKTFSQKSQSYLQCHHR LHTGQKPYK*E*CDKVVSCRQ LKTHRHRIHTG/EKAYKCKVCEK AFWDNSCLSCQKRVHIGEKPYT ALVMHIAJHTGEKPYTCNECG KAFSRKANLALYHRLHGTGEKP YKCEECDKVYSRRSHLERHK
15100	45468	B	15187	1	1347	

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15101	45469	A	15188	I	1446	MWRET KRYAAVLLT PTHY SAS LLPDW/PNLYLHQSGHIVPGVY LKF GISSNPIYP CVD SAKT VFPN APL HDR VQS VRRM GPFG KVFR KVF NSNL GFE YSL STWAT MGSPG SLGVSP PGK TLF VES ASSL D LWPT VKE EISSH KNYQ KH SEK Q IYD VRIEL TGL NALP NISL NFY K NSV SKLL RKK G LHI LQP FIL R LCV SLH KREEN LGIT QD VAM RLS ALP NIV CRL YKK TASE VL K EW STR WDE YTH KEV SQ KAL P TLS VKI YKK NIC QLLN QNNG P SEM NALI T KKS VKS AS GY LES I AAL VEKE I SSY K NYTE AFY NLL CDV YSH VTEM KLS SIE QINT L F VES ASG VWR ALR P RGE VND I FID QIANS VLV DSS K DICK R FEA CGAM V KKEN LHI K TRQ KISE K L HW PFG A PRL TSL T GPE K TG K GE HPG A KAR GEL SGAPPL I HTR K L SLMS N VET LL EKL LQ Y TGA H
15102	45470	A	15189	I	966	
15103	45471	A	15190	I57	531	GDHTT FLCL LMVNA EFK YNF K TII* D L L K K D S G Q Y G H T I F R S M S I G C F S I Y L C I F N F F H Q C F A V F L V E I F T L V K C I P Q V D S I E D T T F G H P E E A T P H P F S F F M R L E Q F S H I F S S W P V S F T A H
15104	45472	A	15191	9	494	P T D R P R P R A L A G R G P P G R A P R V P P P A G G P R P S Q Y G H G R P N P R H G W H D A F C P N N T P Y R E R P L D S R Y L T P G P L D M R G D S G F R T G R G S D V G S L K P T D T R R N G K I Y L N G S / N V F Y Y Q Q R L H P V H R G D G A R R G F S G R T C L H R M V C * Y E Q T G H Q S D Q T * K A R S A Y G
15105	45473	A	15192	I361	2038	
15106	45474	A	15193	I376	1906	L A F P D G M A S L I M M S L P A M R T L A W A M A V S G N C I P E Q F Q S A L S C A D F G I S P K L I L * S S A P N Y L A M G I S C P R A D D L P E A G T A E T D R A C R S I P Q Y G T D L G W Y P A A G P Q S E S V Q G A V * P H R Y E A G * S T / V W K P L K K K * K P L P R R * L A R W Q M I R F R K P S P L T T S L K L T C A W R F L D F R W L E

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15107	45475	A	15194	1	1388	MIEHPRRRDNYRQSGPPVADKP TTKGEPLISDIVSDAQANLLIP VDETPPVINDEQSTSTPLTAQTL MALAAVADKNITKDEKADDL NEDVITASLSALFAMLPGFDNTP KVTDAPlSTVLPTEKPTLFTKLTS EQLTTAQPDDAPGTPAQPLTPL VAEAQSKA^EVISTPSPPSISGV RSKMRQREWLVLPFEDSLVIRR SNKTSQLPAFNVPVLSAAKAAS KPWRASNTACRNSRSPKVCSAE GEQWFSASGRGEIHQSOPARDM AQMCKLA^AEGHF^EARVINQR LMPLHINKLFV^EPNPPIP^VWKWACK ELGLVATDTLRLPMTPI^DSGR ETVSGDETYLEA^PLAELHAPA GMILPVTSGDYA^IPVTNGSAV GSYS^AITEPGAGSDV^GSLKTTY TRRN^GKTYLN^GS/NV^FYYQQLR HPV^HRGDGARRGFSQGQCLHR MVC*YEQTGHQS^DQT^KARSA YG
15108	45476	C	15195	1	1905	
15109	45477	A	15196	285	1706	YARVHSGRSSIRRSIPV^SICIRSSI RGCV^PVVHCIRSSIR^SIPV^DHL YQIIHTKKHTRCPFVSD^H^P^YEE APDYSAS^LLPDWL^PVPSSKV^VI TYPGFTSIC^YYTTSSKAC^F^SVF AWCFVTS^DVPG^GRFS^DE^D^D^SE MWSL^T^ALMGVM^GG^W^K^T^S^ARS EV^S^L^C^S^T^S^K^V^I^H^S^P^Y^AD^RA F^Q^V^W^S^L^D^A^R^F^A^H^I^N^K^P^F^G^V^D^R^F SGEAP^S^R^A^I^T^T^M^Y^G^V^K^V^L^N^R^P^A TGT^A^H^R^L^V^P^P^D^V^P^V^H^P^H^G^G^E^S^N K^P^R^V^Q^T^T^V^S^G^I^S^L^I^P^I^S^A^S^L^A^L Q^N^V^P^D^K^T^H^D^I^S^N^I^T^D^T^V^Y^H^C^P^L S^Q^S^R^W^Y^W^R^F^V^P^V^R^S^P^P^L^S^N^G^Q^ T^A^V^R^P^G^G^S^R^A^G^A^G^P^L^S^E^Y^S^ G^S^G^F^G^V^M^K^W^T^K^D^Q^L^T^V^T^V^K^V H^H^L^P^E^V^V^E^F^L^Y^K^Q^G^G^W^L^S^V^L^ F^G^N^D^E^R^K^L^N^G^H^Y^A^V^Y^V^L^S^R^E^ K^G^T^K^C^W^I^T^D^S^M^D^Y^Q^R^P^A^P^T^ N^D^A^E^T^Y^E^F^I^N^E^L^G^A^R^K^T^T^V^V^P^I^ G^P^L^H^V^T^S^/D^E^P^G^H^L^R^L^F^V^D^G^E^N^I^ I^E^A^N^N^E^*^I^H^R^T^Q^C^
15110	45478	A	15197	3	1396	
15111	45479	B	15198	1	1399	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, <=possible nucleotide insertion)
15112	45480	A	15199	283	796	FVGVK SAGNRIK TIDELANES R SSVGLTQAALKTLESSGAI R IER RGRNCGSYL VEMDNKALLTHVD INNV CAMP LPYTRL YEGLASG LKAQFDGIPF YYAHMRGADIRV ECLLN G VYDMA VVS RLAES Y LPQKGLCL AL*LGPPPYVG E YQ L*QVKAKSEYYKRVGVH
15113	45481	A	15200	48	3376	
15114	45482	A	15201	49	681	DPGADRRGSVWGLS DL RNTY N ALYLTHSGRLSEC PT PANEEKE PT NHN RTLT NQ T QKE KKT R T KDC TTRN KNS TRPGS IIAGPS Y YT VAG PPSA IDP R WLR PTPAL DPQ *MPHTSKRGK RADQSQPN ANKPNT EREKKDKNEGLH HKE QEQ QRP GSG IIAGPS Y YYT VAG P SAIDP R WLR PTPP ALDPQTEPL IFQQL EIDHYVAGLTHEVMS L HLT LVMR WGS VSAAHILA HWA RCR WISTELTPNSITSSPLKD CSSPAMEQ SWL E NDFDEL TED KKT CLCDH
15115	45483	A	15202	3	587	
15116	45484	A	15203	3	774	MVL MAGFTAGNEK GEL VV LG R NGS DYS AAVLA A CLR A DC E I WTDV DGV YTC D P R QV P D A R LL KSM SYQEAME LSYFGAKVLHP RTITP I A QF QJPC LIKNT GNP QAP GTL IGA SR D E D E L P V K G I S N LN NMAM FSVSGPGMKG MVGMA ARVFAAMSRARISVV LIT QSS SE YSISFCVPQSDC VR AERAMREE FYL E L E E S L L E P L A V T V E R L P I I S VGS DGN P P CCGG I SPK FFV A A LA PRP I SKF V ALC S G I P F

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in I USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15117	45485	A	15204	1474	1511	HS*VPANLYMELKACFTGA/NEKGELVVLGHNLAVSYFIALAASLRADCC/WTDVDGVYTCDPRQVPDARLLKSMSYQEAMELSYFGAKVLHPR/TITPIAQFQIPCLIKNTGNPQAPGTLIGASRDEDELVKKGISNLNNMAMFVSVPGMKGMVGMARVFAAMSRARISVGLITQSSSEYSISFCVPQSDCVRAERAMQEEFYLIELKEGLLEPLAVTERLAIISVVGDGDMRTLRGISAKFFAALARANINIVIAIAQGSSERSISVVVNNDDATTGVRVTHQMLFNTDQVIEVFVIGVGGVGGALLEQLKRQQSWLKNKHIDLRVCGVANSKALLTNVHGLNLENWQEELAQAKEPFNLRGLRLRVKEYHLLNPVIVDCTSSQAVADQYADFLREGFHVVTPNKANTSSMDYYHQLRYAAEKSRRKFLYEHNTFVSPHIRPLIERRGRSSTRDKWCARPSTERQQDNAAARILSCQQGNTSFEHTSSIRVGTTNSLN
15118	45486	A	15205	198	462	

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15119	45487	A	15206	31	1981	RWLMRGMGIALPAAMASTVSP STIAETPEPPPLSDW/LRASG/DV WVHLLGLDPHLSSLLSICLFSR SLIWIF*LQP*SV/ALAFQMGAS LFASNGIVIEEGPQAKPL*CLT VSYFEMLNLLNAQGPKGKLSP CQCLSLQVMTMPEYLKKRWT GQRSQWPQMHVSFSS*LPF* A DIFAGAIFIKQPSGEKYMRTH G*NALVLFLSLGGLEVVNIIG CLRFQ*DISFYSDAFLAFNEVGG YESFTEKVVNATPSVVEGDNLT ISASCYTPRADSFHIFRDAVTGK GR*PLPKSSPGLFIIECVFTFSRQV IVQRCLCGKDMSHVKAACIMF LFV*WLLVLPIWASLDSSLNNSP DMVACVPSECVISTLGLARQ CPATNQCLYPFPFAPGLRGLMLS VMLASLMSSLTSIFNSASTRTK AQWK* *CFCLMFKLCCFLRI FVLLLTVVSVIVWVPLVQVSQNG QLIHYTESI***LT*ISFSYFLNILI FFFLLLQAFWGLMVGLAMGL IRMITEFAYGTGSCLAPSNCPKII CGVHYLYFSIKVPFYTTIANICL LLMHFCMVPVQLYRLCWVLR NTTLTRISSSFV*IFCNHLLIFVP DYPEKSRGCLKKAYDLCGLQ KGPKLTKEEEEALSKKLTDTSE
15120	45488	B	15207	1	1392	
15121	45489	A	15208	57	1523	
15122	45490	A	15209	473	589	LPRQLALSCVVHCQTLVPAIRCI DWGWLFW*W*SVTPVPM

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15123	45491	A	15210	1	1297	MGKIMSSYQHVDLIVDCDFEA YHRQPSSGTKSVVTGPAQALI TEKIVTYHWDQHVGDFVLVNLJ YCVINVLDHTVKAVIDDRFMG GITTINLQLMAIIVRYFFASGSA YIVAMLPVFAMLANVSGAPLM LTALALLFSNSYGGMVTYHGG AAGPVIFGVGYNDIKSLCFDER TRIDVADTYASNRWRSRCNQTIF NGECPTNTRQHIAAVRNGIDTLL MNDYLRKQHIDISTRIAGTANN GDFTGQWITAANTVNFCIVAGT HNCHQYFIALRLIFGILKYIQDR AREGLKQRDLAEALSTSPQTVN NWIKRDALSREAAQSIKEKFGY SLDWLLNCEGSPKKDLESNIPP ESEWGTVDADWKNTPLPDDEV EVPFKLKDIEFACGDGRVHDEDH NGFKLRFSKVVVQPRVGC*QG* G*LLYLDVS**GDPLEST
15124	45492	A	15211	62	301	SWMSSPRAFSSSTCLEATAPTR MATALTSAACRLLPPAAGSGSP WAPAPYRWRARRRTGPMMSDR Q*RTSQPCPEPAASR
15125	45493	A	15212	1	1665	MQDSAHLRRLPPAASRRVWLA LGSCPLPLESSPAHRAYERPVSA HQPAVPGARRSLEVPSEVPLTV PALTPPRIPAMLTAVCGCSLSQ HTEAPHASPPRQLDQLQPLQTYQG HTSPEAGDYPSPLOPQGELOQSLPL GPEVDFQSQGYELPGASSRVTCE DLESDSLAPGPFSKLLQPDMS HHYESWFRPTHPGAEQGDSWWD LHPGTSWMDLPHTQGALTSPG HPGALQAGLGGYVGDHQLCAP PPHPHAHHLLPAAGGGQHLLGPP DGAKALEVAAPESQGLDSSL GAARPKGSRRSVPRSSGQTVC CPNCLEAERLGAPCGPDGGKK KHLHNCHIPGCGKAYAKTSHL KAHLRWHSQDRPFVCNWLFCG KRFTRSDELQRHLQTHTGTKF PCAVCSRVMRSDHAKHMKT HEGAKEEEAAGAASGEGKAGGA VEPPGGKGKREAEGSMASSSPD SPCSCDCFVSVPPASAIPAVIFA HELGPTGRGAGGGVCPRRHS HSWEPAAPGL*AVGGGGASGQ AGDRGCHA*EAGRS/CSRRGS GL*RAGTS*ISASS

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15126	45494	A	15213	3	471	GRPSSPGVHGSS1TQTPAHVGSF□PGC GP IPPD/ACRRSKIRGPGGW□GGVVG/CRDGRNSR/DLRLNPLC□PFLFLPGP*AAAPSPPPWAAAGA□APCGQCCLDGWPWHSYSHIGHSSA□AGRGGICRSPPPLLAGELRPPGIQY□YNGRTEVRGLSASPCCPFGSAC
15127	45495	A	15214	3	449	PHQDLEEAMVLL□PPSP/PAWPTP□MTRKRKPSKSVSSTSPRLRKSI MTTYAVPSRAPTPA*PSASKPTNA□FS/HMVGSPEPRSHAHLDRGHRD S R*RKPRPLSGPRTLGGKSLRG SAGAGRRGVPRPRPLPENLDAPLWNSPGNSAGAAVQLA
15128	45496	A	15215	26	1126	EGPSSEAAHPPGGTPREODGAM □DPARKAGAQAMIWTA GWLLL □LLRRGAQALECYSCVQKADD □GCSPNKMKTVKCAGPVDVCT □EA VVA VETIHGQFSLAVR/GCG □SGLPGKNDRGLDLHGLLAFIQL □QQCAQDRCNAKLNLTSRALDP □AGNESAYPPNGVECYSCVGLSR □EACQGTSPPVSCYNASDHVY □KGCFDGNVTLTAANVTVSLPV □RGCVQDEFCTRDGVTPGPGFTLS □GSCCQGSRNCNSDLRNKTYFSPR □IPPLVRLPPEPTTVASTTSVTT S □TSA PV RPTSTTKPMPAPTSQT P □RGVEHEASRDEEPRLTTGAAG □HQDRNSNGQYPAKGGPQQPHN □KGCFDGNVTLTAEPPTVASTTS
15129	45497	A	15216	1401	1983	AQRAQALECYSCVQKAD/GDC □SPNKMKTVKCAGP/VDVCTEA □VGA VES/SHPFWIWPRPFNA APP □LSA WPGPYDTALQARPLY*QL □QARGAES*ELVH/GQFSLAVRG □CGSGLPGK/NDRGLDLHGLLAF □IQLQ/QCAQDRCNAKLNLTS/RG □LDPAGTSPPVSCYNASDHVY/ □KGCFDGNVTLTAEPPTVASTTS □VTTSTSPQ

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15130	45498	A	15217	1	964	MNVKGDTQGNTRVRVDNIGGVGAQTVNGIELIEVGGSNSAGNF ALTTGTVEAGAYVYTLAKGKG NDEKNNSPSPVVRP/EAGSYISNIA AANSLSFSRLLHDRHSCLQPLKI LVTGGAGFIGSAVVVRHIIHNTQ DSVVNVVDKLTYAGNRESLADVS DSERYYVFEHADICDAPAMARI FAQHQPDAVMHLLAESHVDRS ITGPAAFIETNIVGTYVLLAAR NYWSALDSDKKNSFRHHISTD EVYGDLPHDDEVNNTTEELPLFT ETTAYAPSSPYASKASSDHILV RAWKRTYGLPTIVTNCSNNYG PYHFPKELIPLVILNALE
15131	45499	B	15218	44	405	
15132	45500	A	15222	1	498	MTRSLLSVFEEDAGTLDYTNQ LLQAMQRVYGAQNLNLHTELA KQLIETQWFLYSYNEKRSQTL SAMWRGRAAQ/A/TQGHWVWG MVEAVCSKVSTLKDGLGLASN EHDLMSAKYSRLLPKKENEKL AAFGOPTWCDPAERVGFLEPV GPDGAKSAPS PRDRASTL
15133	45501	A	15223	1	1224	
15134	45502	A	15224	1	1353	
15135	45503	A	15225	1	2580	
15136	45504	A	15226	1	3117	
15137	45505	A	15227	1	1260	
15138	45506	A	15228	1	2142	
15139	45507	A	15229	1	1413	
15140	45508	A	15230	1	4049	
15141	45509	A	15231	1	381	MLMLNIGFKNFQFEHLKCSHGS YSEDIGFPNAGALSGAMFLLEE KHLLFGLKEEERLRA SIRRESQ QRRMREKQHQ RQLSASV/WNLIDTMRRRKARSP/YSLAAIKNRY KGGIRDQKPSYD SLNLCMT
15142	45510	A	15232	1	467	DHSSSPAREQNWMENEFDELT EVGFRRWVITNSSELKKHVLTQ CKEAKNLEKRLGELLTRITSLE KNINDLMELKNTARELHEA YTSINSWINQAEERLSEIE DQLNEIK REDKITEKMKNSTTVRAASM QSKLQQVAAEGLPLRLTRSASF
15143	45511	A	15233	1	1140	
15144	45512	A	15234	1	2640	
15145	45513	A	15235	1	714	
15146	45514	B	15236	1	546	
15147	45515	B	15237	1	735	
15148	45516	B	15238	50	1603	

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15149	45517	A	15239	1374	2220	QAENSHININKKDVKHSETPSEG HQRKRPKDHSPPAREQNWME N\EFDELTEVGFRRWVITNSEL KKHVLTQCKEAKNLKRLGEL LTRITISLEKNINDLMELKNTAR ELHEAYTSINSWINQAEERLSEI EDQLNEIKREDKITEKMKNSTT VLVSTWGSQLEQNNLPHIISPLF HSTHDLNISFYGGCLLQACSSK LLQGLAEGGPLRLTRSAFCAA KLCLTKHFLPTEMILIKSRK1TP DTQPRRLYLLQGVVDQTSRKKG PTALNIRQKTFAAAPPKR
15150	45518	B	15240	1	1311	
15151	45519	B	15241	46	212	
15152	45520	A	15242	3	371	EPLPPEPPAVPSEVELQHRLKEL ERVAGELQSQVKNNQQHISLLNR RQEERIREQEEERLRKQEEERLQE QHEKLRLQLAKPQSVELK\SQEV QSLQQQPDHFILGH\QQYVAT LSAARWAAYQQLD
15153	45521	A	15243	392	558	
15154	45522	B	15244	52	689	
15155	45523	B	15245	400	603	
15156	45524	A	15246	5	1158	RKFWRWMVVMAAQHSQAAQ GQRR**VSKGP**PGPMGGPV GHWWHSGGISLAVPSLPPGKS SVFLFLFSASFSDMKLNPGBTVSP RLIFGSYDDGFLVETVVKDFQ LWQKTPHLRAAGERRRAEORG KLSFVMP

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
15157	45525	A	15247	1	1808	MAEETQHNKLAACKKSATGF HREGPTSSATLKDSLPCQERA VVLSDTSVKISRLKNTIKSLKQQ KKQVEHQLEEVTAQDNLVPWV GLSWGIGGILGACLLLCHLCLP LEKKANNERQKAERELEVQIQT LIIQKEELNTDLYHMERSLRYFE EESKDLAVRLQHSLQCKGEI.FS ALSAVIATEKKKANQLSSRSKA RTEWKLEQSMREEALKVQLT QLKESFQQVQLERDEYSEHLKG ERARWQQRMRKMSQEICTLKK EKQQDMRRVEELERSLSKLKN QMAEPLPPEPPAVPSEVELQHL RKELELRVAGELQSQVKNNQHIS LLNRREERIREQEEERLRKQEE RLQEHEKLRQLAKPHCAFSSRS *TMRTRAHLQLEQQVKELE/Q ALARVFLQVELKSQEAQLSLQQ QPDHYLGHFAAEHLEAASQQN QLTAQLSLMALPGEHHGGEH LDSEGEAEAPRPMPSVPEDLESR EAMVAFFKSAGASAQEKAQQL QEQQVKEQRVCQCQLAHPVASA QKEPEAARGPGAPPGPGESSSF MDHLKEKADLSE/PGEKRTLH P/PTG/GDRRHQKTHLLSEPGG CAK/DAALGPGHIHQAGAQGGD
15158	45526	A	15248	2085	2700	YPGKRGLEWV*ANSNRPAAEG PDEVSSLPATEQSWMENDFDE LRKEGFRRSVITNSFLKLEDVQ THRKEAKNLEKGLDEWLTRINS IEKTLNDLMEMKTM*ELHDT CTSFSSRVDQVEERLSV*DOM NEMK*EEKFREK\RVKRNEQSL QEIWNVYVKRPNLHIGVSEIDR ENGTKLENTLQDIFQENFTYLA RQANIQEI

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15159	45527	A	15249	378	1744	QTERNSININKKDIHTKTPSVRH HHQRPKLHKTGKMKHHRSKA ENSKNQSGSLPPKECSSPAVE QSWTIENEFDFTEEGFRVRIESQ MNEIKGEEKFREKRVKRNQSL QEIWDDYVKRPDRLRJIGVPDSG ENGTRLENTLQDIIRENFPNLAR QASIQIQEIQRTPQRYSSRRATP RHIIIVRFTKVEVKEMKMLRAARE KELKIKKLTQNCLTTWKLNLL LNDYWWVHNEMKGEIKMFFETN ENIDTTYQNLWHTFKAVCRGK FIALNAHKRKQERSKIDTLASQ LKEIEKQEQQTHSKASRQEITKI RVELKEIETQKSLQKINESRSWF FEKINKIDRPLPRLIKKREKRNQ IDTIKNDKGDIITNPTEIQTISRE YYKHYANKLENLEEMDKFLD TYTLSGLNKEEVESLNTSITGSE VEAIIINSIPTKKKSRTWIHSRL PEVQGGAA
15160	45528	A	15250	935	1269	LIEGKLTURNSININKKDIHTKT PSVG/PPSSKTKDRSSLPAIEQS WMENDFDDELTEVGFRRSVTNL SKLKEDVRIPHKEATNLKRLD EWLTRINSIEKTLDDLMEKTM
15161	45529	A	15251	401	497	KTFSPFYFS*RRRTVRDINGFE Y*EPEKLLG
15162	45530	B	15252	220	940	
15163	45531	A	15253	1	1476	

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15164	45532	A	15254	1	2423	MNGKNTNIYQEPTVCQALHW TLARIGKEEPRRGQRGEGLLC RERQPRGLSSPGTAAPAAAP TPPALPGHRTSGSPGPEPILR RGGSADAPGRVKTVVNRPAAF VGKCLGDGSADTACDQAMKG QRGSNRKRKTSHSL TFPSSDM HAGGLSAAHPCAHSRAPPASP SPYKGSLGTRTDGLTDSDA ASGARALGVDGQPQPSPPRRAP PRPVGADGSSRGQPQPGRRRVER RGPATQPGDSRALPEPRGVPAV HPAGGSEWERPPAAPSPEHR DKMLPGLRRLQASARRPQPPF EAARVVWSPCFSSGTLCPQSFS ERPLLPFQGASFPGTTLHQRLCP VAALHGSKGQKWWQSHCYA AAVMEEPPAPGRSSESLOQGPLS WAGGAPASACLLMLALPLA APSCPMLCTCYSSPPTVSCQAN NFSSVPLSLPPSTQRQLFLQNNL RTL GARHLWVQPAHIPVALLQQ PLHHLPGHFPPLQALEELDGD NRHRLSLEPDFTQGLERLQLSH LYRCOLSSLPGNIFRGLVLSQYL YLQENSLLHQDDLFADLANLE PTSFLHGNRLRLTEHVFRGLG SLDRLLLHGNRLQGVHRAAFR GLSRLTILYLFNNNSLASLPGEAL ADLPSLEFLRLNANPWAACDR ARPLWAWFQRARVSSSDVTCA TPPERQGRDLRALREADFQACP
15165	45533	B	15255	47	482	
15166	45534	A	15256	1	636	MRDPNTKRSRGFGFVTCATVE EVDAAMNARPCKVVGRTEPK RAVSREDQRPEDETEELHLRDY FEQYKIEVIEIMTDQGSGKKR GFAFVTFDNHDSMDKTVIQKY HTVNGHNCEARKALKSQEMAR ASSSQGRGRSGSGNFGGGRGGGF GGNDNFGRGGNFSGHGGFGGS HGGGGYGG/SGDGYNFGFNDG GGGSYNDFVNYYNNQSSHFGPM

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15167	45535	A	15257	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESRLSHFEQWGTLTDCVV MRDPNTKRSRGFGFV*ATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGRFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMAASSSSQRGRS GSGNFGGGRRGGFFGNGNDNFGR GGNFSGRGFFGGSHGNGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSYGSQRRF
15168	45536	A	15258	1	286	
15169	45537	A	15259	1	1674	
15170	45538	A	15260	235	1370	KREGEGRLLADTFVSLLLSARGR RRRSIVKVSLSLHPAVMSKSESPK EPVQLRKLFIGGLSFETTDESRL SHFEQWGTLTDCVVMRDPNT KRSRGFGFV*ATVEEVDAAM NARPHKVDIGRVV\EPKRAVSR EDSQRPGAH\LTVKV\IFVGWH* RKTTFWGGKKKRAKKHHLRD YFEQYGK\EVIEIH*LDR\QWP RKRGFAFV\TFDDP\DSVDKIVI QKYHTVNGHNC\EVIRKALSKQ E\MASASSS\QRGRSGSGNFGG GRGGGF\GGNDNFQ\QRGNS\G GRGGFGGT\TRGGGGYGG\SVG DGYNFGNDGSNFGGGGSY DFGNYNNQ\SSNFGPMKGGNF G\GRSSGPY\IGGGQYFAKPRN QGGYGGSSSSSYGSQRRF
15171	45539	B	15261	1	660	
15172	45540	A	15262	2	486	KMRQRERAQGKK\VAAPAPAVV K\KQEAKKVVNPLFEKRPKNFG IGQDQPKRDL\TRFVKWPRYIR LQRQRAILYKRLKVP\PAINTQFT QALDRQTATQQLKLAHKYRP/G DKGALAKL\VEAIRTNYNDRYD EIRRHWGGNVLGPKS\VARIAKL EKAKAKELATKLG

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15173	45541	A	15263	3	845	PPKMPKGKAKGKKVAPAV VKKQEAKKVVNPFLFEKRPKNF GIGQDQPKRDLTRFVKWPVYI RLQRIQRAILYKRLKVPVPAINQF TQALDRQTATQLLK/LVAHKYR PATEKQEKKQRLA/LARA/EKCAA WQKGTSPTRKPP/VLR/AGS*HP VTTLVEVNKKASAGWVIAHRR GFPSSLVVFLP\ALCREKGWGSY \\CIIKGKARLGRLVTRKTCITV AFTQVNGLGRQRALLKLVEA RTNYNDRYDEIIRRHWGGNVLG PKSVARIAKLEKAKAK\ELATK
15174	45542	A	15264	1	5796	
15175	45543	A	15265	1	2212	MPRVEKNIPGRRNSKGFDPE VTQDVTRREWAKKVVWKRKA SKINGAYFCGGRVRGEAIRRT MKMRQQATLTMVTDKGDNVN ISFKVVLIKEEDAIVYKNGSFH SVPRHEVPDILEVHLPQAQPQD AGVYSARYIGGNLFTSAFTRLI VRILPPQOPENIKISNITHSSAVIS WTILDGYSISSLITRYKVQGKNE DQHVDVKINNATITQYQLKGLE PETAYQVDIFIAEENNIGSSNPASF HELVTLPESSQAPADLGGGKML LIAILGSAGMTCLTVLIAFLIILQ LKRANVQRRMAQAFQNVREEP AVQFNSGTLALNRKVKNNPDP TIVPVLWDNDIKFQDVIGEGNF GQVLKARIKKDGLRMDAAIKR MKEYASKDDHRRDFAELEVL KLGHHPNIINLLGACEHRERGD RRHLENQVPTTLILRFSNTLSKR HTRRLYPEPGSEGPTPEPRSSL AQQSEIKLHGGSEPLLIFRQTG SGVDLQQTPTNLQLRVLTVRR KTDKRKGPHQKPCSSPSK KEGFRSNYSKLKEEVQTHGK EVKNLEKKLDKWLTTRITNAEK SLKDLMELKTKARELCDECASL TSQFDQLDKRVSVMEDQMN MKQEEKFREKRIKRNEQSLQE WDYVKRPNCLIGAPESDGEN GTKLENTLQDIIQENFPNITRQA NIQIQEIQRTPQRYSSRATPRHI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15176	45544	A	15266	1	743	PPLLIFRQTGSGVDLQQTPTNLQLRVLTVRRKTDKRKGPHPKPICSSPSSKTKEGFRRSNYSKLLKEEVQTHGKEVKNLEKKLKLWLTREITNAEKSLSKDLMELKTAKARECDECASLTSQFDQLDKRVSVMEDQMNEMKQEEKFREKRIKRNEQSLQEIWDYVKRPNLCIIGAPESDGENGTLLENTLQDIIQENFPNITRQANIQQEIQRTPQRQYSSRRAATPRHHIVRFTKVEMKEKMLRAEK
15177	45545	A	15267	1	618	
15178	45546	A	15268	200	618	EVSRNNTRTKTSYKQDMNTSKGF*KDTST*PVT/KERSSPATEQCWTENDFDELREEGFRRSNYSELKEEVRNTNGKEVKNLEKKLDEWLTRITNAEKSLSKDLMELKTMARELCERTSLSRCDQLEERVSVMEDEMNE
15179	45547	A	15269	158	594	SGSSICCSPISTVLOPPLTPRQTTGSGATSSK/SPTDLQLRECSSPAAKEQSWMENDFDELREGFRRSNYSELKEEVQTHGKEVENLEKIDEWLTRITNAEKSLSKDLMELKTMAREQCDECTSLSRRDQLEERVSVIEDQINEME
15180	45548	A	15270	3	1453	LSDLELAQSIIIFIFAGYETTSSLSTFLYELATHPDVQQQLKEIDAVLPNKERSSSPATEQSWTENDFDELREEGFRRSNYPELKEEVRTHGKEVRNLEKKIQRQMVTRIINAEKSLSKDLMELKTMARELRD ECTSLSQQFNQLEERVSVMEDQMNEMKKEEKFRRKRIKRKEQS LQEIWWDYVKRPNRLIGVPESDGENRTKLENTLQDIIQENFPNLAQRQANIQQEIQRTPQRQYSSRRTAPRHHIVRFTKVEMKEKMLRAAREKEIQTTFIREYYKKHYANKLENLEEMDKFLDTYTLPRLNQEEVEETLNRPITGSEIEAIINSLPTKKS PGPDGFTAEFYQRYKEDLVPFFKLKFQSIKEGILPNSFYEASIIIPKPGRDTTKKENFRPISLMNSDTKILNKLANRJQQHIIKKLJHHQDVGFIQGMQGWFNIRKSINIIQHINRTNDKTHMIIISIDEAKAFNQIQPFMLKTLNKL
15181	45549	C	15271	111	269	

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15182	45550	A	15272	94	4505	YLDMMMSFVQKGSWLLALLHP TIILAQQEAVEGGCSHLGQSYA DRDVWKPEPCQICVCDGSVLC DDIICDDQELDCPNPEIIPFGEC AVCPQOPTAPTRPPNGQGPQGP KGDPGPPGIPGRNGDPPGIPGPQ GSPGSPGPGJCESCPTGPQNY PQYDSYDVKSGVAVGGLAGYP GPAGPFPGPFGTSGHPGSPGS PGYQGPGEPGQAGPSPGPPGP GAIGPSPGAGKDGEGRPGPRPG ERGLPGPPGIKG
15183	45551	A	15273	1628	1832	RRRRKARERRRLAAEQGRRMK EQCKDGFSE/QASGALKLMSGN EGEFKAEGNSKFTYTVLEDGCT KHTG
15184	45552	A	15274	1	362	
15185	45553	A	15275	1076	1240	LRQLL*LCPSWRLCLLGGWQL HLFF*RHHFVHLVSQRCISAMS PSPRRCFSLHL
15186	45554	B	15276	480	1167	
15187	45555	A	15277	3	379	
15188	45556	B	15278	13	369	
15189	45557	A	15279	112	1112	WPPASPSASVIRTVKEFALTNP KSSTKETERKETKAEEELDAEV LEVFHPTHEWQALQPQGACPC RNPTYGLNLQTGEREAKLQYE DKFRNNLKGKRLDINTNTYTSQ DLKSALAKFKEGAEMESSKED KARQAEVKRLFRPIEELKKDFD ELNVVIETDMQIMVRLINKFNS SSSLEEKIAALFDLEYVYVHQ DNAQDLLSFGGLQVNINGLNST EPLVKEYAAFVLGAFAFSNPKV Q/EWEAIEGGALQKLLVILATE QPLTAKKKVLFALCSLLRHFPY AQRQFLKLGGLQVLRTLGAGE GHGARRARGHTALRPCHREK CSPRRRLS
15190	45558	B	15280	54	385	
15191	45559	B	15281	274	776	

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15192	45560	A	15282	362	1323	HQLGRSALLDTRTVSMQAKNGDAVTEPVQA/ENEANGKDTAEVDLLTKELEDPEMKKATARA VTGILASHPCSTDVHIIHNLSTFHGQELPSDTKLELNSVRHYGLI GLNGTENSMLLSAVGKHGVPPIP EHIDIYHILTREMPPSDKTPHLHSL VTVSSPRQRDDMSDGHLLCTAR RHTDIRDDRSPDAPDTARSLAR STITTRRIFALATPSRTLQVC ALAYTSHPAARTQPLASTALTR RYMLPSPQLPSLRDHRRTNPLH SAVATIPTTTGEADVSLLCIGL STLHYALVYIIVSVLTALSAQS MSATDASIIFFPEPKR
15193	45561	A	15283	3	537	
15194	45562	A	15284	1	455	MPRPEKLGKTVQVPLAECLTKD SFLGQKQASLGPPLTRDVTIEFS LEEWQCLDTVQQNLYRDVMLE NYRNLVFLVIS/HFTQDFWP QSIKDSF/QRIIERTYARCGHKN LRLEKIVKVSMRKHQHIIHTGKK PYKCEECAKLLASQPQLEMR
15195	45563	A	15285	1	397	FAVLMAHYDVQEEDPVLT YMGLSVSLLCLL\LAALTFLLC KAIQNTSTSLLHQLSCLFLAHL LFLVAIDQTAGHKVLCSSIIAGTLH YLYLATLTWMLLEALYLF RNLTVVNYSSINRFMKLKF PV
15196	45564	A	15286	191	1332	AIETQAITDNCSEERKTFNLN QMNSMDIRCSDIQGDTQGPSVI AFISYSSLLGNIINATFEEMDKK DQVYLNLSQVVSAAIGPKRNVSL SKSVTLTQHVVKMTPSTKKVFC VYWKSTGAG/CSQWSRDGCFI HVNKSHTMNCNSHLSSFAVLM ALTSQEEDPVLT VITYVGLSVSL LCLLLAALTFLLC KAIRNTSTSLL HQLQLSCLFLAHL FLVQGIDRTE PKVLC CSIAGALH YLYLAAFTW MLLEGVHLL FTARNLT VVVNY SINRLMKWIMFPV GYGVPAVT VAISAASWPHLY GTADRM LAF KATAQL FILGCT WCL CLL QVGP AAQV MAY LFT II NSL LQG FFI FLV YCLL SSQAKH KFT PM EV PRQN HRCL QQN
15197	45565	A	15287	263	397	GRPPAPAA RVSGPASV SAG*KR VSASGS VGV RS MRR GS ALL PPN F

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15198	45566	A	15288	1	278	MKFHDHRGQMQPKPSPAEAVNS APQREPEGSILRAADPLVWAAK AMSASR/RGS/CGSSAADPRHTE RTPTEPDADTRFQPAETLAGPK TRAAGAG
15199	45567	A	15289	5	545	SFMTEAKSSPNPAQQLRSTQRP SESRKVPSSSELQTLSCQLQRPC HPGRGPDPYYASASTRTRSPS ARHAVVGRRGCYPEA/AVRAR EGPHPTLAPASTYGLASPRAD SAHPRPRHRSLLTRLPNPKLGG SADPRHTERTPTEPDADTRFQP AETLAGPKTRAAGAGGQPWDS ANASPP
15200	45568	B	15290	121	822	
15201	45569	A	15291	1	1308	MLRMVGIEISNGQWSTPPCQVL HLEGNDIYNPKEQGLGNTCRW GWMAAGTRRNLCWAPFPFLNP VASLVLHSTIQLQESKDRVL GTLINSPLVSTDKANWSLRLA LEVGDDGGGLVGLSPQPVGSGA MSRCPNCTRKLIGSGISPTSSTL AEEQGSVVVKTHSHQGGGARCSK EKGWQII.LILVAGLCLQLVVV QNVGVRKIPRKYLAALRVAIGH ALAIERRRIRVVDVADQAQDTDR DDRSFGDRDRNRDSDKTDIDWR ARSATDSFDDYPPRRGDDRFGD KYRDRYDSQYGRGYWYEYR DGPCRDMDRYGGGSGRRAFG SGY/RRDNDYRGGRDRYEDRY NRWDDGSCSSRDDFSRDCRY NDRRPPQRPKLNLKPHNTPKG DSSASTSQSSRASFVFVGGAKPV DRAARETKVEEWLQKEQDKLQ HQLEAKLE
15202	45570	A	15292	2	293	
15203	45571	C	15293	56	298	
15204	45572	A	15294	1	273	TRGPWCDSVLRGCSLEQRFSI VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFGISLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS

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15205	45573	A	15295	3	1024	CGGIHSVLRGCSLEPAFFYLRSA FSPTISACRHPMEDSMDMDMSP LRPQNYLFGCELKADKDYHFK VDNDNEHEHQLSLRTVSLGAGA KDELHIVEAEAMNY\EGSPIKV L\ATLKMSWQPTVFPWGAEIT PTQWSLRLKCG\SGPVH\ISGQH FSKLLLEDAE\SEDEEE\EDVKL LSISGK\RSAP\GGGSKVVPQKKS KTLLLMKDDDDDEED\DED DG*WMDFGWMEEAEKAPSE RNPIRDTPAKNAQKSQNQNGD SKPSSTPRISKQQESFKKQEKTP KTPKGPSSEDIKAQMOSIEK GGSLPKVEAKFINYVKNCFRMT DQEAIQDLWQWRKSL
15206	45574	B	15296	1	1107	
15207	45575	A	15297	1	1968	MLASMGVVAKEMKY\LSSPYPQ HAFHTRIKSLMTVNFQQLWL PNEAGPTGDDGWGGDTHGCP FSPHLPLRFIQKQPWGTGRRLQ EHFSCKSLVPVIPSRDIEAFLHL ADLILNTLPLSVIIIGQIESHSEEL RARVSTYESGEDTIQCTVTK PKYGATRWKDPGSPDGPLEER RLEDLSTRNNNSIRLFRGCGYRV KQNSSQRPNKVCGLPDTGVLL QTKCGLVRNSQRSAQTNTKQH EELFSTAGIPENLSSRQEVLPGH GFTGWVGTWTWKLTSCEGVTF HHLSATHKLSHASCRQGNFKP KGAMSVTRSTVPHPLAFLSAEI NGKCGRPCVFLGIWAINCGMAI LYERLSALVCVSVERHLDYT MRFLFDIPPSTLEARIGSPWL SLHPLRSSTVTSSVELIPLPECTV AVLEIQYVFLGDTILFTTVGKA RSGTRDRDGRAQIMQVLQGK GRELDAAAQPEGQLLREVRL GVPFIPRARVDAWLVIHTVAVG SADEAHGLLGAASSTGGAG ASVDGGSQAVQGGGGDPRRAAR SGPLDAGEEEKAPAEPTAQVAD AGGCASEENEVLRKEHVAVDH SSQRENEERVSALKENSLQQN NDDENKIAEKPDWEAKTSES NERHLNGADTSFF\SLEDLFQLL

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15208	45576	A	15298	1	2104	MKHLKRWWSAGGGLLHLTL LSLAGLRLVDLDDLYLLLPPPTLL QDELLFLGCPASSAYALSPFSAS GGWGRAGHLHKGRELDPAAAP PEGQLLREVRALGVPFVPRTSV DAWLHVSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGGDPRARSGPLDAGEEE EKAPAEPTAQVPDAGGICASEE NGVLREKHEA/VDHSSQHEENE ERVSAQKENSQQNNDDEENKI AEKPDWEAETKTESGNERHLL NGTDTFSL\EDLFQLLSSQPEN S\LEGISIWGD\PLPGSISDGHF FKHIYHVNFQPRLIISQD\VNLL EAILLCPNNNTFRRDPTARTSQS EPFLQLNSHTTNPEQTLPGTNLT GFLSPVDNHRNRLTSQDLYD LDINIFDEINLMSLATEDNFDP DVSQLFDEPDSDSGLSLDSSHN NTSVIKSNSSHSVCDEGAIGYCT DHESSHHHDLEGAVGGYYPEPS KLCHLDQSDSFHGDLLTFQHV HNHTYHLQPTAPESTSEPFWP GKSQKIRSYLEDTDRNRLSRE QRAKALHIPFSVDEIVGMPVDS FNMSLRSYVLTDLQVSLIRD RGKNKVAACNCRKRKLDIILNL EDDVCNLQAKKETLKREQAQC NKAINIMKQKLHDL YHDIFSR RDDQGRPVNPNNHYALQCTHDG SILIVPKELVASGHKKETQKGK
15209	45577	A	15299	2	342	RRRFRAAAAVGTA*AVVLSA RPSETWTRGRR*RICPSSWP* GI*VNNG*K*RRHSVCQCSLWF PARCICKYHSMARTQPGTRNKE NGPAGPTALDNVASSDDTGRH RPQT

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15210	45578	A	15300	710	1831	IRMKSKIIARCIKPYHSMARTQ PGTRNKENGPGAGTALDNVASS DDTGRHRPOTTQALPGFAHPLQ LASFRRMVLFLSGEGRSRGGPE LQFPASCRRGEGSPGVRESGSG GIAATSTPNYPPNQDSKEHDIR GAEHQKQEOPAKPHTARSAY PPQKSSYPANAKATRHSPETAA AKEARAPAAAQPQRHQPNSP APHTRPAATRQPERRVSPST HRHPAATRLSPRRQSPSPRHH DRRGFPRLAETLQHPCMPLPV ASAGHHRHHIRL LLLAPQAPER EA SDEI^VFSGRSRSGCPTEFQE SAMCPNPGL.PDSCCGESQAVT LILRKFQKVWVIEVPLDYKKG SWEYFSRMETIIMPENIQSE
15211	45579	A	15301	77	1041	IPSCVVSGLAAAF/HPGI.ASDAP ARASSWWTHVEMGPDDPILGV TEGFKRDTNSKKMNLGV SAYR DHNGKPYSIHKAEAQIAAKNL D EDYLSIGRLAEFCKASAEVALG E NSEVSKSGRFVTVQTISGTSAL RIRASFQRLKFSQDVFLPKPT WGSRTPIFRDTGMQLQGYRYY DRKTCGFDFTDTVEDISKTEPQ SLLLHACSHNPTGVDPGPKQQ KEIATVVKKT/RNLFALFD MAY QGFASGNGNNDKAWVRHSAN IRHRCRCSYTKNMVLHSEGVA GFTMVKDADAEKRVESHLKI LMCPMYSNPPNLNGTRLLL PF
15212	45580	A	15302	1	1263	
15213	45581	A	15303	1	1146	MTGRQSLSPVLSLSSLDMSFT TRSIFSTNYLFLGSVQVSNYGA RPASCMASVYAGAGGSSRSIV SRSTSFRGGGMGSGLAAGMAG GLAGMGGIQNKKETMQSLSNDR LASYLDLDRVRSLETKNRKLESKI REHLEKKGLQVRDWSHYLKTI EDLRVQIFANTVDNAIGIVLQID NACLAADDFRVKSLMTNVTWL PLETEMEALKEELLFMKKNHEE EVKGLQAQIASSELTVEIEKSTT VVTTQSTKVGDAEMTTELRR TVQSLKMDDLSMRNLKASLEN SLREVEARYTLQMEQLNRILH LESEMAQSAEKGHQHIGEYEAL LNIVKVKLEAESATVHRLLDDDD FNLDGALDNNSNSMQT/QKTTT RRKVVSETNDTKVL

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15214	45582	A	15304	184	370	
15215	45583	A	15305	40	1411	RGDPRVRRRTQSLSPVLSLSPDS MSFTTTSITFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTSFRGGMGSSGLAT GIAGGLAGMGGIQEKEETMQS LNDRLASYLDRVRSLTEENRRL ESKNPEHLEKKGPQVRDWSHY FKIIEDLRAQIFANTVEQCPTIV L/LRIDS/A/RLA\ADDFRVKYEV/T EAGPCAQSVENNIHGLCKVIDD TNVTRLQLETEIEALKEEELLFM KKNHEEEVKG*AQIASSELTV EVDAPKSQDLAEIMADIRAQYD ELARKNREELDKYWSQQIEEST TVVTTQSAEVGAAETTLTELRR TVQSLIEDLDSMRNLKASLENS LREVEARYALQMEQLNGILLHL ESELAQTRAEGQRQAQYEAL LNIVKVKLEAEIATYRRLLEDGE DFNLGDAALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
15216	45584	A	15306	392	1449	GPWEMLMITKSHPDAAEPRQQR VKKLTQVFVSSASLRLER/GKY LFWPWPLKKAAEIPAAEYREALDE ALGISGGGRDVGERVYKGPSM MANPQKPVLEALSSNNKYLHILC AKHCDRHEGYKDEIKVKEASS RVNGCVEAMLSAPLPLDRRNE HVESKGKPTTMGLSPRVLASR RDGLRERKGSSFRTVVLHDTKT DSNSDTETNSSTPPRTILEMQL SPTWTYEISSSRTLGCGPSVFQQ RASYSPSVSGPRLGCPLMDGGR MRCPPGNPESCVSSEANLIPISVP VAPHAHQHLVLSVFWKITIVIG GKTCVAQNHSNEAKMKQRPEI NHASPPGAFAWSQSGEPIASAM TVPA

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15217	45585	A	15307	1	785	MWDVGQDSSLLRGAGGGPLQL WFGRLQLHLGGRLREHRAWV HSRGLGCSGGMQGAATPTQNG RGSCLSAPASSMEHAAPAVPP CCSWCDSSRSRWPATATTETG PRTVPSAQESAVGLLTASLLKG DSGSGTGFCPPLMSLAAPGTQQC SLGFCCFTFERKRSSVSPAAPGTA APELAALMLMPRNQIAVYE LLFKQGVMVAKEGVHLPRHPE LADKNVPNLHIMKAMQSLKSQ GHREEQFAWRHFYWIILTREGI QSIQ
15218	45586	A	15308	1	392	
15219	45587	A	15309	1	716	
15220	45588	A	15310	150	372	RRSNEWGVPVPVPARTGGG/HG QKTPPSPLPPSSPPSPSPPPPPA /APAKIPPLPLPPLPPLPREAPPAP GPALP
15221	45589	A	15311	218	740	KSCPETVSRRKNVGSIKKHQGD KFNPVCLKMTTKTEFVLCGWV PCRCL/REGEEETVTILDYSHCS /LEQVVPKEI/FTFFKTLEELYLD NQIEELPKQLFNCQSLHKLSLPD NDLTTLPASIANLINLRELDSK NGIQEFPENIKNCKVLTIVEASV NPISKLPDGFSQLLNLTQ
15222	45590	A	15312	96	297	
15223	45591	A	15313	469	5174	KMTSLAQQLQRLALPQSDASLL SRDEVASLLFDPKEAATIDRDT AFAIGCTGLEELLGIDPSFQEFE APLFSQQLAKTLERSVQTAKVNK QLDENISLFLIHLSPYFLLKPAQ KCLEWLIHRFHIIHLVYNQDSLIA CVLPYHETRIFVRVIVQLLKIINNS KHRWFWLLPVKQSGVPLAKGT LITHCYKDLGFMDFICSLVTKS VKVFAEYPGSSAQLRVLLAFYA STIVSALVAAEDVSDNIIAKLFP YIQKGLKSSL
15224	45592	A	15314	267	495	GCLL**CLCIRL/SKRNRAERALR PYSDVEALRLSSDFPFRQPKG GSGWSSLSSVEINQYYGPRVMIG RSNSEVVVLV

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15225	45593	A	15315	3	3027	AMEQAGTRPAATEHPRLLRPM PWLLLLPLLLLLLPGPAASQ LRYSVPEEQAPGALGVNVARA LGLELRLPGPCLRINHILGAPSP RYLELDLTSGALFVNERIDREA LCEQRPRCLLSLEVLAHNPVAV SAVEVEILDINDNSPRFPRPNYQ LQVSESVAPGARFHIESAQDPD VGANSVQTYELSPSEHIELDK PLQENSKVLELVLRKGLDREQA ALHHHLVLTAVDGGIPARSQTAQ ISVRVLDTNDNS
15226	45594	A	15316	1	775	MPCVNGKYNSTIQAGLQMAQI LQDECPYEVGIDEETGSQKGDD IIRSSRKLLFTMALFLETNLKD PLSRERRWRLDDELDSCGREKG VAVFLRSAGIRQVQVAMEQAG TRP/AATEHPRLLRPMWLL/L PLLLLLLPGPAA/SQRYSV PEEQAPGAL/VGNVARALGEL RRLPGP/CLRINHILGAPSPRYLE/ LDLTSGALFVNERIDREACLGS AGANPVA/SAVEEILDIN/DNS PRFPRPNYQLQVTARCWWTSW
15227	45595	A	15317	2	165	
15228	45596	A	15318	1239	2251	TCSSRARRPRRGRTVSQVRGPA PWAPRRARLQQRGSLRGAARS PASPTSA/PSYSRASASAGPAAL QPQGAVTPGPSANLAAPGTL VPAEGPRMPPTAQSASSII/PAP SAQSPSSPAASRSGLSVPQEV ATLLASASSPTLDATRDAPATP RIAAPPGSATSSRGLGSQAQGSS LGTKEISDSFGLGSPAVTQRTT APPDSAALSQDTRPEAAGSWPG PQTGACSVGSGTDRRTAAAT EAQHLLSESKEKTSQAQKSGNCF GILKADFTISTLMDPEEMKDQF LRQVRLPSTDALKQSIISNYRP PGKGPQCYLGDSAWNMSA GTIEGFYKE
15229	45597	A	15319	46	2859	

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15230	45598	A	15320	240	924	NGEQKICILCHIVSSKKRHSHE CRRCGPTEVSL SAYAKHISGQL HKDNVDAQEREDDGKGE <sup>EEE</sup> DYFDKELIQLIKQRKEQS <sup>R</sup> QEPS SSSQEVNSDDSSATFSVSVFV WLKTILLTWPKEVKRLDTPGL ELWLVPNMAELSEPEGPVDWK ERCVALESQLMKF <sup>R</sup> VQASKIRE LLAEKLHHNERLEYRDQRKDS ASFQRKKQFTYKASGIESMASL SKAPEIRG
15231	45599	A	15321	3	755	LRLPRRSTTRRGIVWRTGAAM GKVNVAKLRYMSRDDFRLTA VEMGMKNHEIVPGSLIASIASL KHGGCNKV <sup>L</sup> RELVKHKLIAWE RTKTVQGYRLTNA <sup>G</sup> YDYLALK TLSSRQVVECVGV <sup>N</sup> QMGVGK <sup>E</sup> SYIYIVANEEGQQFALKLHRLR RTSPRNLLKNKRDYHIIHRHNVS WLYLSRLSGMKEFCYMKQFC EQGSQRLRHMMGGQMWA <sup>V</sup> PIC QPRDLFVWWFVLR <sup>A</sup> EACAGCGA TSQRQGALGVTSTCYRD
15232	45600	A	15322	1	1028	MNKTTTQEEVPLQLQADVVQRE EELNSLKQKLA <sup>A</sup> ALLAEQEPQ <sup>P</sup> ERLVSELQL <sup>I</sup> PRKAAVFQDEILR SSRQLV <sup>L</sup> PELGVHRLV <sup>L</sup> VVCC GGLRCPLAGGLAAASVGR <sup>L</sup> GL VDCDVVEMSN <sup>L</sup> AYQV <sup>L</sup> HGEAL AAQAKAASAAA <sup>S</sup> LRGLN <sup>L</sup> APP PAETVTNCADGGMLRVL <sup>T</sup> GVL GCLQPLKVLKIAASLG <sup>P</sup> GSYS <sup>G</sup> LLLFDALRGH <sup>F</sup> CIRL <sup>S</sup> CR <sup>L</sup> DC AACGKWP <sup>T</sup> VTHLL <sup>D</sup> YEAFCGS SATDKCRSLQ <sup>L</sup> LG <sup>P</sup> EDR <sup>V</sup> S <sup>T</sup> TD YKRLLD <sup>S</sup> GAP <sup>H</sup> LLL <sup>D</sup> IRPKMEL PRKAAVFHDEILRSSRQLV <sup>L</sup> PEL GVLRHLLVVGCGGLRCP <sup>L</sup> QA <sup>Y</sup> LAAAIVGRLGLV <sup>A</sup> YDV <sup>V</sup>
15233	45601	A	15323	92	778	QGTRRW <sup>S</sup> SLGTCSLMTR <sup>T</sup> QFEV CTKV <sup>C</sup> VQESLQ <sup>R</sup> PGEELK <sup>T</sup> RCP SVGAGYV <sup>N</sup> YGT <sup>P</sup> AHER/ <sup>G</sup> AAV KTGREADKPEVTKQTQFSTRK DE/TS <sup>L</sup> FGVPLQ <sup>W</sup> LARHR <sup>R</sup> PP <sup>*</sup> RRT/RRL <sup>L</sup> EARTPM <sup>L</sup> PAQ <sup>S</sup> ASR SELAARQDSAWASPAAPASPN/ RSVLRRC <sup>L</sup> SAR <sup>P</sup> PLCG <sup>L</sup> /LRV LPSWRRQQIRENSAED* <sup>L</sup> HSEY RANIRR <sup>R</sup> RGHPEN/WT <sup>S</sup> LE NPENL <sup>N</sup> TRRSSA <sup>P</sup> APC
15234	45602	A	15324	142	500	

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15235	45603	A	15325	3	343	
15236	45604	A	15326	1164	1648	PLMTSAPWPSCCCWRSLLSSGRP AGRQRQLPTSIITANQQPAPSRR KKSTSRKKQRNLPAVSPAMVAI VRRSCDLYRWSVLIHYASQERR VRDAAKPESD\RKRTTTKTRR/H WRYIKELESRQPQGVADMRRQQP TQLVEVPWNEQTPEQRQQTLQ RQHGRETCSV
15237	45605	A	15327	28	417	
15238	45606	A	15328	2	440	
15239	45607	B	15329	1	441	
15240	45608	A	15330	22	584	IRGRVDPPSAVEPPPQKMQIFVKT LTGKTVTLEPVPLGYG*KNVK AQASRDKIEG\NPPDQQR\IIFAG KQLEDRTLS\DYNIQKESTL HIFVLRLLRGGAKKRKKKSYTT PKKVHKHKRKG\GSLAVLKYK WDENGKISRLRRECP\SDECGG WGYGGQVTFDRHYCG\KCCLT LLFQQTMRMTSNCMS
15241	45609	A	15331	3	954	LDARRHWEGTPGFTHTSPDAW ADAWGKMAKEVKEKPDTEKE KPEAKKIVDAGGKVVKGNLKA KKPKKGK\PHCSRNPVLLRGIG RYSRSAMYSRKAMYK\RKYSA AKSKVEKKKEKEVLA\TVTKPV GGDKNGGTRVVKLRKMPRYY PTEDVPRKLLSHGKK\WPSQHV RKLRA\ITPGTILII\LTGRHKGKR VVFLKQLASG\LLVTG\PLVLR WPLRRTHQKFV\IATFTKIDISN VKIPKHLTDAYF\KKKKLRLKPRH QE\GEI\FT\TEKEKY\I\TEQRKIDQ KAVD\SQLPKIAIPQLQGNLRS V\FA\LTNGIY\PHQ\LVF
15242	45610	A	15332	670	1008	WCILGVTPSLMSRTALFLS\RH FFA\RS\HSAAS\KL\EK\KKKEKV ATVTKPVGGDKNGGTRVV\KLR KMPRYY\PTEDVPRKLLSHGKK PFSQHV\KLRPSITPGTILII\LTG RHRG
15243	45611	A	15333	1	708	

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15244	45612	A	15334	1	1754	MRNEISDLTEELHQKEITIAVT KKAALLEKQLKMELEIKEKML AKQKPWACLVNAMPAIQVVFN LGRFRKCQDPHKQAQEWWVPGY SGSDCEVFPEIMTSKRNREEAMP EWKLWKKVVLSGATDAPSWD GPTFTDLNVFAGNMGILSDCTLS LGKIKWKPQGHFLHTSGPVSFHT KGLLNPTKERWVGGFGSEGR GVPEPGCGFGVLAQPRRTPSA AAMTGGERLGRAWAGDRAAA SRSAPVPGTGFMMGWRPVAFG KNAKAYRGFGGIVTSLTPSCDK VTLLFVRLPGSGQSRDQSSPEK LTDTKSTSNAKAYGFPCECLRPE STHIFFYDHQLGSQPRRGTKGT PLKWVSSQKTLERETRQCQALVI WTDCDREGENIGFEIJHCKAV KPNLQVLRARFSEITPHAVRTA CENLTEDPQRVSDAVDVRQEL DLRIGAAFTRFQTLRLQRIFPVE LAEQLISYGSQCFPTLGFVVERF KAIQAFVPEIFHRIKVTTHDKD GIVEFNWKR/LSTL*PHGLPSSL SVVCGVRSLSCRSGVFCWRSTP DPVCLCITSGGCRTASIAEQQQKL LPDPSYRSFPEGQQPI
15245	45613	A	15335	3	125	
15246	45614	A	15336	764	1005	
15247	45615	A	15337	1	3533	MELVNCVLMSTLGNNTCCPMAI AMFRSSSSLPRPGHSLTGSPLRV NLIIHKFPLNDFHQNVVKIKNK DPPLGAAIGKESCPIDNELHSL ERRPLSPKLVQALGVAGLSRPG PPHTGCAIWLLITDHKLSEIL YDLLLHQQLDILADPPDEGGIPR GKNLVELLQLPGLEEDKAFQKE IGLKILVFKAYSTLSSDGPPFLS ALRSLQGVQSSKVGESREEKSQ TEEEDPGNPWVQSQLGASVSSS GKWGCLRTKP

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15248	45616	A	15338	1	2800	SISGPGQEAVPLRPKAEPPEGSG MVWDRQTKMNEYEWKPDSEQGL QQILQLLKKESQSPDPTTQIERTVQQ KLEQLNQYPDFNNYLIFVLTKL KSEDEPTRSLSGLILKNNVKAH FQNFPNGVTDFIKSECLNNIGDS SPLIRATVGILITTIASKGELQN WPDLPLPKLCSLLDSEDYNTCEG AFGALQKICEDSAEILSDVLD RPLNIMIPKFLQFFKHSSPKIRSH AVACVNQFIIISRTQALMLHIDSF TENLFALA
15249	45617	A	15339	8	450	TWSWSPQAPSWARPSSQARAV SLLVARGQLCQGSRRSGRSVGR VDAGAAARTALRTLGLTRPRLRRP CGLGSHETKAAASGQDGQRGS RGRGSLGGRELGANEPFLYQ\WR AHTLTVLFILTCTLGYVTLLEET PQDTAYNTKSEIAVVHLS
15250	45618	A	15340	246	559	MPVAVMAES/AFSFKKLLDQCE NQELEAPGGIATPPVYQQLLAL YLLIIN/GQRJWQRDFPGIYTIN AHQWSETVQPIMEALRDATRR RAFALVSQAYTSIIADDFA
15251	45619	A	15341	129	915	RSGTQGRSAATAALNVIAGATP EGQSWGLAVRTVQRRGRPAK MPVAVMAESA/VSFKKLLDQC ENQELEAPGGIATPKVYQQLL ALYLHFNDMNNARYL*KRIPPA IKSANSELGGI\WSVQGQRQIWRQ DFPWG/IYTTINGHQWSE\TVQP IM\EAALRDATRETA\PLP\WVSA YTSIIAR*FCQPLGLPV\EEAV KGIL\EQGWQ\ADSTTRNGSCP GKPVCRGPWDVFPFNKFISLYS EPVAPV\PPIPNEQQQLARLTDYV AFLEN
15252	45620	A	15342	1	529	MATLTISRAQTEADYYCHRI KLVKEGLDERTHKAYLSSSGK GCEFHMKPGSPGLPDILGSGWA QSALIQPPSVSGSPGQSVTISCT GTSSDVGSDYVSYWYQQHPGT VPKPMIYNVNTQPSRVPDFRSG SKSG\NTASMTISGLQAEADEAD YYCCSYAGSYPVVFGGGTKLT
15253	45621	A	15343	399	737	WISGGNSCATT/LSDAGLSTSNT SIGSAT\GARQAEASSQSGGA LGRHCGASGKCAESLRREPVG ATNQWAPGWVVRPASDSSHVS VIGLGRSAWSPEAVTPSLIPGRG RTK

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15254	45622	A	15344	1	4320	
15255	45623	A	15345	1	966	MNVNLAEESKGKETVGDEIKG GGIQMVMLASQPLTYSYCAARFI TGHGQKLKSELKKTLQVIMLNI QKVRIPTRDGYNEKDLSTGKN VEKLELSNIAGYPSNIKEKEYQE QSVLSCCSERKDANPKSVVCSF FMQEQTGKGEKRFLIPGTLSDV RHLRYFGILPTVSNAAVVKEPV TVSNAAVVTEAPTGSNAAVT EAPTGSNAARVMEVPTGSNAA VVTEVPTGSNAAVVTEAPTGSN AAVKEAPTGSNAARVMEVPT GSNAAVVKEAPTGSNAARVME VPTGSNAAVVKEVPTGSNAAV VKEVPT/GSNAAVVKEAPTGSN AARVMEVPTGSNAAVVKEAPT GSNAARVMEVPTGSNAAVVKE VPTGSNAAVVKEVPTGVTLRW SRKRPRE
15256	45624	A	15346	1	702	
15257	45625	B	15347	238	546	
15258	45626	A	15348	632	2361	FQSRTFLKNWNPGEQSQKII/CF QLGERAYQTDVLVKVPRQSSV FSENQRMNPPERWFESTGCGK TYNQNRQAFNQHQRFHSGEKT EHNECGKAFSbpsILSKHQRIH TGKKLYTCEDCGKSFVHSYFI QHCKIHTREKPYECIKCGKAFS THSSYVQHLKIHTGEKHHECNQ CGKAFSHSSNLIIHQRIHSGEKP YKCKECGKAFNRQSNLIIHQRI HSGEKPYDCCKEGKAFSTQLFL IQHQRIHTGEKPYECNECAKSF LNRTLTVHQRIHTGEKPYRCNE CGKSFSCSQSVIQHQRJHTGEK PYICNECGKSF GARLSLIQHQRI HTGEKPYGCREKPYECSECGK AFSQSFNLIHHQRTHNGEKSYE CNECDKAFLSLLSLVQHQRIHN GDKPYECHCGKAFSQGSHLIIQ HQRIHSGEKPYECNECGKTFGQ ISTLIKHERTHNGEKPYECSDCG KAFSQSAHLIIHQRIHTGENPY ECSECGKAFNVCSSLIQHHRHT GEKPYECSDCGKAFSQHSQFIIQ HQRIHTGEKPYMCNECEKSFSA CLSLIQHKRHTGEKPYVCACK

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15259	45627	A	15349	3	354	EAFGGERVSSTMSGLSPARR GPFPLALLLFLLGPRVLALISF HLPINSRKCLREEIQQGPASDW RVRDLRPVWGRWRPAQ/RTSRS QILLAIIFSTPKRMQPRGNLPLTT EDYDMF
15260	45628	A	15350	283	393	YVYRRYGRFE*NDPSSALMST* GKRCQDCLDQRENKK
15261	45629	A	15351	1	351	
15262	45630	A	15352	1	867	
15263	45631	B	15353	1	1323	
15264	45632	A	15354	1	3669	
15265	45633	A	15355	362	1039	LESYLQLPSAEGKTVSVFGETC ATPVGP/AAGPHTQ/LAQNIVTS WLTGGRFIELKTVQILDRLELE KPCIDAEDCFTNESTWTEFTLL KAWDEYLKAWFALHILLEAMF QPSDSGKSFIFNMSVGYNLEQQ PLNPKNYPSQGVPRVLKSHRQD YLVGKNLWSADIHLVLFYYV EELDSSLISSFPPLKPHTHVDNT KKGSHPHMCAYTDVNNPNND RMPQREITFVS
15266	45634	A	15356	74	208	QRLTKLRETSRRLLSWQRSPSS TTSMHGAEWSPPRWLAAAGV EFEEKFIKSAEDLDKVRNDGYL MFQQVPRLRLMG*SWSRV
15267	45635	A	15357	308	735	NQRCTWASMTMEIFLISCVKT LSVRYAVQQQLKTGVFCSELETQP SKMAPAKKGSKKKGHS/AIIIE VVTQENTINIQKHHIHEVGFKKC APRALKEIQKFAMKEMGTPVV LIDTRLNKAVWAKRIRNVTNR HLCLSRKCNEDEKE
15268	45636	A	15358	3	323	LSSLASMSFTITCSAFTNYWSPG SVQVPSYGTQPVSHASAVYAG LGGSGSRISVSHSPMAGGLAG GGGQNEKETMQSLRDRLASY LDRVRGLETEENWLESKIQEH
15269	45637	B	15359	1	991	

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15270	45638	A	15360	40	1030	RGDPRVRRRTQSLSPVLSLSPDS MSFTTRSTFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTSFRGGMGSGLLAT GIAGGLAGMGMGIQNEKETMQS LNDRLASYLDLDRVRSLETNRRL \\ESKIREHLEKKGPVQRDWSHY FKI\\EDLRAQIFANTVDNARIVL QIDNARLAADDFRVKYETELA MRQSVEN\\DIHGLRNV\\DDTN YHTDLQLETEIEALKEELLFMK KN\\HEEEVKGLQAQIASSGLTV EV\\DAPK\\SQDLAKIMA\\DIRAQ Y\\DELAR\\KNRE\\LDKYWSQQI EESTTVTTQSAEVGAAETTLT
15271	45639	A	15361	1	438	LHSDDLSSLQMLRCSPVATAASY TSGPGAPISSSSFSRVGSSSFQGG LGGGGFGGASGIGGITAVMVNQS LLRPLNLEVDPNIQARF\\VHTQE KEQIKTF\\NNKFAFSDIKVRFLE QQNRMLEAKWSLLQQQKMAQ SNMDNMFQS\\YINNLL
15272	45640	A	15362	176	1455	EIPFLV1QKSYKVSTSGPRAFSS RISYTSGPGAPISSSSFSRVGSSS FQGGLLGGFGGASGIGGITAVM \\VQVLHTEKEQIKTF\\NNKFAF FIDKVRFLEQQNRMLEAKWLSL LQQQKMAQSNMDNMFQS\\YIN NLRWQLETLGQEKLLKLEAELG NMQELVEDFKKYHDEINKHT EMENEFVLIKEKD\\VDEAYKNV ELES\\HLEGLTDEINFRLQLHEEE \\WELQLS\\ISDTSVVL\\S\\DSSHSLD MDNI\\IT\\EVKAQYKEIANCSWAK ADSMYQIKYEDLQMLARKHGD NLRCTKT\\D\\ISEMNQNQV\\WLQA EIKGLKGQ\\RAS\\LEAT\\T\\DAEKR RELA\\IKD\\ANT\\KLL\\E\\EA\\LQW AKQDMAQQLRVYQELMNV\\KL ALDIK\\T\\ATY\\KKL\\LEGE\\E\\SWQ\\ES RMQN\\MSI\\YSKTT\\SGYAGGLSS AYGGLTSP\\PL\\SYGLSS
15273	45641	B	15363	70	915	
15274	45642	C	15364	62	217	
15275	45643	B	15365	1	612	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15276	45644	A	15366	3	841	STPKMPKGKKAKGKKVAPAPA VVKKQEAKKVVNPLFEKRPKN FGIGQD1QPKRDLTRFVKWPRY IRLQRQRAILYKRLKVVPPAINQF TQAL1DRTQAT0LLKLAHKYRP ETKQEKKQRL\LARAEEKKAAW PKGTFPTKRPV\LRAGVNTVTT LVENKKAAQLVVIAHDVDPIELV VFLPALCRKMGVPCIIKGKAS LGRIVHRKTCCTTVAFPTQVNSED KGVALAKLVEA1RTNYNDRYD EIRRHWGGNVLGPKSVARIAK LEKAKAKELATKGLGNVHC
15277	45645	A	15367	2	1006	WINLKGNNLLRKRSLLTSNFWPC LRSRKRRHTRRNLMNLWLSSH PPQQSNTKPWCCQLSCSTSLLT LLGTSPLLSYLIHLIPPGPRQYP VIHRTSTLLLQHISVGKEKFFHKS QHWGFCNNVMMQLQLQPLK GLSLVDKVNRPPALS GTRVLAS KTAWRIFQEP/SEPKTKAAAPG VEDEPLLRRGNP CRFVIFPIEYHD IWQMYEKA EASFWTTE EVDSL KDIRHWESLKPEERYFISHVL VF FAASDGI NENLVERFSQIVQITE ARCFYGFQIA MENIHSE MYSLL IDTYIKD PKEREF L FNAI ETMP CVKK ADW ALRW IGD KEATY G V V A A VEG G IF GS F AS IF W L K K R G L M P G L T F S N E L I S R D E G L H C D F A C L M F K H L V H K P S E E R V R E I I I N A V R I E Q F L T E A L P V K L I G M N C T L M K Q Y I E F V A D R L M L E L G F S K V F R V E N P F D M E N I S L E G K T N F F E K R V G E Y Q R M G V M S S P T E N S F L D A D F
15278	45646	A	15368	3	1368	QAQPMGRVGGMAQPMGRAGA PKPMGRAGSARRGRFKGCWSE GSPVHPVP PAVL SWL ALLRCAS TMLSLR VPL APITD PQQQL QLSPL KG L S L V D K E N T P P A S T G R F T R V L V L A K A P G V E D P L L R E N P R R F V I F P I E Y H D I W Q M Y K K A E A F W T A E E V D L S K D I Q H W E S L K P E E R Y F I S H V L V L A R C F Y G F Q I A M E N H S E M Y S L L I D T Y I K D P K E R E F L F N A I E T M P C V K K A D W A L R W I G D K E A T Y G E R V V A A V E G I F G S F A S I F W L K K R G L M P G L T F S N E L I S R D E G L H C D F A C L M F K H L V H K P S E E R V R E I I I N A V R I E Q F L T E A L P V K L I G M N C T L M K Q Y I E F V A D R L M L E L G F S K V F R V E N P F D M E N I S L E G K T N F F E K R V G E Y Q R M G V M S S P T E N S F L D A D F

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15279	45647	A	15369	2	621	RFIKMLSRHHQHVHHVLPLRA PLPVAMEEEIPALFIDNGSGM/C KSSFA/GDNLRAIIFPSIIGHPRH QGVMVGMGQKDSYVGDQAQS KCGILTLKYPIKHGIVTNWDDM EKIWHHVFYNELCVALEEVVV LLTEAPLNPRANREKMTQIMFK TFNTQAMYVAIQAVALTLHSSC TTGIVMDSGDGVTHTVPIYERH TLPHTILHLDL
15280	45648	B	15370	1	966	
15281	45649	A	15371	2	228	
15282	45650	B	15372	1	816	
15283	45651	A	15373	256	384	RKLLNEAPC*PMR*HSLLNRLA TSCNSWTVPVPKFSLRRGL
15284	45652	A	15374	145	375	KIAKGKRNLRNQCKERKVQVL WISEKKQREAVEDSPSLDCCH KFPFGS*ERLHG*KRGQWF*PP HTVEKQMRSCLL
15285	45653	A	15375	319	482	
15286	45654	A	15376	4776	5910	VCSTAGDVNGVCLLYDLLHIA VASGSAKGECCFARKPLLAEVG IYDCLQEFKEKKLVPATPHAQV LSYEALLSAHDITIAQKDFEPLLP PLPDNIPESEEAMRJCLVKVNQ QPLGATIKRHEMTGDILVARIIH GGLAERSGLLYAGDKLVEVNG VSVEGLDPEQVIIH LAPRPCLSP MSLADLPLPLPREVLVLAGKLPV PSSSFLLQPREDCQGPQPSLLIT WFAPLETEPGVDRAMSRTIMF KVVVPVSDDPPVNSQQMVYVRA MTEYWQPQEDPPDIPCMDAGLPF QKGDILQIVDQNDALWWQARK ISDPATCAGLVPNSNLLK/RIWT EPGICIFTKRLRCSGKQREFWW SQPYQPHTCLKSTLCEYCNCP
15287	45655	A	15377	2	405	WSLVTRRALARVGLPG/PPPPRL LLLPLLGLWGLRVA AASASSS GAAAEDESSAMEELATEKEEAEES HRQDSVSLLTFFILLTLTILTITWL FKHRRVRLHETGLAMIFGLEK ITIGVLDITGWPYCTIQPYNGFL
15288	45656	A	15378	1	3804	
15289	45657	A	15379	349	622	RPDVANLAFLARKEGTKRGFLS KKTAEASRWHKEWFLAYQNV LFYFEQEQSCRPIGMYLLLEGCS GGTSPRSFRSSSRDSPISIPLHPT AK
15290	45658	A	15380	314	483	

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15291	45659	A	15381	352	822	DPRRVQAFPAKMKFNPFTSDR SKNRKRHFNAPISHIRRKIMSSP LSKELRQKYNVRSPMIRPKDDEV QVVRGHYKGQQIGKVQVQYR KKVIVIYIERVQREKANGTTVHV G\HPSRVVITRLKLDK\DRKRIS DRKAKSRQVGKEKGKYKEETI EKMQE
15292	45660	B	15382	80	432	
15293	45661	A	15383	11	888	VKCRKAEGRRESRLQTFEESQA VEAMANVPWAEVCEKFQAA LALSRLVELHKNPEKEPYKSKYS ARANMEEVKALLGPAP\DED ERPEAEDGPGAG\DHALGPAE VVEPEGPVQAQNRLRLAVNEF HLGVNHIIDTEELSAGEEHLVKC LRLLRRYRLSHDCISLCIQAQT WRCIGVRDPPTSSCAFLSTSP VHSVKKIQTPGPLRPSNSTLVD DMESSFQTCFASPLSQDYVN NQEEIGTGVDRCIHKFLDIARQ NISFLQKRLQLSVQKPEQVINED VDVSELNE
15294	45662	A	15384	1864	2705	WPGKVL AHLRGLHPWHRDPHGS GGGAGQELRRQGGCLEQLLYD AAHAQRLPPLDOSVLPAALPQD CQRASACEDPTILLRPSHSPGH PRGAER/VPSTA CLQRWSWEGR/ WNRALQVQVGGLKSPWRGEYK EPRHPPNQANYHQTL/ACPAE R/CFRQGPQGPQGQLRRQQAEPL SSSSLSHQS PQSQTSLLP*L*AR RSLGCGNPYLCPPWSQPLPETP AHQSGKQPSRSRNCSWWK*NYS STACPSHIFLWRSRSKFSRASAST ASPCRMTVRRTHQRPK LARGTP
15295	45663	A	15385	1113	1378	RPHAE SFVSGGIPDPPPGPGGST GPGLERQPCSLTSWPREPSSS SMKMLTQGP SLTAPYKGTILGE VNPAHAISSSARNTSSRTSV
15296	45664	A	15386	285	722	TPAHPGVPGQSGRHRHW/QSA ARSQQLPSAW\PKTGSLFATTW RCQTRASTCSAHWPLMAASPG AGGSSMASWR/DRP\CPPPPAP HLPEAFLLR\CHDACP\NTGSA VPRGSCQPPAQWQDQGLAATR WGQAERLPRIYNWALAPP

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15297	45665	A	15387	207	605	FQASAERFGTEDD/GSLRTPPV MQSHQWPWRRPRPLVSRGRPQ TTPERHDSGGSLPLTPRMEHS EDEDLA/EGCRWP/EAGTVGP GPRAGAAQR/QAVLARKKHR RRPSKRKRHW/PRYLELSWAEK QQRDERQS
15298	45666	A	15388	193	407	ACPKTSKNLRQRRLWNLAKHE F/SVDMTCGGCAEVSRVLISLE VRVKYDIDLPNK/KVCIIEHS MDTLLATL
15299	45667	B	15389	321	625	
15300	45668	A	15390	275	690	SLWPPIRG/SPKGNRPAILTGH DVGLNMANKKSGDHPEREGTP RSFREVVSAGPGSSKLQIPKGS APRCGVPGRGRARRELQSFragP RTQGSPVGPRCQSRRRLRSAQEE SAKARHGGGLRAHRSFSDIRM SSKERKFS
15301	45669	A	15391	2	137	PGRYRPN*LLSDASPAGNEF QSTFLPTTILPSLRFPVLYTPNS
15302	45670	A	15392	1	648	MSLRKLTTIMVEKGKGGPNIPHAC GCRQRSSIKVSLPAVTKSSESP KEPEQLRKLFGIGLSFETTDESL RSHFEQRTTLTDCAVMRDPNT KCSKGFGFVTYATMEEKYHTV NGHSECAKALSKQEVASASSQR/GRSGSGNFGGGGHGGGF GGNDNFHGENFRGHISSFGGSHG GSGYGGSGDDYSFGNDGSNF GGGGSYNDFGNYSNQSSNFGP
15303	45671	A	15393	1	3629	MTGICYTEDERSYKKNAQPTA ASKKQKETQKFCRLRVDGQKVKL SVLQEKSAQLTVQLKSQKFGLGHPTAGRGRSELCLDLPDPPEPD PVALETRSVGTWVVRERDLMGP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAAGAPAQRAQSLPEPYGTG LRALAMPGRPESPPVFRSQEVV ETMCPVPAATSNVHMVKKISITERSCDGAAEMKWEDQNIGD

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15304	45672	A	15394	1	1515	MGQVFRVVTGVGEQPGHPDQF PYIDSWLSIIQNHPKWLQACFET YCKTLMQIKPGTIERDCKAV KEKDSQEKKPKVLPQAPPEELE SPALYAPIYPSLARLRLQEAAPA APRGSDSEESTPQATPCREEPEP IPEKETSSSYRSNAVHFLIHNP WADCKQLLQLSLNTEEHHRV1 QAAFQWLLENNAPAGTGYIRQY AQQLALPIEADTGWDPNQAQGL QSLQWYREALLNGIKAGGKKA TNIGKVSEVCQKPDESPSEFYER LCEAYQLYTPFDPEAGNQCM VNVAFVSQAQGDIKRLQKLE AKAVLRGKFIALNTYIKKAERA QTDLRSHLKELKQEQTKSKA SRRKDVTKIRAELENEIETTTKI QKINETKSWFFEKINTINRPLAR LTKKSRERKLQITSLRKEMGDTT TDTTEIQKIIQGYEHLYAHKLE NLEEMNKFLFKYNAPSLSNQEE HTLNRPIRNSEIEVVVIKKLPTKK/ SPGQDGFRAESYQIFKEALV
15305	45673	B	15395	1	1077	
15306	45674	A	15396	69	290	YYFDSPIHPLHLSGTLRPGGSRQ FPCDPQFLCRLLHTLASL*SLPG DLLRGLLHKLVCRVERLDLASL YAVGR
15307	45675	A	15397	62	201	
15308	45676	A	15398	3	429	LPSSVPRQPKMQARCLSRSLRA VEIYESDLEEGQGLLHEFSQFVL DRPPPTQSRYAQELVHTCYLHT LASL*SLPGDLQRGLLHKLVCR AERLDLASHHAAVGRSELFFW TPYTHSPPGAGVGHPFWHTRL PWGVPAEGHQ
15309	45677	A	15399	303	612	PSSSIQVYHCSLRGICIPVGLKRA AANVGVSLEASPPLLSTPGGLG CLSCGGTRTVGSRVGSIIPW*G EGTTGITGSISCKGSSDVGSNRT SGVDFPRVE
15310	45678	A	15400	1	273	

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15311	45679	A	15401	1	406	MEEGWIRLPDGRVAAPQPLGA AVVLAVQETTHRQQESLEKLL GRYFYISPLSALAKTVQRQDFA DFGTTIKQDFRLLGQTQSVDRLL QLSQGQAVKGQNQLLPSLTSQ CQVYKCVWNWWVVLGTLDFKN EATDPPGVKLQTFLVSVTTHKGN SVDPNSEKQQDILLQRAKEQSFH SVEGDPSPRDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSR*RAI SCCPH*LPSAKCISVSGIGGFL VSLTSRMKPRTLLE
15312	45680	B	15402	1	930	
15313	45681	A	15403	391	617	LQLQPTG/CNFLYFVGYMKIL GFCFHIVEERGGCLWYPCFYC NLSLLGG*RSCSHTRIVPSLLMP KLGPGGQVC
15314	45682	A	15404	1	1860	
15315	45683	A	15405	1	531	
15316	45684	A	15406	2302	2691	
15317	45685	A	15407	520	2883	
15318	45686	A	15408	3690	4727	ENCHWGCEHPCDIGSSIILSPLA YWEQYHRVTYISRDTEGSIIVFP ALVTMLRNLFIILAGRSQSDPHFHT PMYFFLSNLSWADIGFTSATVP KMIVDMQSHSRVISYAGCLTQ MSFFFVLFACIEDMLLTLMAYDR FVAICRPLHYPVIVNPILLCVFFF LVSFFSLLSDQLHSWIVLQFTF FKNVEISNFVCDPSQLNLACCS DSVINSIFIYLDSSIMFGFLPISGIL LSYANNVPSILRISSSDRKSKA STCGSHLAVVCLFYGTGIGVYL TSAVSPPPRNGVMASVMYAV VTPMLNLFIYSLRNNDIQSALRR LLSRTVESHDLSSQDPLLHPFSC VGEKGQPH
15319	45687	B	15409	1	3195	
15320	45688	B	15410	1	1819	

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15321	45689	A	15411	399	1089	LLTPRTDQLEMPLDNAEIEWYT DGSYLRGEVFQWYDHALIFVP QTGIEDVIWHEALPNYIQLVKC RRNPYNQILSLQCAQHEIFLVS WKLVCKQLEGDDDMLVGTTA SNLLESEQSTSNLNEKINHLEY EDQYKDNNNFEGEGNDGQILEDK LISN/NMGGPDSPDSVPNE/P/M PTMTDQTTLVPNEEEAFALEPI DITVKETNAKRKRKLIVDSVKN LDSKTIRAQLNDY
15322	45690	A	15412	3	809	FKDDDMLVSTTTSNLLESEQS TSNLNEKINHLEYEDQYKVDNF GEGNDGGILDDKLISNNNDGGIF DDPPALSEAGVMLPEQPAHDD MDEDNNVSMGGPDSPDSVPDV EPMPTMTDQTTLVPNEEEAFA EPIDITVKETKAKKRKLIVDSV KELDSTKTRAHLSDYSDIGITLD LAPPTKKLMMWKEGGVQKLF SLPAQPLWNNRLLKLFRCLTP LVPQDLIKRRKGGEADNLDEF KEFEHPEVPREDQQQ*HQQRD VIDEPII
15323	45691	A	15413	1	595	MVNRSHFRCVGEPCHQQNSHG HLNSITETNSNPLTLRAAPLQPTR DPSDMAVFEIDELPEGAVKPPA NKYPIFFGTHETAFLGPKDLFP YKEYDKFGKSNKRKGFGNEGL WEIENNPGVFTGYQAIQQQS SSETEGEGGNTADASSEEEDR VEEDGKGKRNEKAGSKRKKS YTSKVTKKLLIVINVICISIKHF
15324	45692	A	15414	41	785	GKGWAGGASGPANHGPAGG RSPGMLRGDQGLPGRGAAGM ARPRSRREVYKAGDLVFAKMKG YPHWPARIDELPEASVKPTNK YPIFFFWHPMKPAFLGPQIDLFP Y*EYRGKFGKSNNRKGFGNEGL WEIENNPGS/RTFTGYQAIQQQ SSFRTEGEGGNTADASSEEEDR RVERDGKGKRNEKAGSKRK KSYTSKKSSKQS\RKSPGDEDID KDCKEEENKSSSEGGDAG\NDT RNTTSDLQKTSEGT

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15325	45693	A	15415	1	1272	MWSGAGPGLAVWPQLVTVLSL SLSRLNCKWGLSFLACLLGD MADAAMQHYGVNGYSLHAM NSLSAMYNLHQAAQQAQHA PDYRPSVHALTLAERLADJILEA RYGSQHRKQRRSRTAFTAQQL EALEKTFQKTHYPDVVMRERL AMCTNLPEARVQVWWFKNRRA KFRKKQRSLQKEQLQKQKEAE GSHGECKAEAPTPDTQLDTEQP PRLPGSDDPAELHLSLSEQSASE SAPEDQPDREEDPRAEGDPKA EKSPGADSKGLGCKRGSPKADS PGSLTTIPVAPGGGLGPSPHYSYS SSPI/SPLPSAGAIPPAHGGHQQ PGALLVRSRGSGPCCSGGCC CALPGRQHGPAGLTA/SASPTTS PCQQPLLP/SQGVVWGSPLLPAPP AGLAPASATLNSKTTSIENLRLR AKQHAASLGLDTLPN
15326	45694	A	15416	1	1152	
15327	45695	A	15417	8	82	
15328	45696	A	15418	1	1350	MGSEKDSESPRSTSLLHAAAPDP KCRSGGRRRLTLHVSASAR GRRARAKPQAEPAAAQPPPA PAPAAAQGPPPEALPAEAAA EAEAAAAAAEPGFDEEEAEG GGPGAAEVECPLCLVRLP PRLLSCPHRSCRDCLHYRLREI SESRVPISCPECSERLNPHDIRLL LADPPLMHKYEEFMLRRLAS DPDCRWCPA PDCGYAVIA YGC ASCPKLT CEREGCQTEFCYHCK QIWHPNQTCDMARQRAQTLR VRTKHTSGLSYQGQESGP PCPRCSAYIIKMNNDGSCNHMTC AVCGCEFCWL CMKEISDLHYL SPSGCTFWGKKPWSRKKKILW QLGTLIGAPVGISLIA GIAIPAM VIGI PVYVGRNIHSRYDGK ENSKH KHKRNLA ITGGVTL SVIASP VIA AVSVGIVGVP IIMLAYV YGVV I SLCRGGCGS
15329	45697	A	15419	2	540	

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15330	45698	A	15420	1	530	SRTTPGKAPKETWGQDAGSGK GGQGPPTRKPPRRTSSHLPSSPA AGDCPILATPESPPPLAEPPTDE AASVAADSDVQVP!GPAASPKP LGRLRPPRESKVTRRLPGARPD AGDGDHLSAVAERPKVSLHFD TETDG!YFSDGEMSDDSDVEAED GGVQRGPREA!AKE!VVRMGV LAS
15331	45699	A	15421	1	2989	MLLVMYWAPAPPVHMSQFLT TGPKCLESLDHGRDSQEITAS GLLWLQHAACGLAQWNQKPH PPFLTLLQAEFPERARSCDIYIR IKMLQTAQQHQVGLAPTERKE ALRGQSPPQKSASGQRPGLSDR ELLMLIKISKCLRVPGPSSVVLG TESTGPVPGELVLCQQDAGATQ EGVCYGRELMICRCDSFPRLME PWGVKGTPVFRTDLITAMKIP DSYQLSPDDYYILADPWRQE EKGVQVPAGAEAIPE
15332	45700	A	15422	218	404	
15333	45701	A	15423	1	422	
15334	45702	A	15424	160	470	LTMLFAACVFSGDEIMASEERQ PMEEEWRSSTISGEDGERWTP DTAGKAAQGIAGDVVWVSPLP PSKVSAASKPPKS!HHPFKWH NFSNLKMFKYMFYFSKN
15335	45703	A	15425	21	375	TFENTRFWDVQIPVPTGERRNE WALPPPAGSVPAGGWRSRPLTP GRCDSQGRGRSRRAAPLSRSPL PPLRRSPTLPGEPAAHRPLRVH PRHGPRPSHL!ACLNSQAPDASR LRASANQ
15336	45704	A	15426	155	340	

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15337	45705	A	15427	1	2658	MIINTIITTTTTTIIIFIITIMSSSPITITNIIITIQQHHHHNDQRPSLGKCRGLYIRVRKVPGERATANSRCPINAQGIESCWNGVMALWLGPNSTCSRPLPELTSEDQCPADSPGDEDPKPWWDPHHEAPLTYFHPYGAAFVPRHAGNFKDRREVPHQDTSFCASAGFWILPSACKTGRVALTLTLLIGAYQTLEADVKGLTAARAASPGAKWRTQFPCPAGTCSSQAGNGQLEDCLPYPPGPSAPVGSLSRSSANGEFIIIGRVIKAMNNSWIPECFRCDCLCQEVLADIGFVKNAGRHLRCRPNHNRKARGLGKYICQKCHAIIDEQPLIFKNDPYHPDHFNANCIGIKLGVFLTDRKDLTADAQELKGELYCLPCHDKMGVPICGACRPIEGRNVNAMGKQWHVIEHFVCAKEKPLGLHRHYERKGLAYCETHYNQLFGDVCFHCNRVIEGDEGDGFRAHRYSPYDSCVEVDQSPLEQQQLKSIRKGPLAQSQPLPTVMLHPGCKTQIREAPGSALESVRRRPRPLVPEEESAAVEAVRHIHLQNFNSRSLLETNGQKLGGHFCDVDTCIHEASLRAHRCGLAIGSPSFQDKLLLGPSEIRVPSVVPVQTVRQLVELLYSGSLVVAQSEAPQVLMMAASVLRIDSYRRMHADYRTRSSAPASTASAPPLTPVPPPLAPEQLRHLRLHLLAA
15338	45706	A	15428	708	892	
15339	45707	A	15429	2	713	
15340	45708	A	15430	212	1246	DLPLAVHGQVSDSGAQAVASRSGDESSIVCLKEESTVNNTFRCSLPLAVISVVSFTAKCQVKSEFIIIGRVIKAMNNSWHPECSAVTSARKFWQILHLSRMLVDRKDLTADAQELKGELYCLPCHDKMGVPICGACRPIEGRVVNAKGKQWHVEREQYMDPGILSALIDPKYLILSHRGLHMKSMDKGFYFAKLYYEAEKEYDLAKKYICTYINVQE RDPKAHRFLGLLYYELEENTEKA VECYRVSVELNPTQKDLVLUKIA ELLCKNDVTDGRAKYWVERAAKLFPGSPAIIYKLKN/DGWVRGQMVPKPDDDEVQVRGRSGRPDAGWRLNRRSSVGGSAWRLRPQ

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15341	45709	A	15431	129	444	WGGPGRQPDGGRVPGRCGP PATWESPAACRPRPQSRHSFE *GGSRSGSSHKRPCPSSPAVLA RDQVVLHTSFEATEGDSSHEDR STPLARRCLCSHRSGEA
15342	45710	A	15432	1	2446	METSLMVQVCGGRDCNALLPG NLCSQPTQVLPLEVDGDDGPG GLPLNAAPPSSVPPVPPSEALPP PACPSAPAPWRSIIISRLFGTSPA AEAHHPPGGALDFGALRTSSC LSQSHGHIPGGPGLGLGAVRVP VPSEEDPASLFTEPVPAAEAPAT VQSVEDFVANDRLDRSFLED TPARDEKKVGAKAAQCDSDTG RASRAPEQQIPHGGHWRGHSRS YERFRPPDMVSAGPGPSDGEAL GGNPIVAGFQDDVDLEDQPRGS PPPPAGPVPVSQDITLSEEAEAV ADPPKGPAAPAQOCSEPETKWS SIPASKPQRGTAPMTAAASPWP GGASVHTGLEKCSSTRPRAEIEP GKGEQASSSEDPEGPIAAQML SFVMDPDPFESEASDTQCRAVR RVLPAQRAENAYGSFQPGAL KPECRPTLKGGPGPVPSKAGKK TEATSPRPTGGASPLAHGATVG AAWGLGMASWPIGSSLAPTRA RTREPRQLRRVGSELPGDPCSG SGASCRQVCARGRATSVRIPAL ESLWPLSSDGSAAREGLEGPR LRQAAAPGGPGPPLPPLSRPPSP ARRMRGGAAVAGRGAAPLE GRVRLGVGFLAETAVRAGAGA LAAADAPPGSRTPRARPLVAAG SGAAGGRCPVPSRRQREAPSP GGAGVDLQLECLTSEKAGVGA ATGGVLEALARAIRQKKEIEI

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15343	45711	A	15433	26	963	FMIWAGQNRKVQDFVIQLRML TPVVPQQAPNAQQPRAAASA PQTRVRAPRWPGLNVVVLGTE DAAGPSRPASEPPASPALPGPAL ELGLPNHPKQT/HRPRLAPRRSH PKDSTIFKLNNSFLKNIKFNNSV GDQVNLDYKLISGTEYDILNFW NFRILAKTGCSDGHNRNPRSRP TQEEGSGPKKSLVKERSGAQE DLPVVPEEKLELSGTSMGPCCFS KTSYGPHIIYILSYKGITATAG HRWPAAYPAPLNCVPPPETTM PVSDLGSPLHWASRIA TPPSMW LCCLLAAALRVLAVNSSAEVY SQS
15344	45712	A	15434	803	1305	RSKPCRSSHNFSWWAHSRPC CPWSGYSSRLCCSCTILGPY QLKNRQQRNGSYKSFQNYLCV GNRLLFWVWJIFQGKGRS/WLP RSDWVTSYKVMVSNSDHTWW TVKNGSGDMIFEGNSEKEIPV NELPVPMVARYIRINPQSWFDN GSICMRMEILGCPPLPGWEH
15345	45713	A	15435	2	377	ARELLKAVWRPHKVAVMHCR GHQRASSTLVGLGNSRADSEAR KAPSAPFRASVTAPLLPQAPDL VPTYSKEENDFLQAKGGQVME EG*IRLPDGGRVAAVVLAHVETT HRGQELLEKLLGWWFYISH
15346	45714	A	15436	77	679	KMKTNQMGLKSKVVEMNATIS EIRLNINRKDVEYQQEILQLEAV WKLHKVAVMHCKGHQRASTL VGLGNSRTDSESPKAASAPLRA SVTAPLLPQAPDLVPTYSKEEK DFLQVEGGQVMEEGCIRLLDG RVAVPQLLGAAIVLAVHETTHL RS/ESSLGKLLGQLFSTISHFVSL CQNLTQRCVTCRQHNARQGPA VPPGMQ

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15347	45715	A	15437	2	881	HARCTGIAARAGLDDPRHTGEA LAARSRIDLARRPHWPRGCGTG GGGGCAGLGGAWLGRNDVA VPARALVTAAAPASSMSPPIPA AARPVSSSI!PAASPSPRCGLRAG PAELRCPRRLRQARAEEPPRAG PAPGRRRPTPGICPAPLSPLRRA GGTAPS!LPGVTRGSRVGRR!RP SLGGAGCRVGKRPRLLPPGRR CSTGLPPPAGTGAPAGVCWED GDPGHELAAALLRRLGGQIRAL AGHRTAGWAQHGLSPREA!VRP APAARTGTLRLRSNSRHLQNP ANFGTTLAT
15348	45716	A	15438	3	502	GRRDCLPGVVAPRACLHPRG QVPRLGSVGKMATPGMSWQQ HYYGGSAAKFAPSPATAQLAG HSMDYSQEMHLMKMSKKIAQLT KVIYALNTKNDHEHESAIQALKD AHEEEQIHLAETREKILQYKS KVTTELDLRRKIQVLESSLEDH KMKQQALTEFEAYKHR
15349	45717	A	15439	29	230	LQIDCKNKPAILRGPPTDPLKEA DCYCRTWERTPQILLPKWEGTR KPILVI*QNKAHQHAPQTLLHQ
15350	45718	A	15440	73	335	FFWGGIEEPCFVILSGSVFWFLL IWVGASASPVVGDVFGRRGGSPF PTSTVGAFTVLGWSVWLKRV CGSSWDC*FVLAINLELKFTM
15351	45719	A	15441	373	513	
15352	45720	A	15442	1585	1649	KNSNIQHSPKITLVHQWQFQTK KKFLIYLKKKNSSGGLVDPD*MVHT TRLCADNPQYQPRARKSHS*VK GESTTLREHPMGQKNLNNSLQP
15353	45721	B	15443	1	696	
15354	45722	B	15444	49	525	
15355	45723	A	15445	113	474	SIPYKNKEEEEGKGGEYYIKGT CHGTGKSEQQPSALDLPDRAY PNEKEPEN*LW*LI*QNKA*LHS PKNHTSSP/RNGSKPRKSSLNL KKNSGG*LLS*LGRHQRKVKPN ARKSKNQYKK
15356	45724	A	15446	47	614	TGCPCKQNSTCIAAVKMEGPL SVFGDRSTGETIRSQNDVTITN DGATILKLLEVEHPAAKVLCEL ADLDQKEVGDGTTSVIIAEL LKNADELVQKQKIHPTSVISGYR LACKEAVFYLTENLIVNTDELG RDCLINAATSMSSDIIGINGDF FAN/MVVDAVLAIHARHRGQ/P RYPVILLY*SHGES

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15357	45725	B	15447	707	1826	
15358	45726	A	15448	108	397	
15359	45727	A	15449	1726	2464	SKAVQLEAGGLQLFCKKMAPDPNITDVFGRITALHYAVYNEDTSMIEKLSSYGANIEECSDEYPPFLFLAVSQRKVKMVEFLKKKA NINAVDYLGRSRDVGKLA DIVILLLQH\NIDVFSRDSVYGKL AEDYASEAKNRVIFELIYAYER KKHEELSINSNPVSSQKOPALK ATSGKEQDSISNIA TEIKDGQKSG TVSSQKQPALDKTSKNDVSN TATEIKDEQKSGTVSSQKQPAL KDTSDKNDSVNTATEIKDEQK SGTSVFSETTGLEGYK
15360	45728	A	15450	2	675	
15361	45729	A	15451	1	467	DHSSSPAREQNWMENEFDELT EVGFRRWVITNSSELCKHVLTQ CKEAKNLEKRLGELLTRITSLE KNINDLMELKNARELHEAYTS INSWINQAEERLSEIEQDQNEIK REDKITEKMKNSTTVRAASM QSKLIIQGVAAEGLPLRLTRSASF
15362	45730	A	15452	2	632	
15363	45731	B	15453	355	894	
15364	45732	B	15454	99	716	
15365	45733	A	15455	1	1140	
15366	45734	A	15456	1	1476	MEVNREKQLNELEVIGSEEQNL EEEGLIMGGVAVRLVPDDIVIP GGVNATNGTEARDALRHKVA MSVTLLSGIIQYLLSALGWSYY TVDGVSQKNPRALGVTAQDQH AIFTTMSDEQASFRFGFVAIYLT EPLVRGFTTAAAVHVFVTSMLK YLFGVKT KRYSGIFSVVYSTVA VLQNVKNLNVCSLGVGLMVG LLGGKEFNERFKEKLPAPIPLE FFADHNSSPAREQKWMENEF EWTEVSFRWVITNSSELKEHI LTOCKEAKNLEKRLLEELLTRITS LEKNINDLMELKNTAQEFHEA YTSINS/RNQTEERVSEIEDQLN E\*CKDKIR\EKKRMKRNEQSLQ E\IWDCVVKRPNLRLTGVPEDG NGTKLENTLQDIIQENFHINLAR QANSQI\QRTPQRYSSRATP RHIIIRFTKVE MKEKMLRAARE KGRVTHKGNPRLIADLSADTL QARRQWEPIFNILKENFQTRISH
15367	45735	A	15457	1	1185	
15368	45736	A	15458	1	2367	

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15369	45737	A	15459	1	744	
15370	45738	B	15460	337	1515	
15371	45739	A	15461	1	1197	
15372	45740	A	15462	1	714	
15373	45741	A	15463	142	601	HQRTKVKFTKMRKNQPKPE NSK/TQNPSSPSKDIHNSLSPAREE NWMEMEFDKLTEVGRRWVIT NSSELKEHVLTQCKEAKNPKDK RLEKLLTRIISLEKNNIDLVELK NTA*ELLEAYTNINSQIDQVEEK I/S/SIEDQLNEIKLEIREKKKK
15374	45742	A	15464	153	474	QTKSNNVNIKKQDVHTKTPSEG HQHQRPK\DHNSLSPAREQNWIE NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNLEKRLQEL LTRITSLEKNNIDLMELKNTA
15375	45743	A	15465	1	2172	
15376	45744	A	15466	1	1640	MKLMETLNQCIAGHEMTKAI AIAQFNDDSPEARAKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRTRLRAEDVFPPVPI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVVDLHIIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGKL PTDPHMLRLAIETVVAHDYDV VIDSAPNLIGITINVVCAADVL VPTPAELFDYTSALQFEDMLRD LLKNVDLKGFPEDHLPAGNC YVVRNEDCIGFFSGFYNVISL GVYLVEQQKGWEDTHSKTPSK GHQHQRSKVDKSTKMRKNWS KNAENSKNQNALSPPNDRNNSP ARAQNWMENKFDKLTEVGFR RQVITNTSELKEHILTSQSKEAKN LDKRLQELLTRITSLEKNNIDL MELKNTARELREAFTSFCVNCE AVSLITSLREDSHWLEDSKGHR M/RRHQE*KCEYFHPPHPGLQF YQLPESDSHSDPLWPHGGSFLS
15377	45745	B	15467	50	1603	

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15378	45746	A	15468	528	1413	QTERNSTSTSKTPSEGHQHQRP KVDKSTKMGGRNQCKKA*NSK SQNACCPPKDHSSLPAREQTW MENEFDDELTEVGFRRWVITNSS KLKEIIVLTQCKEAKNLEKRLE ELLTRITNLEKNINDLMEKNT ARELREAYTSINSRIDIQAKERM SEIVDQLNERNDRENGTKLENT LQDITQDNFPYLARQVNQIQET QRMPQRVYSSRRTVPRHIIVRFA KVEMLKEKMLRAAREKDTSVK QKVNKDIQELNSALHQVNDLIAI YRTLHPKSTEYTFSSAPHITYS KTDHVHSILCDSG
15379	45747	A	15469	368	679	SSQLNKAPSLFNPVSEEFCLWL LLOQKELLTRITSLEKNNDLVL DLKNTA*ELHEAHTSINS*IDQV EERISECEDHLLTEIRHSEKMKTA LLK*DMQTRREKKK
15380	45748	A	15470	865	2055	QTERNSININKKDNYAKTPSKG HQQQRPKVVDKSTKMRKNQHK KA*KFPKPGMPSSPPK/DHNCSP AREQNWMEN\EFNEFDELTGA GFRRWVITNSSELKEHVVTQCK EAKNLEKRL\QELLTRITSLEKN INDLMELKQDITQENFMKHTQ VSIAQADQGRKERVSEIEDEPTL MDIKCEDKIREKK/IKKRNQESL QEIWGYVKRPNRLRISVPEPSDG ENGKX*ENILODIIQENF/PFPNL TRQANIQI\QETQRTLQRYPLRR ATPRHIIIRFTKVEMKEKMLRA AREKGRVTHKGKPIRLTENLSA ETL*ARRE**PILNLKERNFQPR ISYRAKLSFISK/GKREIKSFIDK QTLRDFVTRPALQELLKEAVN MERKNQYQPLQKHTKLKRPLT
15381	45749	A	15471	1	315	
15382	45750	A	15472	1	2775	
15383	45751	A	15473	1	1017	
15384	45752	B	15474	1	3105	

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15385	45753	A	15475	1	1115	MKWLLLLGLVALSECIMYKVLIRKKSLRRTLSEGLLKDFLK KHNLPARKYFPQWEAP!LVD EQPLENYLDMEYFTGIGTTPA QDFTVVFDTGSSNLWVPSVYCS SLACTNHNR!NPEDSSTYQSTS ETVSITYGTGSMGTGILGYDTVQ SGYHHGNHRLNLKGLCSSKRSS TIPPLYDGLGVASPPSGVSSC DDQSGSVVIFGGIYSSYYTGGL NWVPVTVEGYW!QITVDSITMN GEAIAACAEGQQAIVEPGTFFVT GP!TSP!A!NIQSDIEA!SEELDG!D SVLICSAISSL!PDIWFT!NGQY PVPPS!AYILQSEGSCISGFQG!M NLPTESEELWLGDVFH!PASTLT V!FDRANNQVGLAPVA
15386	45754	A	15476	1	765	
15387	45755	A	15477	470	479	PRNPSSFLQVQVQHRLFLQLEVP FHFFFLASLYVMVTLTTWFR* DPCVSGMALNCNSFLKIASSSGE YLRPTPSYLNQVVRVTMT
15388	45756	A	15478	1	896	CLPFGGPKNPWNKDDGGCQGR PQPRHLPGPGTAAQRRQQCPSE KSLL/CRWPPLTASTCSRLFYIL LHV GAS/CNLLPPAVKDSSKG VGQDTQVLSGSGAVYRVCAGT ATFHLLQAVLLVHLHSPTSPRA QLHNSFWLKLFLGLCAIAF CIPDEHLFPAWHYIGICCGFAI LLQLVLITIAFAHSWNKNCNEAS YLAEVFGPLWIVKVYVSYEFQKP SLCFCCPETVEADKGQRGAA RPADQETPPAPPVQVQHFLQL FCLPLRLLPWLTLCHGYPYQLV QASAGCGCKPAPYSL

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15389	45757	A	15479	1	1016	MERRPGAAATARGRARPGGP SVGLLATGSSLNPSFHGVARI PGRFIRIARPRDGSFAYESV PWQQS ATQPGAGSLSVVTTVWGVGNAT QSQVGLNPMGPAGSPSGSSMM PGVAGGSSALTPQCLGLQQQAF AEGGANKGYYVQQGVYRGGYP GAPGTTGYAGGPGGIQLGLPSH AARPSTDFTQAAAAAAVAAAA ATATATAT/GHRGCGSPGEAEPG AEP\DGAMGAGGQSFNSQFLQHG GPRGPSPVAGMNPTGIGGVGMG PSGLSPLAMNPTRAAGMTPLY AGQRLPQHGPQGPQQAQLPLRQ GVKRTYSEVYPGQQYLQGAYP VHSGLSQFPTWQETPRHP
15390	45758	C	15480	1	585	
15391	45759	B	15481	1	885	
15392	45760	A	15482	3	440	GPWPRPVAYLSKQLYRVSKGW PPGLRALAEMALLAQEADKLT LRQNPNI/GPHAVVTLMTKG HH*FTNARLTYVKIPT*PLKF/G NTLNPTTLLPVSESPVEHNCVD VLDSVYSSRPNLRDHP*TSVDC ERYVDRSSFTNCKVTR
15393	45761	A	15483	3	368	
15394	45762	C	15484	109	276	
15395	45763	A	15485	1	1710	
15396	45764	A	15486	221	784	QNSLRSMCQKEKKMAAGVLT HTCWPWPRPVAYLSKQLDRIS KGWPPLRALAATALLAQEAD KLT\GKT*P\PPHAVVTLMT KGHHWLTNARLTKYQSLLCEN PHITTEVCNTLNPTLLLUVSESL VEHNCVEVLDSVYSSRLNLD HP*TSVDW*LHVGDGSSFTNPCK VTLKKMTSAAPVTPRS
15397	45765	B	15487	509	661	

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15398	45766	A	15488	1370	2243	LGKLRLCESCGLVAAVRPHSGGL AMPLPNATRPASGRSED/AELK LALEHGHRSQESLQGRKHIGRVH DNSDIPQAALVGGTTMIIHGHLV PDKETSLVDAYEKCRGLADPK VCCDYALHVGITWWAPKVKA EMETLVREKGVNFSQMFMTYK DLYMLRDSELYQVLHACKDIG AIARVHAENGELVAAEKAEL DLGITGPEGIEISRPPEEAEATH RVITIANRTHCPIYLVNVSSISA GDVIAAAKMQGKVVLAETTTA HATLTGLHYYHQDWSHAAY VTVPPRLLGIPPH
15399	45767	A	15489	307	600	VSRRASSGSPVPLGLSILQHSPA/PSAAPKPRSPPARLSRPHL GESAAPSPLSPGPASLAAAAAA RVPQAQSPAPSTTPAPRTTLAPR VPHLAPAP
15400	45768	A	15490	3	222	
15401	45769	B	15491	1	1131	
15402	45770	A	15492	136	201	
15403	45771	A	15493	3	556	ELPRLRVCSKLRADPGRLTPD CARPGMSRYLLPLSALGTVAG AAVLKLDYVTGGACPSKATIPG KTVIVTGANTGIGKQTALELAR RGGINILACRDMEKCEAAKVID IRGETLNHHVNARHLDLASLKS IREFAAKIIIEEEERVDILINNAGV MRCPHWTTEDGFEMQFGVNHL GHFLTTWC
15404	45772	A	15494	11	559	
15405	45773	A	15495	1	312	MAPAADREGYWGPPTSTLDW CEEENYSVTWYIAEF/SWLMSGF/LPTPSSLRDLTASRWVRSLPPSR SPAGRQPGPAEELPKASPCPWG KSLSRPFASFASSGPS

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15406	45774	A	15496	2	1605	WQLPHPPAAPSARQILRACQLS SVTAVAQSCLYGKQLC/GLTTG NIAGAGLFFFGGGIGGTILYAK WASHFRVERVEKTIPIYSDKLFEV VLGSAPYNVPLPKKSTQSGPLK ISSVSEVTKEFKQPASQLQKQK GDTPASATAGDTVLVPGVQHE ESLKTIDHPAIDEGKPTPALEEEA SSSSIRERPCEEIAACLAQEEKQ EQVKTESLAKSFEDALRQTA TLQAIAAQNTVQAVNAHSNIL KAAMDNSEIEGKKSAKWH QGALK KEEVQAAQFESKLVSQYHE GQAQDDFKRQLDSITPEVLPGW KGMSVSDPADKLSTDDLNSLIA RAHRHIDQLNRELAEQKATEK QHITLALEKQTLEEKVQE YEFEQNLSEKLSEQUELQFH HLSQE QEQVH NFTLDINTAYARLRGIE HAVQSHAVAE EEARKAYQLW LSVEALKYS MKTSSA EMPAVPL GSAVEAI KANCSDNE FTKALAT AIPPE SLTHGVY SEETL RVRFYA VQKLARRV AMID

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15407	45775	A	15497	89	2490	PKCCFFCLLSGETAAASQCLCG KVVLRLPLRPCRRYRSTGSSGLT TGKIAAGAGLFLVGGGGTILY AKWDSHFRESVEKTIPYSDKLF EMVLGPAAYNVPPLPKSIQSQP L*ISSVSEVM KESNRPASQ LQK QK GDTPASATAPTEAAQISAA GDTLSVPAPAVQPEESELKTDHP EIGEGKPTPALSEEASSSSIRERP PEEVAARLAQQEKQEYVQKIESL AKSLEDALRQTASVTLQIAQ NAAVQAVNAHNSNLIKAAAMDNS EIAGEKKSAAQWRTVEGALKER RKAVIDEAADALLKAK*LLMDF NKEELEKMKSVIENAKKKEVA GAKPHITAEGKLHNMIIVDLD NVVKVQAAQSEAKVVSQYH ELVVAQARDDFKRELDTSITPEVL PGWKGMCSVSDLADKLSTDDLN SLIAHAHRRIDQLNRELAEQKA TEKQHITLAL EKQKLVEEKRAF DSAVAKAFRNIHRKLKYRA*TG QKR*KEVRDAME NEMRTQLR RQAAAHTDHLRDVLRVQEQUEL KSEFEQNLSEKLSEQELOFRRLS QEQQVDNFTLIDINTAYARLRRGIE QAQVQSHAVAEEEARKAHQLW LSVEALKYSMKTSSAETTS P GSAVEIA KANCSDNEFTQALT AAIPESLTGVVTVKRPLGAR FIYAVQKL ARRVAM DETRNSL YQYFLSYLQSLLLFPQQQLKPPP
15408	45776	A	15498	1	1212	MPKKRQALVEFEDVLGACNAV NYAADNQIYIAGHPAFVNYSTS QKISRPGDSDDSRSVNSVLLFTI LNPIYSITTPTRLNVFKNQDQT WDYTNPNLSGQGDPSGNPKNR QRQPILLGDHPAEYGGPHGGY HSHYHDEGYGPPPPhYEGRRM GPPVGEYGPPhADSPVIMVYGL DQSKMNCDRVNFVFCLYGNVE KVKISLKKQSPGGGRPMGEEWL DGYAVDRAITHLNNNFMFGQK LNV/CVGAQAREGSRGTGERK GGEWGPAAEHSEAEVLTHTEM GCGSVSKQPAIMPQGSYGLEDG SCSYKDFSESRNNRFSTPEQAA KNRJQHPSNVLHFFNAPLEVTE ENFFECDELGVKRPSSVKVFSG KSERSSSGLEWESKSDALET GFLNHYQMKNPS NLV

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15409	45777	A	15499	1	645	
15410	45778	A	15500	3	677	SPPNPRAPYLFPASLQNPANWS PHFOYLPLSQPRPSVLTAFRQQA QPRISMPCQATPFRPQMERLDQ NIRRSNQPHSLKPKLQSKALT LFNSVKAEKDEEAAEKEFEVTR VVHIRGLIDGVVEADIVEALQE FGLISVVMVMSKKRQALVEFE DVLEACNAVNNTADNQHIIAG HPAFVNYSSTSQKISRPGNSDDUR SVNSVLLFTILNPPIYSITTDVLYT
15411	45779	A	15501	2	1712	DEQRRRSGAMVKMAAAGGGG GGGRRYGGGGSEGGRAPKRLKT DNAGIDQHGGGGGGGGGGAGAA GGGGGGENYDDPHKTPASPVV HIRGLIDGVVEADLVEALQEFQ PISYVVVMPKKRQ\SLV*FEDVL GAGNAVNNAADNQIYIAGHPA FVNYSSTSQKISRPGSDDDSRSV NSVLLFTILNPPIYSITTDVLYT\  CNPCGGPVQIVIFRKNGVGQAMV EFDSVQSAQRAKASLNGADIYS GCCTLKIEYAKPTRLNVFKNNDQ DTWDYTNPUNLQSGQGDPGSNPN KRQRQPPLLGDHPAEYGGPHG GYHSHYHDEGYGPPPBPHEGR RMGPPVGGHRRGSPRYGPQYQG HPPPPPPPPEYGPADSPVLMV YGLDQSKMNQDRVFNFCLYG NVEVKVFMKSKPGAAAMEVEMA DGYAVDRAITHLNNNFMFGQK LNVCVSKQPAIMPGQSYGLED GSCSYKDFSESRNNNRFSTPEQA AKNRIQHPSNVLHFFNAPLEVT EENFFIECDELGVKRPPSSVKVFS GKSERSSSSGLLEWESKSDALET LGFLNHYQMKNPNGPYPYTLK
15412	45780	A	15502	1	528	NHQIRNDFITISPGVKADSRTPSI PQQPASSFDITEAAVSFAKDSLAA GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP\  TQALNFTFKDKYKQIFLDGVDK RSQFWRYFAGNLASGGATGAT SLCFVYPLDFAHTRVAADVKG AGAERELRGFGDCLVKIYKSDG IK
15413	45781	A	15503	1	1452	

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15414	45782	A	15504	2	991	RSAGVKAGSRPSPVLLQQSASSF NMTDAAVSFAKDFLAGGVAA AISKTAVAPIERVKLLVLQVQIH ASKQIAADKQYKGIIIGCVVRIP KEQGVLSFWRGNLAVNIRYFPT QALNFAFKDKYKQIFLGGVDK RTQFWRYFARNLASSGAAGA TSLCFVYPLDFARTLAAADVKG AGAERERFRGLGDCLVK1YKSDG IKGLYQQGFNVSVQGIIYRAAYF GIY\DTAKG\MLPDPK\INTHIVS \W\MAQTV\HCCPG\*LPYFDT RS\VRRNE\*MQSGRK\GT\DIMY TGT\DCWRKIA\REDEGGKAFKK GAWSNV\LRGMGGAF\VLVLYE *KSKKYT
15415	45783	A	15505	1	613	
15416	45784	A	15506	1	1695	
15417	45785	A	15507	131	723	LLEGKLTNRKDIHTKNPSVRH/ RSSKTKEVSAKEDENEMKRE EKFREKRVRKRN\QSLQEIWWDYL KRPNLR\IGVPESDGENGTKLE NTLQDIQENFPNLARQANIQIQ EIQRMPQRYSLLRATPRHIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRE WGP\IFN\ILKEKNFQPRISYPAKL
15418	45786	A	15508	1	3156	
15419	45787	A	15509	1	879	
15420	45788	A	15510	1	804	
15421	45789	B	15511	1	1230	
15422	45790	A	15512	2	827	
15423	45791	A	15513	1	1011	
15424	45792	A	15514	1	1722	
15425	45793	B	15515	1	780	
15426	45794	A	15516	1	2712	
15427	45795	B	15517	1	855	

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15428	45796	A	15518	3	1263	GRTIQTGKGEVIEFENFEKNEECI TRITNTEKCLKELMELKTKARE VREECRSLSRSQCDQLEERVSAM EDEMNEMKQEGKFREKRIKRN EQSLQEIJWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQRERQRTQRYSS RRATPRHIIVRFTK VEMKEKMG LLVPVWTNHSPLFRALFDYKG FCRGFTTHQTGFSPAGANQRGP LAATLSGGGEGQGSARVLTG IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQRTPQR YSSRATPRHIIVRFTK VEMKE KMLRAAREKGRTVLKGKPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSSFISEGEIK SFTDKQMLRDFVTTTPALKELL KEALNMERNNNRYQPLQNHAK
15429	45797	A	15519	1	1137	
15430	45798	A	15520	1	1578	
15431	45799	A	15521	1	1656	
15432	45800	A	15522	1	1120	
15433	45801	B	15523	1	1541	
15434	45802	B	15524	1	1632	
15435	45803	C	15525	53	352	
15436	45804	A	15526	1	973	MGKKQRKTGNNSKMQSAPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKGE VENFEKLNLEECITRITNTEKCLK ELMELKTKARELQRVSAMEDE MNEMKREGKFREKRIKRNEQS LQEIJWDYVKRPNLRLIGVPESD GENGTKLENTLQDIIQENFPNL ARQANIQIQRIPQRYSSRRA TPRHIIVRFTK VEMKEKMLRAA REKGRVTLKGKPIRLTVDLSAE TLQARREWGPIFNILKEKNFQP RISYPAKLSSFISEGEIKYFTDKQ MLRDFVTTTPALQELLKEALN MERNNNNRYQPLQNHAKM
15437	45805	A	15527	1	2896	
15438	45806	B	15528	50	658	
15439	45807	A	15529	1065	1260	RSHALALDSAGSSSPESP*RAS IPHTALGQNAGSWAGTAHSHH GPFLWSDPRHQPQVPHRTCCP
15440	45808	A	15530	96	219	EFSTKPRLSGP*SSWEMLILEPL APDTTIDLKLLYSDRDF

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15441	45809	A	15531	5459	6324	LLANVSQQLADISQLLANFTQL FSHFSQLLTYLSKLFTHLPLQLLT HFPKLLTHQPELFSNQSQLHPNI TRYSPSTSPTSPSYSPNVTPTSPN YSPTSPSTSPTSPSYSPS/RLDTKL PFQPTIHTTVSNLYPKLTLQLPQ FAQLQPNLTQV/PPTSPSYSPSSP EYPTPSPKYSPSTSPTSPSYSPK SPTSPSYSPPTPKYSPSTSPTSY PLQSTPQPLPSTHLLAPLTRLPL PSTRPPAPPTPRPPPQKAQPTLPLP LVTRPPAPPTVSQARLSSARMTV TRRTEGTWGAAG
15442	45810	A	15532	13	941	SVVLRPLLVVAAATATTPVAA AAATNTAKKTATVMVGEMVA GERGVLQMGHDITRFFYFSNIQT VINNWLLIEGHTIGIGDSIADSK TYQDIQNTIKKAKQDVIEFTEN QVPRILNDARDKTGSSAQKSL EYNNFKSMVVSGAKGSKINISQ GGGSQGGRGGPPISMWLALLC LVGLAGAQRGGGGPGGGGAPG GPGGLGLGSLGEERFPVVNTAYG RVRGVRELNNIELGPVVQFLG VPYATPPLGARRRFQPPPEAPSW PGVRNATTLPPACPQNLHGALP AIMLPVWFTDNLEAAATYGGC FRVPKA
15443	45811	A	15533	207	696	TNLQEKNKQPHQKVGRKYKQT LLKRRHLCSSQQAHEKMLIJTGH QRNANQNHNIEIPSHTS*NGDH* KVRKQQMLERMWRRNRAFTL WVGV*TSSTIVEDSMAIPQGSR TRNTI*LSHPITGYIPKGL*IMLL *RHMHITYAYCGSIHNSKDLEPT QRSINDRLD
15444	45812	A	15534	1	307	
15445	45813	A	15535	1	381	LPPPHDRLWCVMFPTLCPSVLI VQFPPMSENMRCLVFPCPNSSL RMMVSSFIHVPTKDMNSGIL*S RPADIELFSNLVNKKFLKGKF GDPLSLQRQLRNIVFSPMPCCFPS FLLPWVFSQLSVKPH
15446	45814	A	15536	134	278	DPAFLAPSPV/LMKQAPQATSG LMEPPGPSTPIVQRPRILLVIDD AHTD
15447	45815	B	15537	1	840	
15448	45816	C	15538	1	891	

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15449	45817	A	15539	1	3102	MYSHVITVCRHVKGNDILLNR QPTLHRPSIQAHRARILPEEKVL RLHYANCKAYNAIDFGDEMN AHFPQSELGRAEAYVLAQTDQ QYLVPKDQGQPLAGLIQDHMVS GASMTTRGCFFTREHYMELVY RGLTDKVGRVKLLSPSILKPFPPL WTGKQHINRTKDKNHIISIDA EKAFDKIQQPMLKTLNKLGD GTYLKIIRAIYDKPTASIIHLNGQK LEAFPLKTGRQGCPPLSPLLNFN VLEFLARAIQEK
15450	45818	A	15540	1	779	IPMKDHDAIKLFIGQIPRNLDEK DLKPLFEEFGKIVELTVLKDRAFT GMHKGCALTYCERESALKAQ SALHEQKTLPGMNRPIQVKP SESRGEDKKLFVGMLNKQSE DDVRRLLFEAFGNIEECTILRG ERQTAKGCAFVKYSSVHAEAG RPSTRLHGSQTMPGAFVPVW GQVSADTDKERTMRIRMQM GQMGMFNPMAIPFGAYGAYA QALMQQQAAALMASVAAGGYL NPMAFAAAQMQQMAALNM NGLAA
15451	45819	A	15541	1	1413	MEYYAAIKKDEFISFGVTWMK LETIILSKLSQMQKTKEHRIFSLIV LCDITDILKEFTVAEAGGFALNE IMKEICKSRSFAKVSLLHWKMW HSTASLGYHRVNVNTNPDPNLNC LGHCWGLRLDTGQKQACGGP GVCPCMFRACGGNAPCKEAP SVTEASSPDGSVLLCQSHVPITP APLSSAQMVCHMVEDRRRTVEL ILGATHNLFFSTSPLTWSLRAIP GNCVFLFLKDYVTEPVRSQSILHI AGPTFKQTPNLPFLKPEATKA HGPNVYQNDSTCPEPTAQVSH WSSVSTLIASPVPGPEDRKL GMLNKQSEDDVRRLLFEAFGN IEECTILRGPDGNSKARPLASSQ GAPSVKYSSHAEAQAAINALH GSQTMPLMQQQAAALMASVAQ GGYLNPMMAAFAAAQMOMQMAA LNPNGLAAAPMTPVQANGQP AAEELFANGIHPYPAQSPSTA PLQQAYAGVQQYAGR

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15452	45820	A	15542	254	883	DLRKDSPWEHRQCDKREPGNS APPAPHSWGFAVNPRA/PFGSAGA QLCKRADTRTPSPRA/PFGSAGA CRGCGRAGARSLASPKARTCIS SARRRAGGPLQLGAGSGOAKR PDR*TRREGANA*KTLHL/HSSL APSPGVLAGFQEPPGRPQVAC CAATAAGGIRAGERP/AAAAAA AAPWAQKLRLRLRQLRGPPGC R**MVSFPRLFGSTSR
15453	45821	A	15543	1	768	MCDFGKSTSPLPASPTSSSANGR DNSTYRLKEQGGFMHSVASRD SCAESARYTDAHYAKSGYGAY TPSSYGANLAASLLEKEKLGFK PVPTSSFLTRPRTYGPSSLLDYD RGRPLLRPDITGGGKRAESQTR GTERPLGSGLSGGSGFPYGVTN NCLSYLPINAVYDQGVTLTQKLD SQSDLARDFSSLRTSDSYRIDPR NLGRSPMLARTKEELCTLQGL YQTASCPEYLVDYLENYGRKG SASQVPSQAP/PSRVP

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15454	45822	A	15544	85	2249	SAEAMSGDGateQAAEYVPEK VKKAEEKKLEENPYDLDawsili REAQNPQDkarktyerlvqaQF PSSGRFWKLYIEAEIKAKNYDK GEKLFRQRLMVKLHIDLWKCY LSYVRETKG!KLPsyKGKMAQ AYDFALDKIGM!MSYQ!WV YINFLKGVEAVGSYAE[NQRITA VRRVYQRGCVNPMinIEQLWR DYNKVEEGIN!HLAKM!EDRS RDYMNARRVAKEYETVMKGL DRNAPSVPQNPQEAQVQDM WKKYI!QWEKSNPRLTEDQTLIT KRVMFAYEQCLLVLGHHPDIW YEAAQYLEQSSKLLAEKGDMN NAKLFSDEAAN!YERA!STLLK KNMLLYFAYADYEESRMKYEK VHSIYNRLLA!EID!DPTLVYI!QY MKFARRAEGIKSGRM!FKKARE DTRTRHHVYVTAALM!EYYCSK DKSVAFKIFELGLK!YGD!PEY VLA!YIDYL!SHLNEDNNTRVLFE RVLTSGL!PPFKSGEIWARFLAF ESNIGDLASILKVEKRRFTAFKE EYEGKETALLVDRYK!FMDLYP CSASELKALGYKDVSRAKLA!AI IPDPVVA!SPVVLKDEVDRKPE YPKPDTQ!QM!P!FQPRH!APPGL HPVPGGVFPVPPAAV!VLMKLLP PP!CFOGPFVQVDELM!E!FRC!K IP!NTVEEA!VR!ITGG!A!PELA!VEG NGPVESNAVLTKAVKRPNEDS
15455	45823	A	15545	12	427	SAEAMSGDGateQAAEYVPEK VKKAEEKKLEENPYDLDawsili IREAQV**YR!T!PSLWVQSHYL VLPVNNIFI!LTL*MLFIGFQF!N Q!P!DkarktyerlvqaQF!PSSGR FWKLYIEAEV!T!L!F!Y!F!L!Y!Q!C IHL
15456	45824	A	15546	150	469	SAEAMSGDGateQAAEYVPEK VKKAEEKKLEENPYDLDawsili REAQNPQDkarktyerlvqaQF PSSGRFWKLYIEAEV!T!L!F!Y!F!S Y!S!IA!FTV!ENKLGT
15457	45825	A	15547	I	834	
15458	45826	A	15548	443	732	SFMRWQKGQLPQLCLHRESHC SPY!PQPSFLGMEP!AD!HETTFN SIMKCDVD!H!KGLYANAVLSSG TTM!PG!A!NRMQKEITALAPS MMKIKIIAPA

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15459	45827	A	15549	1	1214	MEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPSIVGRPRHQGV MVGMGQKDSYVGDEAQSKRG ILTLKYPIEHGIVTNWDDMEKI WIHTFTYNELRVAPEEHPVLLTE APLNPKANREKMTQIMFETFNT PAMYVVAIQAVLSSLYASGRTTGI VMDSGDDGVTHTVPIYE\GYALP HAILRLDLAGRDLTDYLMKILT ERGYSFTTTAEREI\VRDIKEKLC YVALDFEQE\MATA\A\SSSLEK SYELPDSPRSSTNWQLSGFRLPL RHSFQPSFLG\ME\SCGHI\HETTF\ NSIMKC\CDV\DIRKDLY\ANTVLS GRTPPCTLGIADRMQKEITALA PSTMKJII\APPERKYSV\WIGGF HPWAWLSHLSSKM\WVQQARS MTESGPLHSSTANG\FLGGLLTL VAFTPFLWTKP
15460	45828	A	15550	1	2355	MKQITFAPRNHLLNTNTWTPD SQWLVFDMRTSGASFTGETIER VNIPTGYVEKPNKQCRHSVTRY GHGGHSDHTPSLT\ATVATQIT PRHSGHGSHCDRNL\SLATATA ATLTPH\HLLWPRWPLGSHSVT WCGHGGHSDHTPSPTTA\TAVT RITSRHP\LRPQQS\LSGHPVTHYS HGSHSDCIPVTRY\AHGGHSDHT PSLAMATAATQ\MALCHSLWPR QPLGYLVNKIRRKRC\TDGVSPS GKAPVFDT\GIPWFESR\YPSHLL RVSGSPPGYWGI\KRHQILNVS NMFGKF\KTNLLGYRQAVRHRI LIPAFRGSNPRT\PA\NLFKT\LLTIS NMRALENDFFNSP\PRKTVQFG GTVTEVLLKYKTAIEKRL\KLA VD\PHRDRAQMLK\VENVQQAW QQWINKLPPARREDEDV\K\IR WMIEELRV\SYFAQQLGKNSRA E\SM\LSWFHKA\IEAARTNIIQA QTRVEAAQATERRIA\ADIDSE LKAPR\DGRVQYRVA\KPG\EVLA AGGRV\LN\MV\DLSDVY\MTFFLP TEQAGT\LLKGGEAR\LLD\A\PD L\RI\PA\TISFV\ASVAQ\FTPKTVET S\DER\LLKLMF\RV\KARI\PP\ELLQQ HLEYVKT\GLPGVA\W\SLF\Y\SI\NQ TICLRLDSIEAKLQ\A\LEATC\KSL E\EKLDL\VTN\KQH\SP\I\QV\PMVA GSPLRT\TQMCN\KVR\CVNP\*AT VVPPPV\Q\PTT\QQY\Q\GLDAGA

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15461	45829	A	15551	1	956	MSSGRRDALARGLGNNSGDGAP HLGEHRQLEDVGGVTVTVWT GRLQAAAGCWRTRSVSSSTAAGR REPSTRDGAALSTEPPDPPERLG HRGSRALTALGHVTRGSSQ RGGRPEPWEHWLENGTRRTEL VDGVSYESWRRRPCRGQLESR LVLENHVATDEDEPALKQQLR EINCQDPSIKSFLYSINQTCILRL DSIEAKLQALEATCKSLEEKLD LVTNQKHSPIQVPMVAGSPLRT TQMCNKVR/CAMHWLCVSCIF TCLPGWRPAAPDQGPAAISLCS LPSSSGHREPLALGILPSALPPA HRQRIRGSATVPIPP
15462	45830	B	15552	161	925	
15463	45831	A	15553	31	856	GGFLHHASFVGRGRTLLMYFS LLGATPKPEPEPEQVKNYTEEL KVPPDEDCHCMEKLSAAGSYS DVTDSKAVGPLAVGCLTKCSH AFHLLCLLAMYCNGNKGPEHP NPGKPTARGFP\ASATFQITPA GPQELVPYTPQITAWDILEGKVT ATTFSLEQPRCVFDGLASTNDT VWLVVAFNASRGFQNPETLA DIPASPLLTGHDYMTLPVSPD QLPCDDPMAGSGGAPVLRVGH DHGCHQQPFCNAPLPGPGPYR WVVTGALGLGLCLG
15464	45832	A	15554	827	1371	GSSAGEASSLRLRSPSQPISRPL LPAGEKVLVWIEDQTSHNIPL SQQSKT/TLFNSMKAERGKEVT EEKLEARRGWFMRFKERSCFPN VKVQGEAANADIEAVACYPEY LAKITDEGGYTYEQQIFSVDETA LYWKKMPSRTFLARRKNCHSH PSFSSQHLVQSAAINIKAKSSTS KKIMTP
15465	45833	A	15555	799	906	FLNKLAFAFLRCGLALNSFLRKI QEPLSGISKSGSLs
15466	45834	A	15556	143	560	

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15467	45835	A	15557	1059	1940	QQMQQQEMRRSKWMAMLGK WETYQNS/TKGHLMKRVYKG PMNVRAEVWSVLLNQEIKAK NPRQYRVMKEKGKRSEHIHQI DLAVSQTLRNMFRDRYVTG QQELFVILLAYSKYNPVGVYCR DLSHIAALFLIYLPEEDETFWAL VQLLASERHSCRVGEQLPLGLH AARPGDGHPGQPRHLPVCASLL GAFRTSLLTVKPEPGTDPPEPKS DAFHPHQQKASHPPRGCPCLPG ATPSGSDSVQLALRNLRVLLPF SCSGSCPWPYPRKEALHPGGLE EQRLQPLMGLVTC
15468	45836	A	15558	123	448	ALAAAVYPSHSERTGEEAKKIC SVR*LLRSAQEEI/FLRGKNSRT GVL*KLLQRK*RYQRALGLAM LSEWTISPKGPVSTGITKPMFTA SRVTVPRTMTSALLDFIHGA
15469	45837	A	15559	1	6387	
15470	45838	A	15560	52	3218	
15471	45839	A	15561	3602	4015	GSVESPLGQKTPRTSSASPCWPS TNLYRMELELYGPHVTQVVK STRCAPRSAAPSILCEVRVPV TMWTCPLPATGRLSMWW*IWP RQWPVCVLTTSATQS*LTRCGGGT RAVSLAPQSHL*VCPAQSSWTS IILWT
15472	45840	A	15562	932	1316	RVQDIPAKRGIPQFRPKIKGIGQ SYKQHYPARPWNVLAQKVVF FEDQDALLPCLLTDVPLVEAGVS LVRVRGRPLMRHTNYSFSPWH GFTIHRAKFIQSQDYQCSALMG GRKVMSISIRLKVQKAVNRA
15473	45841	A	15563	1	263	
15474	45842	A	15564	66	185	
15475	45843	A	15565	1	4217	MRLAERAALAAENADGEPGA DRRLRLGTYVAMSLRPAAGA WERCAGSAEAEQLLQAFGLRD AAEGRPRLVVRPGPRLGAIKP GLEVGPEGLAGAKALFRLTG PEPPGPDSFRGAVVCGDLPAP LEHLAALFSEVVLPVLANEKNR LNWPHMICEDVRRHAAHSLQCD LSVILEQVKGKTLPLPAGSEK MEFADSKSETVLDSDIKSVIYAI ESAVIKWSYQVQVVLKRESSQP LLQGENPTPKVELEF

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15476	45844	A	15566	26	494	RPGCGEWLGNAELWGQECQL HYSPPVSPWENSSGPRFSISKTG SLIPPLLNNDICQNQKPOQILSHPA RCLGLLDHFPQQWERRQAQNR AETG*GQRSAQGQTFRQRPLSV SGNCRVPPRATVSRK/PRPAPAY ALSLKSPRRRPPRTGPAPPGLVP
15477	45845	A	15567	1	1242	
15478	45846	A	15568	114	1219	VDLPPGAPVRQSGSHGSVLRDH KTEGEARVLPLHQRVGKGAGR GATPGPHVHEDPVTCICGHSFC R/P/C/ICLSWEEAQSPANCRACR EPSQKKDFKTNILLKLNLTiar KASLWQFLSSEKQICGTHRQTK KMFCDMDKSLLCLLCNSQEH GAHKHYPIEFAAEEHREKLLKQ MRILWKKIQENQRDLYEERRT AFLWRKRRTLRLKGMTSGAOGT SQKVALGLLQQPLCHTVRAQS NSARVHKQRGGDAVSSGAGIP DPKAQRFPATLRSQAFICTAGR RWGSGETVLHPLQRAVGVRGAV AELHRQLLSSSAAGFEECEGL CTSGPHITQGPDHQELYLHSHEG  VWTLFTCTGDRWKVLSGVPCP

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15479	45847	A	15569	1	2694	MRMAATAWAGLQGPPPLTCP AVRTGLYCRDQAHERAATDV LLAPFCOPKTRSHGTCPPTERDP RGEGSTEYGRVWDGIQGWGTR ALTGWTDRRLLCQACQTLPPR HWFLPGARGWLGGSPCAHGQE SLPSQSPILLRVEVKSRLMRR RAQEEDSTVLDVSPPEAKRG SYGSTAHASEPGGQQAACRA GSPAKPRIADFVLVWEEDLKD RQQDSAARDRTDMHRTWREDF LDNLRAAGLCVDQQDVQDGN TTVHYALLSASAWVLCYYAED LRLKLPPLQ/DYPTRPTGRPAC/ CAWLGIPNVNLLEVPDVPPVEYY SCRFRVNKLPRFLGSNDNQDFFF TSTKRHQILFEILAKTPYGHHEKK NLLGIHQLLAEGVLSAFLPLHD GPFTTPEPGPQAPRLNQRQVLF QHWARWGKWNKYQLLDHVR RYFGEKVALYFAWLGFYTGWL LPAAVVGTLVFLVGCFLVFSDI PTQELCGSKDSFEMCPLCLDCP FWLSSACALAQVREAGRLF DHGGTVFFSLFMALWAVLLE YWKRKSATLAYRWDCSDYED TEERPRPQFAASAPMTAPNPTIG EDEPYFPERSRARRMLAGSVI VVMVAVVVMCLVSIILYRAIM AIVVSRSGNTLLAAWASRIASL TGSVNVLFILSIKIVYVSLAHV LTRWEMHRTQTKFEDATLKV
15480	45848	A	15570	1	924	MISQFIPENYFSQKSSATSGWA RAQRDFRVGAGSARPALLSGRL APPALGSERLSTRASSCGGLPR ATPRGRAPPPATRHPVPSSTAQR LRSAAARQRLAGSSAGRDA GKASWAPESVLEVLARAVRQE KEIKGILLGKEEVKLSLFLAGDM VYLENPISQAQNLLKLMSNFSK VSGYKISVQKSHAFVYTNNRQS ESQIMSELPTVATKRIKYLGIQ LTRDVKDLFKENYKPLLNEIQE DTNKWKNIPCSIVGRINIVK AILPKVIVYRFNAPIKLPMTFFTE LEKTKAFIWNQKRAHIAKTIL
15481	45849	A	15571	1	825	
15482	45850	A	15572	1	1488	

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15483	45851	A	15573	1	1476	MPIKVDWIKKSRTHTPRDTMSP KRGINISIQEYRNTPDAISLSEL LERDTNTQVYTYEQEHTKNN GHQAIQKQNKGHIRRESDRGEY YPLDCRPTGSLTDKGWGMLLC GMMTAGKPTPILTFLLDVGLPG GTAINKSSVIRVRNREGNVEK WGERQVDQRDAVMRVRCGIR NNVEAGLKYGPGTMKVSLSVF YTTQQCRRYLSVLCAGFLARAS VPFNEDFQMSLDEKLFSNLHPL GSSSSPPKSLLHCPLLEHQFTML GFSDLGAQLASPMSGHTRAAGV AACQPAPITLTWLSLPRVARGL TLEQGVVLVGEARAAQEPMEW VGGSCMVGCRSRALPRGKA AWREIQRSAGAGGAPVSPWSG GAPSRACPPSASSVRFLCAARR LACNTYSPVLYCVRNNWWILGL TDFNNEATDPRDPFLANVPGQL AAVAIGTCDGNVYSAQRD YRFALESILKACTLALALEEVGPPA VQDKIGADP\TGLPF
15484	45852	A	15574	140	448	GFLGACAGCREFKMAPP*SSLG *KLSVSPCPGILLISAEPEAVFSI V*NARVRGFILEVSETKNPPID TISTKHASLMSDSYREKKLVPV VYPHSSTPSFQ
15485	45853	A	15575	1	1001	MEAPOGALEQDGPAVLSQQRH RKKPFTATPDPYSYHRSHAISLS VIIGYCVPPSHAAEMAAYGWT MGKSKLMAGQWITQSQVFCDS STDGPRQHKAQTAITLTKLQSQQ RSTNSTVSHRQOWVNCRLLR VKCQRLRAHKELLPVQRWLWR QGRCPVTTSLVAVSETAGAGA AALALSRCLCRLQVSASARPF SRTLSPOPCKWAMAASHQPIKG ILKNKTSRTSSMVALSEQPCRT VHEELSKKKCQKWDEMNLISTY HPADKDYGGLMKIDEPSPPYHG LTGDDENACSDTETTEMVSDI LAKKLAAGLEPKYWVQE SSGEEDLAAEE
15486	45854	A	15576	1	1851	
15487	45855	A	15577	73	418	GKPDGDKVSQHLLWKG/YSF/ PPSLMKSLAGYEILS*KFFSLR TLNIGPPLSSGFRVSAERTVSL MDFPLCITQCFSAPAALNIFSFIST LVNLTIMCLGVALLEQYLCCVL
15488	45856	A	15578	2	460	

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15489	45857	A	15579	1	2031	MATEVFLIPYALLQCSLASYSPSKPGIYVPSMQMVGVSVTCSDQKNTIEVLVPKAYTLARQQYKSLSEQVY SCHQGTLNTRAQESAASLLKPARPRTRQKKEPTPNTSEHQKEQTLDTPPLRTVTLITRVRGFILEVSETKNPPISDTMGLDISKQEVLGRESDEQGEQSQGLSEMQTALAMLLTREPISAKQAPHEPPRRQEDNTQAREGETRSRKTRAEGQKGHAHENAENERNAKERESERKRQEAEEDENGKEKQERNEGHARHMKRRKRDEKKRQGQNKPGNKRPEGNEEAQRRRKKNREQRQFSFYQSGPSAAGLLVFAGGLPQLSFLAWVSPLEAAEQQRFLSVPSSGPLRKFCLYFGFVGNAATPLRGLNTHGRLLTPAHTGRRRHTRPLNSPVPEKAGSTTESNGSPYQGQNPGPLPKGNRAQGEKWMGRRIQGTTRPRAREANHKKMTQIMFETFNTPAVYMAIQAMLSLYTGCCTGIVMDSSDGVTHITVPYIYEGYALPRAILC LDVAGRDLTNYLMKILTEHSYSFTTMAEREIVCDIKEKLYYVTLDFEQEMATAASSSLEKS YELSDGQVITIGNELSCCPEALFQPSFLSMESCDIHKTIFNSIMKCDMDIRKDLYTNTVLFGNMYPGIANRVQKIVT VWMGSSILALLSTFQOMWVSK
15490	45858	A	15580	485	886	VPVFHFTCSHSSASQLPFLQMMKIAKTCSDLGLNRLPEAKLKAPPTRVTSI WPRQRGRPRR\CGGRNRSGLVSAARGVGGRSQAAAARRDAPSPATSRMPPRQGSVSWGCARNAPGRRADPEVRRQPGPSCT
15491	45859	A	15581	1	435	
15492	45860	A	15582	2	339	HRCSTGAFSTAASNSNADRPPPARRRGLPR/RGPP/SRRRSPRPPRREPWPRTTRPRTAKARRATLEGRCRRACGHWQPRAAAAAA AAAAAAVAAAAAAAAGASATW

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15493	45861	A	15583	1067	2093	RRNTSSKRSRNCRCPSPRHR RPSLRPRSRQQPKCKCRPRSRSS RAPSSRRSRPQGLVPC*RAPPW PTSRWPSPGPFLNNCSRKGRC RPRHPSQPRCPCRSLRWCPSRQ LWSPHRESPPCP*TSRGSAWRS VSHRRQQDRPWWTQPVHMQQ LLKLKQQAVQQQKAIQPOAAQ GPAAVQQKITAQQITPPGAQQK VAYAAQRALKNPVSYTHLPG PETGRGPASADPDPGCKTSSCS TANTRGQHPASCLCFPAGFSTD CGAHAGDGGRAAGADDCPSDR DCPGGSAETHSAAGGDHGVP APDSRRSQPSPGARQLRQPKPA AQVTDEGPCCQAKDTY
15494	45862	A	15584	10	607	RALCGESRLPLARKL\$*AKKSV QRSTLQSRRRIWVWCWFHAN\$L F*KQGRT*ESPL*L*LI\$PAS*RPS TSESPPL*KANFQOPHRGL*EKV AEGRGP**EVYTSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SNSSSSNSRHRRRRRRLSFLSR RRRHRSRCCLSRSRPRRPRRHP ARLWLRSCRTDQRKNFQLPRK TV
15495	45863	A	15585	217	1012	AKNDSKRQNFGHGRGQPTFGAD KAKGERVRTSSTIRRTSYLDIT GPyLTGQWPRDPHG\$HYPSCMK DKATQT\$PSCWAEEGAEKRSHQ RSAWSGSADQLKEETPTDLQQ NAQQKLYKPEEVGCLISDFLKE KENCQPRILYAGKLSSECTPDE EAVNIVEMITKDLEYINLVDK EWQGLRGLTPILKEVLRVKCY QTASHATKSGMKGVSVQFGK LHCYFKKLPLPLPSATAILSQ LTSTRQELHHKKDCNLLKTQMI
15496	45864	A	15586	2	387	
15497	45865	A	15587	1	165	LFMFCCLLYIR*QLLHPGYNAPF QNTAA\$TRGRGIAQTAPEAAFQI FLHQ\$VRFHC
15498	45866	A	15588	172	359	PDGGDIESINYLGQYGHFHIDDS SYP*AWNVLPLFVCLFYFIEQWF IVLLEEVFHIPCKLDS
15499	45867	B	15589	1	2850	
15500	45868	C	15590	1	2835	
15501	45869	C	15591	78	491	

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15502	45870	A	15592	1	5721	MAVLSLPLAAPPTLMPAAHFNLV EMQVKATLKEYWQRKSPGP GANRKKKINGSSPDTATSGGYH SPGDSATGIYGEGHASSATLED LELRQPTPSTSPNDCSLYPSPQS SSNSSLHAPHSQYRELAVALH SSSAIISQLSENIISLNENKNSAL QLERQVKELKLGELETVTS SNNGWEAVTSLWEGFRLPARG AEEPRGSESTAAARPVPVSPA VRGRLVAGEPGSYQPAETAAK AQLSLMALPGEGY
15503	45871	C	15593	178	1287	
15504	45872	B	15594	52	855	
15505	45873	C	15595	1	1698	
15506	45874	A	15596	302	617	NLAVNPSGPGFLIGKLLIASIS EHVIGLFRDSTSSWFSLGRVYV SRNLSVSSRFSLVFDGDVQMG FWCGCPLCLLVFLLTAGPSAA GLLEFAGGPLQLTFLA
15507	45875	A	15597	1	2762	MYGTGYRDVAGKWAIDPDSK REFLDVTQEGIQGGCDSGTCRQ TLSILTQPLRQWGLEGIKKPNS WIISEESVSNGGPPLIIPRQTAS GVDLQQTPTDLQLRVLTVRRK TNKQKGIASTTKRTSTPKPHL YVTIKDQSYIKPQRWGKNAIE KLKIKLKVVALSLQRNAAPHQQ WNKAGRMSLMSQQKASEVI ESQMNEIKGEEKFREKRVKRNE QSLQEWDYVKRPLDLRIGVPD SDGENGTRLENTLQDI
15508	45876	B	15598	1	1989	
15509	45877	B	15599	1	762	
15510	45878	A	15600	686	850	GQPERKVGLPTKGSPSD*QRJSR QKLYKPKESGGQYSTFLKKRIF NPEFHIQPN
15511	45879	A	15601	2	382	
15512	45880	A	15602	1	993	
15513	45881	A	15603	3	460	SPCWGQLLQATQP/ATAFAKD LLVGAVLFGHNGSLSSRNTLAF SMDVGPSPQWMWGLLNCGGAS AHRQCTRCTLQVTLALEGPLAP LKLAWHKKIYJFLGEAAEIRR QLEARELFHSSRAEQGRFLFVGR PGQAAHMLPPGDCVSINTQH MIT
15514	45882	A	15604	1	130	
15515	45883	B	15605	1	561	

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15516	45884	A	15606	94	420	EKAVGRWIFQSCKYRSPCEKPY SKGLQVQRTVPEGPSKAARAA QAPGPNLLPCLPT/PQTPFEISEP LANMYSCGNQNTLMEELAEQA QQHDEMLHMHHALKEALSIIS
15517	45885	B	15607	46	747	
15518	45886	A	15608	186	364	AFAPAPCTLVPGVLRGPPILLRE TGLAH*CPAVISPCKSLPWLPTA YSVESQQVILFGL
15519	45887	A	15609	155	511	GAAVAGTQNLCCLGGGAVGG S*RGALNCEGGLIHPGYNAPFQN TAATRDRGIAQTAPEAAFQLFL HQRVRFH*FLLWREGRGR*AR REPLSLRQPFPAGPLGGALPAPL PDASTLVGVG
15520	45888	A	15610	1352	1684	MSIRSAWCRAEFNSWISLLTFC LVLDLSLVFDDGDIQMGFWCGC PFCLLVFLLTAGPSAAGLLEFA GGPLQTLFAWASAVVAAEQI LVSSKCCCLIVPLEVLSQRSTWP
15521	45889	A	15611	98	367	
15522	45890	A	15612	426	738	VCVWGDPPGPAGGHGEAAATL WKEKVVLKERVKEKLELQFIHLS GQTDTIGRKYIISQGAVSETQHW ERRTSSGWP/GPGGDEGEPAGA AGQVQLVGDHKEGHGF
15523	45891	B	15613	86	1411	
15524	45892	A	15614	950	1493	GTVFVLWRRRGTLJFRVSGFSAL FFPPSLWFYLPFWFDDGDLQME FWYELSFLLMLLLFCACWCSF *QSGPSAAGLLEFAGGQLQTLF AWVSAAVAEEQWILVNRKCC LIVPLEVLSQRSTRPCEVSHPY VHCLCLGIEELNLYCSLHISLGLFE AILLGKAEEELGCCDPSLFATV
15525	45893	A	15615	1	5731	MDSHRPTAWPAAVLAGRSPVA AESERYCSRQPPPLPRQALLSV LVLASDTRLPPFWSSQTFCGILS KPLVLSGPLQTQGETNNENGLV GGGEVGMQPLVLFERSLFPGRC CVLERRIVPWMRQESYSSSSPI WFVDSDELNLTSVLECLEDDK NNNNLHQQQLKWLICLRLYN LPKHLVDAMPDQLPMLPMGQSGP SAAGLLEFTGGPLQTLFAWVSA ALAAEKQILVNCKCCCLIVPLE VLSQRSTWQYELKEYW
15526	45894	A	15616	2	521	

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15527	45895	A	15617	1	1261	MSEHNITEECQQENQSIEQWRSIAHSDSIEVSWLHEVIKTYLAKASTKLDLMKKLKELESSQPSRKPKPFIPSQEGTGDNDVIVYSTERLSKLLNQKKGSTRLYDKPLPSNLLNQKKVSTRTEGLTVDSRADMRNVTTILLSTESSSTDSSSMDSSSMDSSSMDSSSISIGRVETATCAMIPVQKSKRSGPPQGPSAATGDGAEGRFLPRCSRWPWADRLAWSQPRRHLAPGPSAATGDGAEGRFPPLCSCCGTDRLAWPQPGHALLPRCGECGRARELPGDCCLAEGGCVSLEVLARAIRQKKEIEEIQIGKQEVKLSLVADDIIFCLENATDSSRNLELIKEFSKVSRVYKINGHKSAVALPYINSYQAENHIIKNSPTFTIAATNNNNKK\KNLGIYLAKESKDSYNENYKTATERNHRWSQAR
15528	45896	B	15618	60	499	
15529	45897	A	15619	134	1416	RTSICWTMDSSVQNTVLGPTRSVKGVMEWLQYLQMERR/CTL SISMESMPRVAEDAGDVGAELPLHLEPPAGPLEVEQQQLQAEIKHLRKTLESLAGQLQAOVEANE GSSHLLNRQQDERLREWKAELWEEQGETGRSSVQKDRTTISHALSQNHQLEEQQLAKERLEATSQQNQQLQSQMSLMLAPGEGDELGSKEEEEAQPMPMSILEDLKSREA MVAFLNSALVSAEEEQQAQLH GQLKEQRVCCQHLAHPVALAQKEPEAAAPTPTGGDSAVWTV DLQVEKTKFIMFTIKPGEVNNKDMAQSIYRSGKNLKDMDYGH DLEARRKTNRPLETTFYFLSYE LDYSRCFIGCLKCLCLPSPSATIGSFALKPSQKQPKVCLLYSLQNH EPIKPLFFINYPDSDSYRHTQVIRILLSGSIHVQVPATKTPL

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15530	45898	A	15620	1	1665	MGGHVGGRHRMLTPKLIPE AAGSMKINPEEPNRPINGAPG GPALPLAAGDSGSEQAGEPALA ASELQGWDSTLGSPGSLRGTTI VATRSRGSRGFLSPASLGRRSR DRKTKELAFAAGSGLATRGQRA SSDAAGPPLSRCSPARTPQLPV RGSLTGPRAPAPPRARVCLLSC SCRQFPPLTGGI NVGRPSGPS WKICPRSLPSAETGIRRRRAA AHPPPLQQPLLCGESLPSVQCSA NADSSIPVPSRWSQDACRNTGA AGPPGYPACVNNRNRTDKNSQ LDETHHMKTVTDRQGFGAFT MLURVVDTGHSTCSGSVEWDP RLYGDQADLSRSRSGHLDRPGAH HDYYTAIKCEEGKSLLDTTVK VKAGVNGFGRIEHLVTKPAFNS GKVDIVTINDPFVDLNNMVYM FQYDSTHGFCTVKAENRKL VASGNPITVQ/ERDPISKW\YI AESTCIFTTMEKAGADLQGGA KRVIIAPSADAPMFVMDVNH KYDNSLKIVSNASCITNCLAPL ANVIIHNGIVEGPMTTVHAI TQKIVDGPSPGKLA
15531	45899	A	15621	2	1105	GRVGCVTSRIFSCVASRATSLR TPMGKVKGVGNGFGRIGRGLVT RAAFNSGKVDIVAINDPFIIDL YMVYMFQYDSTHGKFHGTVK AENGKLVINGNPITIIFQER\YPS KIKWDAGAEYFVESTGVFTT MEKAGAHL\QGGAKRVIIAPS ADAPMFVGMVNHKEYDNSLK ISIVASCTTNCLT\PLAKVIHDNF GIVEGLMTTVHAIATQKT\LD GPSGKLWRDGRGAF\QN\IPAS TGAAKAVGKV\*AERGKLTG\ MAFRVPTANVSI\VVDL\TCRLEK PAKYDDIKKIVVKQGVGGPPQG AIGYTEH\QV\VS\SSDCNSGPV FPPFDAG\VGAGLNDHFVKL\JSW YDNEFGYSNRV\VVDL\MAHMAS
15532	45900	A	15622	121	221	
15533	45901	A	15623	189	538	

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15534	45902	A	15624	3	1015	DRAGPPGAPRLGQLLCAIIL GLAAKKKEINITIIKQLKKFLN KKPSYGLERQMETTQNQLVDSY MAIVNKTVWDLMVGVMPKTI MHVMINNTKEFIFSELLSNLYS RGDQKTLMEESAQAWRDE MLRMYHVLKEALGIQDINTTTI STWPWGPVDNSWLQVQSVLARR R/SPGLAPTAPELPTPHRI.SLGA LGTGSVPPLLHHPGSSSSVSSLG LVA/DCFGLPKARGGPQRLPF PSLPGRLFCDLAAPPAPKAAP FICDFVYCCDQASEPVGCGQQT APHLRHGSPLGIPQAPPQGSIQA WLRAAVFWKGALCPRCGRHIQ EFLLHRCTLVSL
15535	45903	A	15625	547	1242	PKALIKTSNKSSLSYQLTTHSGT MACPWIRHEVLLSRLGFLVLEN TNMDKRPKSLLRWLERQMETT QNLVDSSYMAIVNKTVWDLMV GVMPKTMHVMINNTKEFISE LLSNLYSRGDQKTLMEESAQ AQWRDEMLRMYHVLKEALGII GNINTTISTPWPVDNSCLQV QSVLAGCSFIILVQAVFLLYQA WWLLFWAPQGERWPWTSGLE DTVTREEGSPKGLSISL
15536	45904	A	15626	108	308	AQKHLT*LSFLPRH*ILT*NLT KIPTSKIKKTPRSRSPRSTSCL DNLAPSCGCSKGSSWRIC
15537	45905	A	15627	687	1910	KDHQLRKKLRRRGKQGAFTAA LPPGSPRPPRLRGGRGSGVGLGV RGQRTPQAPQAVTPSEGPPEPLW GPVLGGGEHRRGTGASAAG ASMRRLGAAGGGAGAGPQRG VGARVVVSEEEANSPGAIAITSNR ETQDANEGLSAPRPECLLHPTC RLYVPLIVRDWVCHTRSVVLL QVVNVGTIAVGTGLASAYDTL MSQSGFGVKNLKRGIIILQRGVL ILMLCCFPCWADLVTTERILIL LKQDPKSPGWTRECFQEWGSYI HLVIPSMMFVCTEQWTFEIGNF LAGLIDIVMELGTQGIICELASV AYMNYFRLNPQPPISDFTINLAF LTTERKILGYIQLRKGPDIVGP YGLLQPFTDAVK\FTKEPLWPS TSTITLYIIAPTLALSIVVLLALPT RMLAAATPRPRGT
15538	45906	A	15628	1	1173	
15539	45907	A	15629	3	1447	

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15540	45908	A	15630	1	215	MDPKQEEIPDSPEKEFRRYRIA WIRIHQPIICCLQETHLTHKDSH KLKV/KGWNKAHFANGHQKSA ARETK
15541	45909	A	15631	1	1524	
15542	45910	A	15632	1	575	MALSERSQPQDHVSHDRIYVK HPEYANLYRQKVDTYTLPRVSIS IHVGQAGVQIGNARWELYCLE LAIQPDGQMPMSDKTIGGGDDSF NMFFSEIIGAGKHVPRAVFVDE PTVVDRCLGHWMAAFLGE\EV HTGTYRQLFHP\QQLISGKEDAA NNYSRGHHTIGK/EDLVLDRIH KLLTSQCRKPKATMWLSQAT
15543	45911	A	15633	208	465	
15544	45912	A	15634	107	827	EARRPCTLHLRSALHPATMCEL YSKRDTLGLRKHHIGPSCKVFF ASDPIKIVRAQRQYMFDENEQ YLDCCINNAVHGHCPIEVVKA ALKQMEELLNTNSRFLHDNIVEY AKRLSATLPGETLCLLFYKFRG YWPSSTNPSSRPAAPASPPAAE RAGDFRAGRKPSVPGSRSVSGS PRGPCSRSLSLSTFCTRYCPLSAL TSGPGCPYPMCFFLPSRVSRLLY SSHMVAGCRALRRCKNSH
15545	45913	A	15635	3	1218	GGLWEKMAAAA/QSRRVVRYLS MSRSAITA\ATSVCHGPPCRQL HHALMPHGKGGRSSPHSGIVAT VFGATGFLG\RYVVVNHILGTAW GSQVIIIP\YRV\IKY\QSMHILSFP WG*PGGQLSVFLGNWGTARD* RFLFRVSYNTGNVGSSILFGTR LGETKNFDFWRDVFVFKIPQAIA QLSKGSWEFEKFISCFHIWNGG II*KAL\\$*DI*GNKAVGKEVKVRD AFP\EAIIVKPBSDIFGR\EDRFLNS FASMRFG\PIPLG\SLGWKTV KQPVYVVVDVSKGIVNAVKDPD ANGKSFAFVGPSRYL\LFHHLVK YIFAVAHRLFLPFLPLFAYRW VARVFEISPEPWITRDKVERM HITDMKLPHLPGLEDLGQATP LELKAIEVLRRRHRTYRWLSAEI EDVVKPAKTVNI

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15546	45914	A	15636	2	799	GLWEKMAAAQSRVVRV\LS\ MSRSAITAIATSVCHGPPCRQL HHALMPHGKGGRSSVSGIVAT GFGAVTGLRYYVVNHHILGRMG SQVIIPYRCDKYDIMH\URPMGD LGQLLFLFLEWDARDKDSIRR VV QHSNNVVINL\ GTRP/WKSNSD YEDVFVKIPQAAQLSKIEAGIV EKFIHV\ SHLNANIKSSRYLRN KNRKREKEEMKKDLSKKEPE PEDLENSQLIHIAKNEKACFEEN TKSVAEQPFDEEIVDATHQLTS YLGRSQE
15547	45915	A	15637	560	1394	RKSSSVHNAASGLLGSRGAH RHLGRCRCCRHLVSPSPAMAE DLSAATSYTEDDFYCPVCQEV L KTPVTTACQHVFCRKCFLTA MRESGAHCPLCRGNVTRRERA CPERALDLENIMR\ KFGSCRC C AKIQIKFYRMRHRYKSCKKYQ DEYGVSSIIPNFQ\ QSQDSVGNRIE NNTGIKQIPGAPAFGDRGVGCR QRNAKTELLAAAGESPCTMSL GSGPNLGPSPRSKSSVTPQPC FTEHPRERFVFSFPV\ HYVLEGSR MSFLLWSLKTDRIFGH
15548	45916	A	15638	1	1026	MKVVKCEVKFEKQCPCEAVLLH WEQTDDDENKRCDLREPRKPE THTKGPGLLVPTTQPGRNQEGQS GADGKHARCSKTSCCLSGKEPS FIITEHCPVPVQNTTIIKPDSGIR ILQTLDSRETFMTSTALDVLQM KEEDVLKFLAAGTHLGGTDL DFRMEQHICKRKSGGIY\ INLKRS WEKLLLVAAPAIVAIENPADSV I SSSSTGQRAMLKCAAATGATP IAGHFTP GTFTNQI QATFPNPRV L VVTDCRTGHQPLAEASYV\ NN LPTIALCHTDSPLHHV DIA PCNR/KAHSV DLMWMLAREILPM\ R GTIARKHWW\ DPEEIEKEEQA AADKALTKEEFQGE
15549	45917	A	15639	20	441	TAEIAIPCNNGAHSVG*MWR MLAREDLRMRGTTISGEHPWEV MPDLYFYRDTEE\ EKEEQAAD KAVTKEEFQGEWTAPAPEFTAT QPEAADWSEGVQVPSVPIQQFP TEDWSAQPAT EDWSAAPTAQA TEWVGATTDWS
15550	45918	B	15640	88	531	
15551	45919	A	15641	1	1302	

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15552	45920	A	15642	150	957	KAGASCCGSANPYVSVGKSCV LLAMAQLQTRFYTDNNKKYAVD DVPLSIPAASEIADLSNIINKLLK DKNEFHKHVEFDPLIKGGQFLRM PLDRHMEMENISSEEVVEIYV EKYTAPQARSNAWFHDDWISSI KRGRO\RLITGSYDKTTSRIWSLE GKSIMTIVGHTDVVKDVAWVK KDSLSCLLSASMDQTILLWEW NVERNKVKALHCCKGHAGSV NSIAVDGSGTKYFGLRIEPKPA VSLVEEINSLSYRWTADNYKV GSGGKEEDD
15553	45921	A	15643	3	393	VFCCPHICSLTFSKSFSSFSRLVR HQQTTHWKQKSYLCPICDLSFGE KEGLMD/HLEGL*RQPGQSSH HKCRVILGQWLGFSHDVPPTMA GEEWKHGGDQSPPRIHTPRRRG LREKACKGDKTKEAVSILHK
15554	45922	A	15644	335	537	VYFKQVTLDSSCRL*ERQVKST SSWNILSSTWRLPFCPTSVVLRF LTWICLRTISTSSISWFPADSS
15555	45923	A	15645	153	828	

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15556	45924	A	15646	I	2002	MLESAGNQDIEDDIVLRLQIQV KNRSTTEVGQNGNLQVEVSYT QAHIAPRPLASQGTWPHFVSSA PQPCFQVQNHSKYQNLVYSGFI RETEPISKGDVGEWLSAGKGES SAMFASEQEISKDEQGTPVLGS FYWEVDSPRKESSQAWAPGQE WIKLERDTTEEKMFEQLKPIEP VQKTLPLWVGEVAATLQEAMK RDCWREARVKKKPVTEDWAV NFTQEEWDCLLDAQRVLYQDV MSETFKNLTSVEGKKELREQ HPSLRDEGTSDDKVFLACRGA GQCPLSAPAGTMDRTRLVQAS QAGPP/FFFATTVGKCFCSRSSL YSHQFVHNPKLTNSCSCGKLF RSPKSLSYHRRMHLGERPFCCT LCDKTYCDASGLSRHRRVHLG YRPHSCSVCGKSFRDQSELKRH QKIHQNQEPVDGNQECTLRIPG TQAEEQPTIARSQRSIQLLVDN HAPVARSQEPIFRTEGPMQANQ ASVLKNQAPVTRQAPITGTL QDARSNSHPVKPSRLNVFCCPH CSLTFSKKSYLSRHOKAHLTEP PNYCFHCCKSFSSFSRLVRHQ THWKQKSYLCPICDLSFGKEKG LMDHWRGYKGKDLCQSSHHK CRVILGQWLGFSHDVPTMAGE EWKHGGDQSPPRJHTPQQGLR EKACKGDKTKEAVSILKH
15557	45925	A	15647	I	1048	MPSLAELEFGGSSKAFAAGAAASQL NPVVASGEMILKFKYGLRNPLH AVAAEPIASRTSRLNLFQGKPP FMTQQQMSPLSREGILDALFVL FEECSQPALMKIKHVSNFVRKY SDTIAELQELQPSAKDFEVRSLV GCGHFAEVQVVRKATGDIYA MKVMKKKALLAQEQQVSFEEE RNILSRSTSPWIPQLQYAFQDK NHLYLVMEYQPGGDLSSLLNR YEDQLDENLIQFYLAELILAVH SVHLMGYVHRIKPNENLVDRT GHIKLVDFGSAAKMNSNKMVN AKLPIGTPDYMPEVLTVMNG DGKGTGYGLDCDWWSVGVIAY EMIYGRSPFAEGTSARTFNNIM

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15558	45926	A	15648	101	220	KRQQAFGLLDLHQWFARGSGF FRLQTEGCGIIGFPPTFEV*RHSGFL SCQSCTGSFSVWADVPLMFE GAAQPV*PVPSRGSDAFLPLSIC *RSRRILVKRCENSQVR
15559	45927	A	15649	597	808	ITMKSQRQIJKKAVTTKEMKSV CRRD/PAFMFIAALFKIAKIRIQ RLCLSTDEWIKKMWYIHTMEY YSTLK
15560	45928	B	15650	161	3156	
15561	45929	A	15651	14	270	
15562	45930	B	15652	787	1821	
15563	45931	A	15653	1	2412	MAKSKGCSAATLASTHQILVTP WSCDNQKCLQTLPNVPGGTKL LLCEDHWFRNDSCNQAIPTIAT LLSFPSLQLASLWTTTHFLSPLNH HPVNPDSHLEQPPGQSPRLNFE AGDPERAPHALGCKRSRTRATS DRQPMASRDPGWGKASVGKA CALGSAVLPAGNDCTTDNLGL GSAGFEDLRLRLGQGPPRRQGA LQAAPRKASSCCAAGQRLAPDSS FSRKRRPSRQLGCETAAVADT AEAKSSEAPAFGWSTMDEAGS SASGGGFRRALDEPPNSRIFLVI SKYTPESVLRERFSPFGDIQDIW VVRDKHTKESKGIAFVKFARSS QACRAMEEMHGQCLGPNDTKE IKVRVPGSGCPRGKEWASWTS HLLLCRGEGGVVEHPFAADQT APGLGTGAALRRGSPTTKLRRV AGKGTGCGVFAPRERTRQPRP GDRTAVAGLPSPSPSLHQQLSS LPNSS*TLSTFLTSQMPRFP YIKNGKTL/PFPQVFIAQSRSSSG HRDVEEELTRIFVMIPKSYTEE DLREKFKVYGDIEYCSIIKNKVT GESKGLGYVRYLKPSQAAQAI NCDRSFRAILAEPKNKASSE QDYYNSMRQEALGHEPRVNMF PFGHGVVQYFNVASAIYAKYK LHGFQYPPGNRIGVSFIDDGSN ATEKMATQMVAALQASMVWN NPSQQQFMQFGGSSQLPOIQ

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
15564	45932	A	15654	375	2059	DSSVWQTPQKQRAVRPLHSGG APWTKLAA LRATRGRFPGVDS LDEPPNSRIFLVISKYTPESVLE RFSPFGDIQDIDWVVRDKHKTKE KGIAFVKFARSSQACRAMEEM HGQCLGPNDTKPIKVRVPGSGC PRGKEWASWTSLSHLLCRGEG GVEHPPA ADQTAGL GTGAA LRRGSPPTK IRRVAGKGTGCG VFAPRERTRQPRPPGDRTA VAG LPLSLALTNP PPALEFTAKL VLA YFEYFSDLPLSDA QISIYKKRN STFPQV FIAQS RSGSGSH RDV EDE ELTRIFV MIPK SYTEEDLREK FKF VYGDIEYCSII KNKVTGEK SGL GYVRYLKP SQAAQIAE NCDRSF RAILAE PKNK ASESSE QQD YSN MRQE ALGHEP RVNMPF GHGV VQYFNVASI YAKYKL HGQY PPGNRIGV SFID DGSN ATD LLIK MATQMVA A Q/ RLHWC GII QV SNNL/WQFGGSSGSQ LPQI QT D VVLPSCKKKP AETPVKERLFI VFNP HPLD VLED IFCRFGNLI EVYLVSGK NVGYAKYAD RISA NDAIATLHWKDSEWGET
15565	45933	A	15655	257	412	
15566	45934	A	15656	3	866	HAAS PCCC YEEKQSP LQKHL RV CSLRTW SLSAAR VAE GT AETVD PSAA PKTS VWS SRVC WGRLLA TISPSV NET DTCG MED RRL VVC RPW RAOC HMK A WGWRH PEEG GTHSGAPS A VLQ ALA VAIQLGG HLADPL LQV DP LSS CGAV SLDI LIYL VFY YRTA SVP ETYIV KTLF KKL E S QSLI QSNV LTR SNSMKA ERGEE AAK EKSEAS RGRWF MRF KERSCL HNIK M QGEA A SAD VE AAAS YPKD LAKIT DEH GY TKQ QFDV YKTA FCW RVMLK KVVK LLF VU CPLP

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15567	45935	A	15657	333	1034	RLSTTVMRGAFVFVFMHKMPRL WLDYCQFLMDQGRVTHTRRT FDRALRALPITQHSRIVPLYLRF LRSHPLPETAVRGYRFLKLSP ESAEEYIEYLKSSDRIDEAAQR LATVNVNDERFVSKAGKSNYQL WHELCDLISQNPDKVQSLNVD AIIRGGILTRFTDQLGKLWCSLA DYYIYRGHFEKIRKAPVNNGPT WMVVGQNSVPRFQTRRLTPLKR KGPLVTDFREKQPTPLAQE
15568	45936	A	15658	172	346	ARPCCRWCPS*TSASA PGPGLR PCPP\GGDRTPASPPLHNQAAA APPGPGTWRGAAAS
15569	45937	A	15659	293	482	
15570	45938	A	15660	468	791	LAKCGCLEARGRARQTSGRPRP TDGGP*SPCWETGKHPVLR RGS/PKGQL*SLPQSCQGQWR CAASRLLSSKNSWACMGSREA VSQETGTSSSLGLMRPSDKKP
15571	45939	A	15661	366	609	
15572	45940	B	15662	321	739	
15573	45941	A	15663	1	1815	
15574	45942	A	15664	1	1911	
15575	45943	A	15665	437	1125	PVSCSGHRSWAAAISIALSMIE TVNMFVTFYSRHHGTISTRVL/I GKRPERQDGQDTVNLGTLEET ASPPSPVVTTSPPQPMPLPSAFPPL SEEINPALPEATVMASPEAVAR QDNVDSAQEPPPTPLCASRPTT RQKSWWGARGEVESVTHEEM HYTGKELLEFSNLYKEKSGEQA WEWILRVWDNGGRNQLDHPE FVDLGPLSRNSAFNVAVRGVK KGSKSLFAWLGEI
15576	45944	C	15666	49	186	
15577	45945	A	15667	80	877	GAERLPEGPGKRMVFRKFVE\W GRVAVYVSFGPHAGKJ/VSAMVD VFVDQNKGFWSNGPCTQVR RQ AIMPFKCMQLTDFILKFPHSAH QKYVRQSLGRREDINTKLGQP TRWGQGRFESQEEKEPRLTDF *SVF*S**RAKEN*RDRINPRNE V*EAFKRAAFPGKASSQKKAPG Y*GVLLAAAAAAAAAAAAAAA AAAAAAAKVPAKKIT\AASKK APAQKVPAAQK\ATGQK\AAPAP KAQNGSKSSKPQKAPAKPASG KESISGNHKK
15578	45946	A	15668	253	1218	
15579	45947	A	15669	1	1819	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
15580	45948	A	15670	1	2422	MCPILREHRGSTEKGRRQKRLP LELTALKDEEVLAHRQEIVAKA SPSKGNIIHFYGKGVVEYHDQQ DVTSNFLGAMWLISITFLSIGYG DMVPNTYCGKGVCLLTGIMGA GCTALVVAVVARKELETKAEK HVHNFMMDTQLTKRHCWAA TIQPKLISFLISLPGCDYRGESAR ARPLSHPPLQLGLGKDARYLRI CDRSLLCVCAAAGNAGLPRD SPHTLLHWRSRSPYFFSPKPVPP QLLGQQPAAHISRRDDLEAGV GRGGCCFAALRGVQSEKWSGF HTVPEPA PGQGDVMPIVLVRPT NRTRRLDSTGAGMGPPSHQQQ ESPLPTITHCAGCTTAWSPCSFN SPDMEPLQFQRGFFPEQPPPP RSSHLHCQQQQQQSQDKPCPPFA PLPHPHHHPHHLAHQQPASGSS PCLRCNSCASSGAPAAAGAGDNL SLLRTSSPGAFRTRTSPLSG SSCCCCCSSRRGSQNLNVSELTP SSHASALRQQYAQQSAAQQSAS ASQYHQCHSLQPAASPTGSLGS LGSGPPLSHHHHHPHPAHHQH HQHQARRESNPFTEIAMSSCRY NGGVMRPLSNSASRNLH DSEAQPLQPPASVGGGGGASSP SAAAAAAA VSSSAPEIVVSKP EHNNNSNNLALYGTGGGGSTGG GGGGGGSGHGSSTKSSKK NQNIGYKLGHRRALFEKRKRLS
15581	45949	A	15671	1	246	SEPPHRGPTGALPSGA VRRGPL SSRPQIGRSTDLSLHCVPGKATD AQRQPVKAAGSGAVPKATG WSCPKL*EPISCINVTC
15582	45950	B	15672	43	741	
15583	45951	A	15673	687	1012	FHTSRPFWNISELSRFCIJKLMNOP PWHSVSDFYRYQFFICQGTACC PASLRM*HCPN*ILQGTSSQNCC SCSGKSCSPMQRHRSTVCSSG GTFCVGSCESFEGTYFSR